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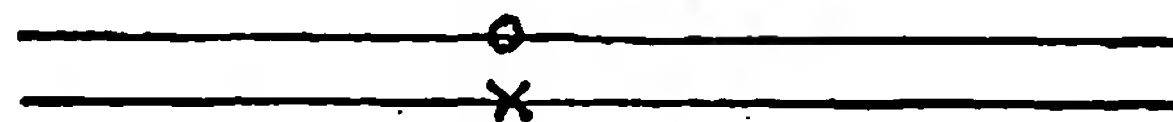
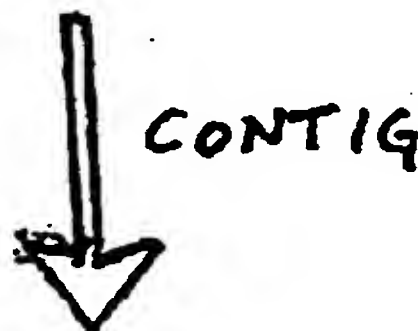
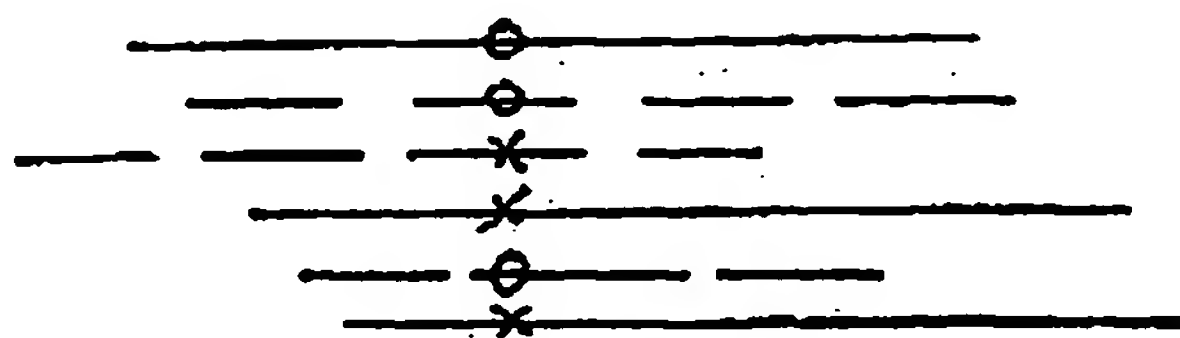
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(54) Title: NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE
THEREOF



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(57) Abstract: The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

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NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

BACKGROUND OF THE INVENTION

5 Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in
10 identity and paternity analysis, and in genetic mapping studies.

 One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

15 Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

20 Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA.

 SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a
25 substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

 Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an
30 insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele. Some SNPs



occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7867) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-7867), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.* 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

5 In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

10 In another aspect, the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a
15 fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in
20 addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 -
25 7867), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5;
30 and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The invention also provides a method of detecting a polymorphic site in a nucleic acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1,

column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-7867, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, the polypeptide can be related to an ATPase associated protein, cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7867, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen
5 complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig,
10 goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a
15 gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the
20 gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally, aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can be administered to a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic
25 sequence. The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

30 Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any

one of the polymorphic sequences SEQ ID NOS:1 - 7867, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of
5 SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or
10 more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7867); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence
15 comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described
20 nucleic acids. The kit can include, e.g., a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, e.g., a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7867) and which includes a polymorphic sequence, or a fragment
25 of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-7867), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific
30 oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic

sequences (SEQ ID NOS:1 - 7867), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. Many SNPs have been identified in genes related to polypeptides of known function. If desired, SNPs associated with various polypeptides can be used together. For example, SNPs can be grouped according to whether they are derived from a nucleic acid encoding a polypeptide related to particular protein family or involved in a particular function. Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins which are associated with metabolic pathways, including fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc. Specifically, the present invention

provides a large number of human cSNP's based on at least one gene product that has not been previously identified. In contrast, and as defined specifically in the following paragraph, the cSNP's involve nucleic acid sequences that are assembled from at least one known sequence.

5 The present invention provides a large number of human cSNP's based on at least one gene product that has not been previously identified. In contrast, and as defined specifically in the following paragraph, the cSNP's involve nucleic acid sequences that are assembled from at least one known sequence.

10 7867 distinct polymorphic sites were identified by the present inventors, using the following procedure. Raw traces underlying sequence data were drawn from public databases and from the proprietary database of the Assignee of the present invention. The sequences were obtained by calling the bases from these traces, and included assigning "Phred" quality scores for each called base. For each allelic set, at the polynucleotide level, four or more nucleotide sequences were identified having at least partial overlap with one
15 another.

As illustrated in FIG. 1, these four or more sequences could be clustered and assembled to make a consensus contig that included an ORF. In this way, the inventors found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by an SNP at a particular polymorphic site. In order to be confirmed as a SNP
20 site, the nucleotide change from the consensus sequence had to occur in at least two individual sequences, and had to have a "Phred" score of 23 or higher at the site of the presumed SNP. Furthermore, in a window of 5 bases on either side of the SNP, no more than 50% mismatching with the consensus sequence was allowed. In the assembly leading to each of the contigs defining the allelic set, the SNP alleles occur in polynucleotides found in public
25 databases. Furthermore, it was found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by an SNP at a particular polymorphic site. These associations were not previously known. The SNPs are presented in Table 1.

At the level of translation of an ORF contained in the contigs, however, the inventors identified allelic sets in which one allele defines a known polypeptide sequence that includes
30 the polymorphic site and another polypeptide allele is not previously known. Then, various associations of alleles are possible. For example, it is possible that an allelic pair is defined

in a noncoding region of the contig containing an ORF. In such cases the inventors believe that the invention resides in the recognition of the allelic pair; this association has not heretofore been made. Alternatively, sets of allelic contigs may exist in which the polymorphic site is within an ORF, but does not result in an amino acid change among the allelic polypeptides. Here too it is believed that the invention resides in the recognition of the allelic pair; and that this association has not heretofore been made. In yet another alternative, the polymorphic site resides within an ORF and results in an amino acid change, or a frameshift, among the alleles of the allelic set. In the sets of gene products that fall within this group, at least one of the alleles at the polypeptide level is a known protein. At least one of the remaining allele or alleles in the set, carrying a variant amino acid at the polymorphic site, is a novel polypeptide not heretofore known. The invention resides at least in the recognition of the polymorphic allele as being a variant of the known reference polypeptide.

Table 1 provides information concerning the allelic sequences. One of the sequences may be termed a reference polymorphic sequence, and the corresponding second sequence includes the variant SNP at the polymorphic site. Since the reference polypeptide sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele, while its SEQ ID NO is provided in the Table. A reference to the SEQ ID NO that corresponds to the translated amino acid sequence is also given. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and a description of each, are given below.

SNPs disclosed in Table 1 were detected by aligning large numbers of sequences from genetically diverse sources of publicly available mRNA libraries (Clontech). Software designed specifically to look for multiple examples of variant bases differing from a consensus sequence was created and deployed. A criteria of a minimum of 2 occurrences of a sequence differing from the consensus in high quality sequence reads was used to identify an SNP.

The SNPs described herein may be useful in diagnostic kits, for DNA arrays on chips and for other uses that involve hybridization of the SNP.

Specific SNPs may have utility where a disease has already been associated with that gene. Examples of possible disease correlations between the claimed SNPs with members of the genes of each classification are listed below:

Amylases

- 5 Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

Amyloid

- 10 The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-
- 15 stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. Amyloid deposition is also associated with type II diabetes mellitus.

20 Angiopoeitin

- Members of the angiopoetin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an essential step in tumor growth in order for the tumor to get the blood supply it needs
- 25 to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

Apoptosis-related proteins

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of antiaging drugs.

Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I

diabetes mellitus, meningitis neurological disorders such as Nemaline myopathy, Neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

5 The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

10 Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

15 Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

20 G-protein coupled receptors

 G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological
25 conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a "SNP" is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

"SEQ ID" provides the cross-references to the nucleotide SEQ ID NOs: for the polymorphic sequences, which are numbered consecutively, and, as explained below, amino acid SEQ ID NOs: as well, in the Sequence Listing of the application. Conversely, each

sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label "CuraGen sequence ID". The first SEQ ID NO: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic acid sequence for the polymorphisms. If a polymorphism carries an entry for an amino acid in a coding region, then a second SEQ ID NO: appears in parentheses in the column "Amino acid after" (see below) for the polymorphic amino acid sequence. The latter SEQ ID NOs: refer to amino acid sequences giving the polymorphic amino acid sequences that are the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one SEQ ID NO: is provided, in the first column.

10 "Base pos. of SNP" gives the numerical position of the nucleotide in the nucleic acid at which the cSNP is found, as identified in this invention.

"Polymorphic sequence" provides a 51-base sequence with the polymorphic site at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5' side and the 3' side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a "slash (/)"; and third, the polymorphic nucleotide. In certain cases the polymorphism is an insertion or a deletion. In that case, the position which is "unfilled" (i.e., the reference or the polymorphic position) is indicated by the word "gap".

20 "Base before" provides the nucleotide present in the reference sequence at the position at which the polymorphism is found.

"Base after" provides the altered nucleotide at the position of the polymorphism.

"Amino acid before" provides the amino acid in the reference protein, if the polymorphism occurs in a coding region.

25 "Amino acid after" provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated polymorphic amino acid sequence if the polymorphism occurs in a coding region.

"Type of change" provides information on the nature of the polymorphism.

"SILENT-NONCODING" is used if the polymorphism occurs in a noncoding region of a nucleic acid.

"SILENT-CODING" is used if the polymorphism occurs in a coding region of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

"CONSERVATIVE" is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

"NONCONSERVATIVE" is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

"FRAMESHIFT" relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

"Protein classification of CuraGen gene" provides a generic class into which the protein is classified. During the course of the work leading to the filing of the four applications identified above, approximately 100 classes of proteins were identified.

"Name of protein identified following a BLASTX analysis of the CuraGen sequence" provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely. (The next paragraph explains how a sequence was determined to be "novel").

5 "Similarity (pvalue) following a BLASTX analysis" provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of $pvalue > 1 \times 10^{-50}$ (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel.

10 "Map location" provides any information available at the time of filing related to localization of a gene on a chromosome.

The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-5696 are nucleotide sequences for SNPs that are silent.

15 SEQ ID NOs: 5697-6011 are nucleotide sequences for SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 6012-6740 are nucleotide sequences for SNPs that lead to nonconservative amino acid changes.

20 SEQ ID NOs: 6741-7867 are nucleotide sequences for SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

25 SEQ ID NOs: 7868-8182 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 8183-8911 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative

amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

5 SEQ ID NOs: 8912-10038 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

10 Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

15 Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

20 Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, 25 Oxford); and U.S. Patent 4,683,202.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, *i.e.*, a "polymorphic protein"

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containing an altered amino acid at the site of translation of the nucleotide polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein,

refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence. "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1989)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox. Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A., 82:4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res, 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984

(1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (T_m) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A “polymorphic” marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR’s), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple

sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation.

Oligonucleotides probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1 862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984). Purification of oligonucleotides may be carried out by either native acrylamide-gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be can be obtained using either the dideoxy chain termination method or the Maxam-Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al." ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific

aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

5 In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding
10 region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to
15 the entire coding region of an mRNA, but more preferably as embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An
20 antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between
25 the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-
30 2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine,

7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et*

al. (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window",
5 "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window
10 may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized
15 implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described
20 generally in Sambrook et al., The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as
25 well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a
30 triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based

on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assays of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified before analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be
5 complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short
10 subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989). This
15 primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch
20 prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be
25 analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation
30 polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or

otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

5 The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
10 hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

 Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases,
15 inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach,
20 leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

 Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
25 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least
30 several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the

invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

5 The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match
10 between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the
15 probability that a match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism are (see WO
20 95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

$$\text{Both Heterozygotes: } p(AB+BA)=2xy=2x(1-x)$$

25 The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID)=(x^2)^2+(2xy)^2+(y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$cum p(nonID) = 1 - cum p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc)=xy(1-xy)$$

- 5 where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site $p(exc)=xy(1-xy)+yz(1-yz)+xz(1-xz)+3xyz(1-xyz)$), where x, y and z and the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(non-exc)=1-p(exc)$$

- 10 The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$cum\ p(non-exc)=p(non-exc1)p(non-exc2)p(non-exc3)\dots p(non-exc_n)$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

15 $cum\ p(exc)=1-cum\ p(non-exc).$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

- 20 The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous
- 25 sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some

polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the

possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic

trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the
5 relative likelihood of obtaining observed segregation data for a marker and a genetic locus
when the two are located at a recombination fraction RF , versus the situation in which the
two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in
Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the
human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter
10 4). A series of likelihood ratios are calculated at various recombination fractions (RF),
ranging from $RF=0.0$ (coincident loci) to $RF=0.50$ (unlinked). Thus, the likelihood at a given
value of RF is: probability of data if loci linked at RF to probability of data if loci unlinked.
The computed likelihood is usually expressed as the \log_{10} of this ratio (i.e., a lod score). For
example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a
15 coincidence. The use of logarithms allows data collected from different families to be
combined by simple addition. Computer programs are available for the calculation of lod
scores for differing values of RF (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci.*
(USA) 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be
determined from mathematical tables. See Smith et al., *Mathematical tables for research
20 workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150
(1968). The value of RF at which the lod score is the highest is considered to be the best
estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values
suggest that linkage is less likely (at that value of RF) than the possibility that the two loci are
25 unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than
1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked.
Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence
against linkage of the two loci being compared. Negative linkage data are useful in excluding
a chromosome or a segment thereof from consideration. The search focuses on the remaining
30 non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an
exogenous variant gene and/or having one or both alleles of an endogenous variant gene

inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be
5 achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292 The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

10 The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug
15 targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the
20 cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

25 A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by administering a normal
30 or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid

may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is
5 incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

10 A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by
15 administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect
20 leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-
25 specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or
30 polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences
5 complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is
10 prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. *Gene* 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either
15 mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, *Science* 196:180-182 (1977). Colony hybridization is carried
20 out as generally described in M. Grunstein et al. *Proc. Natl. Acad. Sci. USA.* 72:3961-3965 (1975). DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of
25 the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of
30 protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from

analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by A, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin,

tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., Gene 8:17-24 (1979); Broach, et al., Gene 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glucanase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, Nature (London) 275:104-109 (1978); and Hinnen, A., et al., Proc. Natl. Acad. Sci. USA, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., J. Bact, 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. Immunol. Rev. 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987)). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known

methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

5 The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

10 General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control
15 sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

20 The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated
25 nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells,
30 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells,

BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida* or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

10 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as
15 described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

20 The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic
25 means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography.
30 For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard techniques well known in the art, including

selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl® or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP- HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, monoclonal,

chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, a Laboratory Manual*, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the

invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, e.g., hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp.

77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in
5 detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymorphic pos. of sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similarity (pValue) following a BLASTX analysis	Map location
1	cg44131670	631	TTCTCGTTCCTG ACAAGTGCAAAT TTTCJTTACACCA GGAGAGGATGG ATGTTT	T	C	Phe	Phe	SILENT- CODING	amyloid	Human Gene SPTREMBL-ID:Q60496 PUTATIVE AMYLOID PRECURSOR PROTEIN - CAVIA PORCELLUS (GUINEA PIG), 695 aa.	0	21
2	cg44131386	1635	AAACATCCATCC TCTCCTGGTGTA A/A/GJAATTTGCA CTTGTCAGGAAC GAGAA	A	G	Phe	Phe	SILENT- CODING	amyloid	Human Gene SPTREMBL-ID:Q13764 AMYLOID-BETA PROTEIN - HOMO SAPIENS (HUMAN), 547 aa.	1.20E-304	
3	cg43323142	246	GGCAGCCCCAT GGTGGTGCTG GGG[A/G]CAGCC TCATGGTGGTGG CTGGGGGC	A	G	Gly	Gly	SILENT- CODING	amyloid	Human Gene Similar to SPTREMBL- ID:Q16409 PRP AMYLOID - HOMO SAPIENS (HUMAN), 97 aa (fragment).	4.20E-55	20 (20pter)
4	cg43323142	342	GGCAGCCTCATG GTGGTGGCTGG GG[A/G]CAGCCC CATGGTGGTGG CTGGGGGC	A	G	Gly	Gly	SILENT- CODING	amyloid	Human Gene Similar to SPTREMBL- ID:Q16409 PRP AMYLOID - HOMO SAPIENS (HUMAN), 97 aa (fragment).	4.20E-55	20 (20pter)
5	cg43921977	2720	TATTATCCAATGT TAAGAGAGTATG A/GJAAATTATTCA TCCAAGTTTCCA TAT	A	G	Phe	Phe	SILENT- CODING	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
6	cg43948568	2108	TCATATGGGGCC TGAACAGCTCGC G[A/G]CTCAGCA GGACGTCCCAG AGCTGGT	A	G	Ser	Ser	SILENT- CODING	apoptosis	Human Gene SWISSPROT-ID:P55211 CASPASE-9 PRECURSOR (EC 3.4.22.-) (CASP-9) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) (APOPTOTIC PROTEASE ACTIVATING FACTOR 3) (APAF-3) - HOMO SAPIENS (HUMAN), 416 aa.	2.00E-222	1

7	cg44001801	1601	AGGAGCCTCTTC CTGGGCTCCTCC A[C/T]GAGTAATA GCCTGGAACCGT GGAAT	C	T	Ser	Ser	SILENT- CODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
8	cg42913771	334	TACTGCTCAAAA TTCATGAGGTGT C[G/A]ACTTCCAG CCACGTAGATGC CGATT	G	A	Ser	Ser	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
9	cg42913771	340	TCAAAATTCATG AGGTGTCGACTT C[C/T]AGCCACGT AGATGCCGATTG CTTCC	C	T	Ser	Ser	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
10	cg42913771	364	CCAGCCACGTAG ATGCCGATTGCT T[C/T]CTGTGTGT CTTCCTGAGCCA CGGGG	C	T	Phe	Phe	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
11	cg42913771	397	TCTTCCTGAGCC ACGGGGAAGGC AA[C/T]CACATTT ACGCATACGATG CCAAA	C	T	Asn	Asn	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
12	cg42913771	406	GCCACGGGAA GGCAACCCACATT TA[C/T]GCATACG ATGCCAAAATTG AAATTC	C	T	Tyr	Tyr	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
13	cg42913771	412	GGGAAGGCAAC CACATTTACGCA TA[C/T]GATGCCA AAATTGAAATTC AGACCT	C	T	Tyr	Tyr	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	

14	cg42913771	418	GCAACCCACATTT ACGCATACGATG C[C/T]AAAATTGA AATTCAGACCTT GACTG	C	T	Ala	Ala	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
15	cg42913771	424	ACATTTACGCAT ACGATGCCAAA T[T/C]GAAATTCA GACCTTGACTGG CTTGT	T	C	Ile	Ile	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
16	cg42913771	436	ACGATGCCAAA TTGAAATTCAGA C[C/A]TTGACTGG CTTGTTCAAAGG AGACA	C	A	Thr	Thr	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.2E-116	
17	cg43271933	435	GGTTGTGGAGT GCCAGGTCAGC CA[A/G]TGTGTC GCAGTTCACCT TCTACT	A	G	Gln	Gln	SILENT- CODING	apoptosis recep	Human Gene Homologous to SWISSPROT-ID:Q93038 WSL-1 PROTEIN PRECURSOR (APOPTOSIS- MEDIATING RECEPTOR DR3) (APOPTOSIS- MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN) (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED RECEPTOR QF DEATH) (LARD) - HOMO SAPIENS (HUMAN), 417 aa.	6.7E-103	1
18	cg43271933	3985	GTTTAACCATTT CTAGCGATGTCA GT[C/G]ACGCTAT GACAGACCACGA GATGA	T	C	Ser	Ser	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)

19	cg43252813	1690	TCAGCCTTCATC GGAAATGCCGCT TTT/CJTGACTTCA ACTAATGAATTTT ATAC	T	C	Leu	Leu	SILENT- CODING	ATPase_ associate d	Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa. COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0 X (Xq12)
20	cg43939527	1245	AAGATGACCTCT CTGGTGCTGACA TTC/AJAGGCAAT CTGTACAGAAAGC TGGTC	C	A	Ile	Ile	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P49014 26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 440 aa.	14 1.5E-233
21	cg43933946	961	ATATGTGGTCC GACCCTCTAGAT C[G/A]GGCAAGC TAAATTC AATTT TCTAT	G	A	Pro	Pro	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7 5.2E-231
22	cg43933946	826	GTGCTCTGATGG CAACATACCCAG C[C/T]TCTGTGCA GACGCTTCTAAT CTCAG	C	T	Glu	Glu	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7 5.20E-231
23	cg43933946	838	CAACATACCCAG CCTCTGTGCAGA C[G/A]CTTCTAAT CTCAGCACCCAGT GCTAT	G	A	Ser	Ser	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7 5.20E-231
24	cg43933946	937	TCATTGAACGAG CGTGAATCTTAA A[T/G]ATGTGGT CCGACCCCTCTAG ATCGG	T	G	Ile	Ile	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7 5.20E-231

25	cg43916747	445	GCATCAAGGAG GAGACGGAGAT CCTT[C]GAAGG GGAGGTGGTGG AGATCCAGA	T	C	Leu	Leu	SILENT- CODING	ATPase_ associate d	Human Gene SPTREMBL-ID:Q12464 CHROMOSOME XVI READING FRAME ORF YPL235W - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 471 aa.	4.00E-163	19
26	cg43284434	2039	AGATGGGCCAC CTGACCTGCTTC GC[T]GjGGGGC ATGTTCCGCACTC GGGGCTG	T	G	Ala	Ala	SILENT- CODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
27	cg43251803	2941	TGAGGTAGCAG GACACTGCCATC TG[A]GjATCTGCT CGGTACGCACTC GTTTCA	A	G	Ile	Ile	SILENT- CODING	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.10E-105	
28	cg43986887	320	CAAAGTGCCTGT GATCCACTCGGT C[G]A]AGGAAGG CTTCCGTTCAA TGTAAC	G	A	Leu	Leu	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
29	cg44022155	1125	TCCAGTACCTCA TCCTGGCTGCAG C[T]C]GTGTCCAA GGGGCGGCCCT TCCGCC	T	C	Ala	Ala	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
30	cg44022155	903	GGCAGCGCTG GTCCTGGGACG GGT[A]G]CGGCC ACCGGGGGCGC TGCTCAGCG	A	G	Val	Val	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
31	cg43920913	364	GTGCAGATTTTG GAATGGCTGCTG A[T]C]AAGAATAA GTTTCCTGGAGA CAGCG	T	C	Asp	Asp	SILENT- CODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288 3 (3q21)	

32	cg41562164	2748	GGCTGGCAATG CTCTCTCCAAAG TG[C/G]GCATTGT AGGCACCATCCC CAGTCA	C	G	Ala	Ala	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:Q13797 INTEGRIN ALPHA-9 PRECURSOR (INTEGRIN ALPHA-RLC) - HOMO SAPIENS (HUMAN), 1035 aa.lpcis:SPTREMBL-ID:Q13797 INTEGRIN ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1035 aa.	0.00E+00	3
33	cg43918042	3955	ACAGCCCAAGCA TGCGGCGATACA G[G/A]TCCGTTAA TGGTGGGCCCG GCAGTC	G	A	Arg	Arg	SILENT- CODING	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTOCOLADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
34	cg42483174	1386	GTTAGAGTTAAA GCGGCTCCATAC N[T/G]GATCACAG CCCCTCAAAATC TTGIG	T	G	???	???	SILENT- CODING	cadherin	Human Gene SPTREMBL-ID:P97686 ANKYRIN BINDING CELL ADHESION MOLECULE NRCAM - RATTUS NORVEGICUS (RAT), 1215 aa (fragment).	0	7
35	cg43957225	2759	GGCCTTCCGGATC CAGCATTGCTGT T[C/T]CGGCAAG GAGAGAACTCG GCATAGG	C	T	Arg	Arg	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0.00E+00	10
36	cg43857225	2783	TCCGGCAAGGA GAGAACTCGGCA TA[G/A]GCGCTG AAGTTCTGAATT GCTACAT	G	A	Ala	Ala	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0.00E+00	10
37	cg43312078	1430	TCCTAGCGTGTA CCCCCTTGACCG GTTCTGGAGATT GAATTACTTAAG GGGGA	T	C	Leu	Leu	SILENT- CODING	cadherin	Human Gene SPTREMBL-ID:Q28260 VASCULAR CELL ADHESION MOLECULE-1 - CANIS FAMILIARIS (DOG), 739 aa.	0.00E+00	1 (1p32)
38	cg44026834	1209	CGGAGGTGAGG GTGGAGTAGTCC CT[G/C]GGCAGT GTGGTCGAGTGT GAGTGT	G	C	Pro	Pro	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P18144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)

39	cg44026834	1221	TGGAGTAGTCCC TGGGCAGTGTG GT[C/T]GAGTGTG AGTGTTCTGAGC GGGTCA	C	T	Ser	Ser	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)
40	cg42558238	2054	AGAGTGCAACCC TGACCTGTGAGA G[C/T]GACGCCA ACCCCTCCCGTCT CCCACT	C	T	Ser	Ser	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. ipcl:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	19 (19q13.1)
41	cg42558238	2225	AGGGCCGTTCC CCTCTCAGCAC CT[C/T]ACCGTCT ACTATAGCCCGG AGACCA	C	T	Leu	Leu	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. ipcl:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)

42	cg42558238	2228	GCCGTTCCGCTC TCAGCACCCCTCA C[C/T]GTCTACTA TAGCCCCGGAGA CCATCG	C	T	Thr	Thr	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
43	cg44923512	657	AGGAAATGGACC CAGTGACTCAGC T[G/C]TATACCAT GAGTTGCACCCCT GGAGT	G	C	Leu	Leu	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q13740 CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE) (ALCAM) - HOMO SAPIENS (HUMAN), 583 aa.lpcis:SWISSPROT-ID:Q13740 CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE) (ALCAM) - HOMO SAPIENS (HUMAN), 583 aa.	1.7e-310	3 (3q13.1)
44	cg43956560	1283	GGCTGGCAAGG AGATTAAAAAA GG[C/T]AAGAAAT CCAAGAGAAGTA TGAATG	C	T	Gly	Gly	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)

45	cg43956560	521	CGTGGGTGGGA ACCAACAAATCT CTT/CJACTGAAG AAGCAGAGAACT GGGGAG	T	C	Leu	Leu	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)
46	cg43977366	1646	CCTGGAAGAA TTCTGAACCTCC TIG/CJTACAAAT GCTGGCTGCTCT CATT	G	C	Leu	Leu	SILENT- CODING	calcium_ channel	Human Gene TREMBLNEW-ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	0	15
47	cg43280376	1374	CCTGGGACATGA TGGTGCACTCCC G[C/T]TCCCACCA GCACGTGAAGAT CACCT	C	T	Arg	Arg	SILENT- CODING	carboxyla se	Human Gene SWISSPROT-ID:P38435 VITAMIN K-DEPENDENT GAMMA- CARBOXYLASE (EC 6.4.-.) (GAMMA- GLUTAMYL CARBOXYLASE) - HOMO SAPIENS (HUMAN), 758 aa.	0	2
48	cg43307396	285	TTGTCCAGGGAA GCCTGGACAGC CT[G/A]CCCCAG GCAGTGAGGGA GTTTCTCG	G	A	Leu	Leu	SILENT- CODING	carboxyla se	Human Gene SWISSPROT-ID:P35558 PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC (GTP) (EC 4.1.1.32) (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-C) - HOMO SAPIENS (HUMAN), 622 aa.	0	20 (20q13.3 1)
49	cg43919581	709	AGCCCTACAGCG GGCGGAGGCCA GA[T/C]GCCATCA GGCTGGGCCTG GGGAACC	T	C	Asp	Asp	SILENT- CODING	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T- PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0	8 (8p12)
50	cg42094324	835	CTGGGGGTCCA CTTGCTCTGTAAT GG[T/G]GTGCTT CAAGGTATCACA TCATGGG	T	G	Gly	Gly	SILENT- CODING	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	2.1E-147	19 (19q13.2)

51	cg43980411	1251	GCCACAGTTTG TGGCAGATCATC GT/GJTTCITTT TCTTATTATGCAT AAGA	T	G	Pro	Pro	SILENT- CODING	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
52	cg43266931	673	GCGTGTCACC GTGGTGAGGT GAAAGJGGTAC GCCCTTGAGGA GCAGGACCA	A	G	Pro	Pro	SILENT- CODING	chloride_ channel	Human Gene Similar to SWISSNEW- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa. pcis:SWISSPROT- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa.	3.1E-59	9
53	cg43970982	2113	AGGAGAACAG GCATTCTGGAC CTC/AJGGGAA GCGGAGGTGCC GCTGGTGC	C	A	Arg	Arg	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
54	cg43970982	2138	CTCGGGAAGC GGAGGTGCCGC TGGT/CJGCTCCT GGAGAACGAGG CAGAACCG	T	C	Gly	Gly	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
55	cg43970982	2307	GAGGCAAAAAG GAGAAAGAGGAT TTC/TJCCTGGATA CCCAGGACCCAA GGGTA	C	T	Phe	Phe	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
56	cg43970982	2460	CTGGCTACCCAG GACCAGCTGGTC C/C/AJAGGGCA ACAGGGGCGAC TCCATCG	C	A	Pro	Pro	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2

57	cg43131198	5627	GCCGGCAGGGA ACTTGCCACTTT TT[C/T]GCAAATA AGTATAGCTTCT GGCTCA	C	T	Phe	Phe	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P53420 COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1690 aa.	0	2 (2q36)
58	cg43970983	2931	GCGTGAGGCTG AGTGTCTTAGGG CC[G/A]GCTGGA GAAGGGCCCTCT GCAGAGG	G	A	Pro	Pro	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
59	cg43970983	9092	GTCCGTTATTTC AGTGACTTGGTC C[C/A]GTGGGTC TAGCCTTCCCCC CTGTGG	C	A	Pro	Pro	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
60	cg40339378	4366	TACCTGGCATCC CCGGTAAAGATG G[C/T]CCCAGTG GGCTCCAGGC CCACCTG	C	T	Gly	Gly	SILENT- CODING	collagen	Human Gene SPTREMBL-ID:Q12823 A TYPE IV COLLAGEN - HOMO SAPIENS (HUMAN), 1690 aa (fragment).	0	X (Xq22)
61	cg43011543	391	CGCCAAGAATGG GCAAGGAAGCC GT[A/T]CCCCAAGA AAGGCAAGAA TACCAT	A	T	Val	Val	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P27658 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
62	cg43991318	3003	CTTCGGGGCCCT GCTCTCCCTTTGG G[G/C]CCGGGCT GCCCAGGCCGT CCTGCCA	G	C	Gly	Gly	SILENT- CODING	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
63	cg43281450	1145	CCATCTTGGCTT TTTGCCCTCCGA T[G/T]ATGCGCTG CCTCTGTTCCAC GGGGT	G	T	Ile	Ile	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0	12 (12p13)

64	cg43084083	4497	TTCTCAGTCCTG CCACTTTCACAG T[G/T]TACGAATA CCACAGACCAGAA TAAAC	G	T	Val	Val	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:P01031 COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN) - HOMO SAPIENS (HUMAN), 1676 aa.	0	9 (9q34.1)
65	cg43029279	578	AACGAGGATATG CAACAGCAGATG G[G/A]AATTCTTC AGGATCAATTAC ATGTT	G	A	Gly	Gly	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
66	cg43029279	659	GCATTAATCTT CAGAAAAGTGTC G[G/A]CCTCCTC CACCTATTAGCA ATGGTG	G	A	Gly	Gly	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
67	cg43956185	890	TAGAACTCTTTC ATTGAGGTGGTT C[C/T]GTCCAGTT TCCATTTAAACA CATCA	C	T	Thr	Thr	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
68	cg43956185	536	CCAGTTTCCCAT CCCAACATGTTG T[A/T]CGCAATGT GTGAGAACGTGA TGAAA	A	T	Arg	Arg	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
69	cg43956185	572	GAGAACGTGATG AAAGACGATATC C[A/C]CGTTTACA CACAAATTCAGC TGATT	A	C	Arg	Arg	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
70	cg43956185	809	ATGAAGCTGGAG CATATACTGACA A[C/T]GGGAATGA AGTAATGTCCCC ATTGT	C	T	Pro	Pro	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1

71	cg43956183	345	AGTAATGCCATT GATTCTATTTTC [T/C]TCACAACTG GGATATACCAGT TTCC	T	C	Glu	Glu	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:P36980 COMPLEMENT FACTOR H-LIKE PROTEIN DDESK59 PRECURSOR - HOMO SAPIENS (HUMAN), 270 aa.	9.20E-154	1
72	cg21644442	1753	TGGAGCAACCAG AGGGCAGCCCC CTTG/CJACTCAG GATGACAGACAG GTGGAAC	G	C	Leu	Leu	SILENT- CODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5.00E-304	1 (1p21)
73	cg42542496	942	CAAACTTCACTG CCTCAGCCAGAA CTT/AJACTGGCTC TGGGCTTCTGAA GTGGC	T	A	Thr	Thr	SILENT- CODING	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
74	cg43931046	2043	AACAGATTATTG TTCATGCTTTATC [G/C]CCAGAACAT TTGTTGAACACA AGTG	G	C	Ser	Ser	SILENT- CODING	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7
75	cg43927697	992	TAGTTAGTTCCA TCAGGTATTTGG C/C/T]AAAGTATG TTGCTCGACATC AACCT	C	T	Leu	Leu	SILENT- CODING	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
76	cg43926592	1705	AGAAAGTGCACT CTTGATCACTGG G[T/A]GGGAGC TGCTGAGACTCT CCTCTC	T	A	Pro	Pro	SILENT- CODING	cyclin	Human Gene SPTREMBL-ID:Q16589 CYCLIN G2 - HOMO SAPIENS (HUMAN), 344 aa.	8.50E-183	4
77	cg43957094	2212	GCTTGCCCTGAT AAAAAAGCACCA G[C/G]CGGCGGA GCGGCCGCGGA GCGACCA	C	G	Arg	Arg	SILENT- CODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6

78	cg43242733	222	CTGCAGTCTCTG TCAAGATGATAG A[A/G]GTACTGAC AACAACTGACTC TCAGA	A	G	Glu	Glu	SILENT- CODING	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
79	cg43996855	3862	TGGTCAGGTCCT TGTTGATGAGGC C[G/A]TCCTTGTC CAAGAATCGAGC TGGAT	G	A	Asp	Asp	SILENT- CODING	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)
80	cg40333008	1612	CTGTAGTCTTGG TGCCCATACGAA C[C/A]GAATAGAT GGGGCCATATTT TTTCT	C	A	Ser	Ser	SILENT- CODING	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa. pcIs:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.90E-274	10 (10q24.3)
81	cg40333008	1669	TGAAGAAGTTGT TATGCATATGGC C[A/G]TGCTGG GGAGGAATGGC AGGCTGC	A	G	His	His	SILENT- CODING	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa. pcIs:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.90E-274	10 (10q24.3)
82	cg43966704	1243	ACTTGAGGCCAG TGGGGAAGCCA GC[G/A]CCTCCA CGGCCCTCAAA CCCGATG	G	A	Gly	Gly	SILENT- CODING	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11

83	cg43966704	1279	CCCTCAAACCCG ATGCTTGATCT C[G/A]CCCAGGA TCCAGTCGGGC CCCTTCA	G	A	Gly	Gly	SILENT- CODING	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
84	cg43966704	1294	TCTTGATCTCGC CCAGGATCCAGT C[G/C]GGCCCT TCAGCAGGATCT CCTTTG	G	C	Pro	Pro	SILENT- CODING	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
85	cg43966704	1375	CTTTCAGCCTCC AGTCATGGCGG CC[G/A]TACAGGT TGGTGAAATCC GGTCTT	G	A	Tyr	Tyr	SILENT- CODING	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
86	cg43962888	563	CCTCCATCTCCA ACAAGAGAATAG T[A/G]GGCTGCAT CTGTGAAGAGGA CAATA	A	G	Val	Val	SILENT- CODING	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.10E-66	2 (2cen)
87	cg43962888	620	TCGCTCTGTTT GGCTGCACAAAG G[C/G]GAGGCC AGCGATGCCCC CGCTGIG	C	G	Gly	Gly	SILENT- CODING	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.10E-66	2 (2cen)
88	cg39454979	2375	ACTTACTACGCT CCAAGATTACCA A[A/G]CCCAACGT GTACCATGAGTC CAAGC	A	G	Lys	Lys	SILENT- CODING	deaminas e	Human Gene SWISSPROT-ID:P51400 DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) - RATTUS NORVEGICUS (RAT), 711 aa.	0.00E+00	21
89	cg43275625	1124	GCTTGGACTCAT GGTACACGTTGG G[T/C]TTGGTAAT CTTGGAGCGTAG TAAGT	T	C	Lys	Lys	SILENT- CODING	deaminas e	Human Gene SPTREMBL-ID:O00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa.	0.00E+00	21

90	cg42476357	891	ACCGGCGCCTG AAGTTCCTCTCC TC[G/C]AAGTTCC AGTCCATCAGA TGCTTA	G	C	Ser	Ser	SILENT- CODING	deaminas e	Human Gene SWISSPROT-ID:P23109 AMP DEAMINASE 1 (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) (AMP DEAMINASE ISOFORM M) - HOMO SAPIENS (HUMAN), 747 aa.	0.00E+00	1 (1p21)
91	cg39454981	2495	ACTTACTACGCT CCAAGATTACCA A[A/G]CCCCAACGT GTACCATGAGTC CAAGC	A	G	Lys	Lys	SILENT- CODING	deaminas e	Human Gene SWISSPROT-ID:P78563 DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	
92	cg41626024	635	TTGGGCGCTGAG GACCTGCAGAAG AC[T/C]CAGTGAC AGCCAGAGAATG CCCACT	T	C	Thr	Thr	SILENT- CODING	deaminas e	Human Gene Similar to SWISSPROT- ID:P23230 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) - HOMO SAPIENS (HUMAN), 146 aa. pcds:TREMBLNEW- ID:E1228801 CYTIDINE DEAMINASE (EC 3.5.4.5) - HOMO SAPIENS (HUMAN), 146 aa.	8.80E-78	1 (1p36.2)
93	cg34396112	3375	CAGTTCCTCTGG TGCCTCTGGACA C[A/T]AGTGTGTCAG CTTGGCCCCCACT GGCCA	A	T	Leu	Leu	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
94	cg34396112	3660	TCAGCTCAGGGA TCCAGGCTGGG CA[G/A]ACAATCA TAGGAAACAGCA TATTCT	G	A	Val	Val	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
95	cg34396112	3870	TCAGCAACTCTG GGGGAATAATG GG[C/T]TCCTGG GTTGGATCCAGG GGCGTGA	C	T	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
96	cg34396112	3876	ACTCTGGGGGAA AAATGGGCTCCT G[G/C]GTTGGAT CCAGGGGCGTG AACTCCT	G	C	Thr	Thr	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)

97	cg34396112	4245	TTCCTATTCCCTTC CACAGTTGTCAC[T/A]GCAACATGG TGCAAGGAGCA GATGG	T	A	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
98	cg34396112	4254	CTTCCACAGTTG TCACTGCAACAT G[G/A]TGCAAGG AGCAGATGGGG GCCAGGC	G	A	His	His	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
99	cg34396112	4362	TCACTGTGCAAG CCCCGCAGCCC CC[C/T]TCTCCAC AGCCGAGCTTG GTCCAC	C	T	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
100	cg34396112	609	TCTCCGGGGTG GCAGGGCTGTCT AG[G/C]CGGAAG AGTTCCCTTCACG TTATTAC	G	C	Arg	Arg	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
101	cg43314766	1860	CGGAAGCATCCA TAGTACGCCACG G[A/G]GATCCAAT CTGAAAAGCCTG TCTTG	A	G	Ser	Ser	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALHDII) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.20E-273	9 (9q21)
102	cg43996714	1683	TAGATTCAGTTA ATCTCTTGGCAA T[G/A]ACTCTTCG AATATTGCTGGC GGGGA	G	A	Val	Val	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266	11
103	cg43996714	2433	ATCTCCAATTAG CTCCGGCGGCTTA C[A/G]GACCAACC CAAGAGCCCCCT TCACCA	A	G	Ser	Ser	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266	11

104	cg43959104	779	ACAGGATCATTCTTCAGTAATATTC [A/T]GCCCTTGACA AGCACAGCGGC TACAA	A	T	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P51648 FATTY ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) (ALDEHYDE DEHYDROGENASE, MICROSOMAL) (CLASS 3) - HOMO SAPIENS (HUMAN), 485 aa.	1.30E-250	17 (17p11.2)
105	cg43259523	654	AGATGTGGATCAGCAGTCTGAG CA[C/T]GCAGGG CTCCTTCTGGTG ATGGCAA	C	T	His	His	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2.00E-229	10 (10q25)
106	cg43057018	1242	TCAATCCTAGAGACTTACATAAAC C[G/T]ATCCAGGA AGTTATCATTGA ATTGA	G	T	Pro	Pro	SILENT- CODING	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa. pcls:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)
107	cg44917703	1198	AGAAGGTGATCA AAGTTGGCAAGG T[G/T]CGGACTC GAGACATGGGC GGCTACA	G	T	Val	Val	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
108	cg44917703	1218	GCAAGGTGCGGACTCGAGACATG GG[C/T]GGCTAC AGCACCAACAACC GACTTCA	C	T	Gly	Gly	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
109	cg44917703	1222	TGCGGACTCGAGACATGGCGG CTA[C/T]AGCAC ACAACCGACTTC ATCAAGT	C	T	Tyr	Tyr	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13

110	cg44917703	1243	GCTACAGCACCA CAACCGACTTCA TTC/TJAAGTCTGT CATCGGTCACCT GCAGA	C	T	Ile	Ile	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
111	cg3000385	566	TGGGCACTGCTG GAAAAGTTATTA A[A/G]TGCAAAGC AGCTGTGCTTTG GGAGC	A	G	Lys	Lys	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.40E-202	4 (4q23)
112	cg43923979	863	GAAAATCTTTTG ACTGAGCTTCCG G[A/G]GGAAATTC AAAAGGAACCCC ATAACA	A	G	Pro	Pro	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4.00E-192	3 (3p13)
113	cg43948373	1642	CAAGTGGGGCT GAGATTGGAGGT GC[C/A]TTTGGAG GAGAAAAGCACACA CTGGTG	C	A	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
114	cg43948373	1678	AAAAGCACACTG GTGGTGGCAGG GA[G/A]TCTGGC AGTGATGCCTGG AAACAGT	G	A	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
115	cg43948373	1741	CTACTTGTACTA TCAACTACAGTA A[A/G]GACCTTCC TCTGGCCCCAAGG AATCA	A	G	Lys	Lys	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5

116	cg43960596	903	CCAACAGGGTG GTGTGGAGGCG GGA[A/G]GAGGC CACCCGCTGCA GGTCCTCGG	A	G	Ser	Silent- CODING	dehydrog enase	Human Gene SWISSNEW-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.lpcis:SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.	4.40E-170	12
117	cg43969759	566	CGTCTCGGATGG TGCTGAGTGGTG G[G/A]TAGAGTCT CCCCTGGGACA GATGCT	G	A	Tyr	Silent- CODING	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.80E-109	11
118	cg43104003	710	ACCCAGCGCCTA TGCTGGCCCGG AC[G/A]TCACTGA TAGGTAAGATGA AGTCCC	G	A	Asp	Silent- CODING	dehydrog enase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.lpcis:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6

119	cg42717491	384	CTGTCTCTTTGG ACTGAACAAAAG A[G/A]CACTCGAT GACTCCTTCCTT CCCAT	G	A	Cys	Cys	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
120	cg43248620	2294	TCTGTACCCCTCA CGTGCAGGCTC CG[C/T]GATGTTT TGCTGGAAAGCT GAGCAG	C	T	Ser	Ser	SILENT- CODING	dna_rna_ bind	Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa.	0.00E+00	1
121	cg43273880	4271	GCTGTGTGTCAG CAATGCAGGAAT A[C/T]GAAAGAGCA GCTGAAAGAAAA TGCCA	C	T	Tyr	Tyr	SILENT- CODING	dna_rna_ bind	Human Gene SWISSPROT-ID:O14647 CHROMODOMAIN-HELICASE-DNA- BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
122	cg43273880	4952	CTAGAAAAGACA AAGAAGGGGAC AA[A/G]GAAAGAA AGAAAGGAAAG ATAAGA	A	G	Lys	Lys	SILENT- CODING	dna_rna_ bind	Human Gene SWISSPROT-ID:O14647 CHROMODOMAIN-HELICASE-DNA- BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
123	cg42175288	1364	ACAGAAAGTGGG GGTGGCTATGGT GG[A/G]GACAGA AGCAGCGGTGG TGGCTACA	A	G	Gly	Gly	SILENT- CODING	dna_rna_ bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0.00E+00	17
124	cg43988816	2369	TCCCTTCCCTC GGGAGTTGCTCC A[C/G]GTACGGA TCTGACTTTTGT GGTAA	C	G	Thr	Thr	SILENT- CODING	dna_rna_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00 (17p13.3)	17

125	cg44005808	3412	AGACCACCTCTC AGGCCCACTCG CT[G/C]CCTCTCT CGCCTGCCTCCA CAAGGC	G	C	Leu	Leu	SILENT- CODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.[pcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
126	cg43276473	311	CATCTGCTCCCA CCGTAACCTCTAG T[A/G]CAGCTGC CCAATGGGCAGA CAGTTC	A	G	Val	Val	SILENT- CODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q62347 TRANSCRIPTION FACTOR/DNA BINDING PROTEIN - MUS MUSCULUS (MOUSE), 287 aa.	5.30E-142	2
127	cg44031583	307	CAAACCTGATTG TACATCAGAGAA C[C/T]CATACAGG AGAGAAACCCCTA TGCTT	C	T	Thr	Thr	SILENT- CODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	7.10E-125	12
128	cg43969880	580	AACGGATACACA CGGGAGAGAAG CC[C/T]TATCAGT GCAAGGAGTGT GGGAAA	C	T	Pro	Pro	SILENT- CODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	9.40E-58	10
129	cg43946971	1334	TGGCCATGCACA AGCGCAGTGCC CA[T/C]GGCGAG CTGGAGGCCAC GGAGGAGA	T	C	His	His	SILENT- CODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52 (6p21.3)	6
130	cg43946971	1361	GCGAGCTGGAG GCCACGGAGGA GAG[T/C]GAGCA GGCCCTCTATGA GCAGCAGC	T	C	Ser	Ser	SILENT- CODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52 (6p21.3)	6

131	cg43949306	1784	TGGAGTCTGTCC TCGTCTTCTTCT C[A/G]GTCTCTGC GTAGGCCAGGT CGTCCT	A	G	Thr	Thr	SILENT- CODING	dynein	Human Gene SWISSPROT-ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	0.00E+00	14
132	cg43958656	565	GAACCGGCATG GCCAAAGCCGC GGC[G/A]ATCGG CATCGACCTGGG CACCACCT	G	A	Ala	Ala	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
133	cg43958656	763	AGAACACCGTGT TTGACGCGAAGC G[G/C]CTGATCG GCCGCAAGTTCCG GCGACC	G	C	Arg	Arg	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
134	cg43958656	769	CCGTGTTTGACG CGAAGCGGCTG AT[C/T]GGCCGC AAGTTCGGCGAC CCGGTGG	C	T	Ile	Ile	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
135	cg44017749	10249	CCATTAAACCGAG CCCACAAGACCA C[A/G]GGCACCA ACAAAACGCTCC TCATCA	A	G	Thr	Thr	SILENT- CODING	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0.00E+00	12
136	cg43982507	2646	CCAATAAATTCA CTGGATCAGAGC T[A/T]GCCACTCT AGTCAACAACCT GAATG	A	T	Leu	Leu	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	
137	cg43982507	636	CCATGGGCACGTG CCGCGCTCTGG GC[G/C]CTCTGG CTGCTGCTCGCG CTGTGCT	G	C	Ala	Ala	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	

138	cg43953981	2111	CTTGAACAAGTT TAGCTCCAATGT TTC/TTTGTATTT ATCTTTTAAGTCA ATTG	C	T	Lys	Lys	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P10809 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (HUCHA60) - HOMO SAPIENS (HUMAN), 573 aa.	8.30E-295	9
139	cg43945167	1149	AGAGCTTGTCCTCA GTTCTTCGCCGG A[A/G]AATTTCCTCC AGAGGTCCTTCGC CTTGT	A	G	Phe	Phe	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191 (4p16.3)	4
140	cg43918531	1596	GCAAAAAGCAAC AGATATCTCTTG C[A/C]ACACAAAT GGTAGAATGAT TTTGA	A	C	Ala	Ala	SILENT- CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. [pcis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
141	cg43918531	1611	TATCTCTTGCAA CACAAATGGTTA G[A/G]ATGATTTT GAAGATTGATGA CATTC	A	G	Arg	Arg	SILENT- CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. [pcis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5

142	cg43918531	1618	TGCAACACAAAT GGTTAGAAATGAT TTT/CJTGAAGATT GATGACATTCGT AAGCC	T	C	Leu	Leu	SILENT- CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. pcIs:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
143	cg43944783	1309	TGTTGTAGTCGC CCTTTTCAAAGT A/C/TACCGCTGC TTGATTGGTAAT GTAAG	C	T	Val	Val	SILENT- CODING	eph	Human Gene Similar to SWISSPROT- ID:P15705 HEAT SHOCK PROTEIN ST11 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 589 aa.	2.80E-74	11
144	cg42889246	592	TCATTCAGACCT TCGAAGGCTGG CT[A/G]CTGATAA AAGCACAAACACG GAACCA	A	G	Leu	Leu	SILENT- CODING	eph	Human Gene Similar to SPTREMBL- ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.50E-73	
145	cg42889246	679	CCCGACAGTACA AACTACCAGATG GTT/CJGTGGAAAT CAAAGATTGTGC TGCAG	T	C	Gly	Gly	SILENT- CODING	eph	Human Gene Similar to SPTREMBL- ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.50E-73	
146	cg43984905	2206	ACCTTGCCCTCA TCCGCTTCTTGG TIG/AJGAAGATTA TGATGCCTCCTC CAAGA	G	A	Val	Val	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

147	cg43984905	2227	TGGTGAAGATT ATGATGCCTCCT C[C/T]AAGAATGA CTTCATTGGCCA GAGTA	C	T	Ser	Ser	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
148	cg43984905	2233	AAGATTATGATG CCTCCTCCAAGA A[T/C]GACTTCAT TGGCCAGAGTAC CATCC	T	C	Asn	Asn	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
149	cg43984905	2239	ATGATGCCTCCT CCAAGAATGACT T[C/T]ATTGGCCA GAGTACCATCCC CTTGA	C	T	Phe	Phe	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
150	cg43984905	2254	AGAATGACTTCA TTGGCCAGAGTA C[C/T]ATCCCGTT GAACAGCCTCAA GCAAG	C	T	Thr	Thr	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

151	cg44011461	2429	GGATGAGGGCA TAGATGCTGCTG AA[G/C]GTGAGG TTGTCAGTCAAG TAGTATT	G	C	Thr	Thr	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
152	cg44011461	2432	TGAGGGCATAGA TGCTGCTGAAGG T[G/C]AGGTTGTC AGTCAAGTAGTA TTTCA	G	C	Leu	Leu	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
153	cg44011461	2750	CATCACTGAAGG ACAGCTTGGCAT C[G/A]GCAATGG CGCAGTAGTGCC GAGTCC	G	A	Ala	Ala	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
154	cg40343531	592	AGGATCACTTAC TCTCACTCCCG C[C/T]GCGGGG TGGTGCTCAGCT GCTTGG	C	T	Ala	Ala	SILENT- CODING	esterase nhib	Human Gene SPTREMBL-ID:Q14432 CGMP-INHIBITED CAMP PHOSPHODIESTERASE - HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	12
155	cg43937658	1406	CATCTGCTGGGG CCACCTTTGCTG C[G/A]TAACTCCA CATCTCAATCCG GTCA	G	A	Tyr	Tyr	SILENT- CODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16

156	cg43320667	1510	CAGGAACGCCA GCCCCGGCTGA GGC[C/G]GCCAC ATCAGCAATGGA CCTCTTGG	C	G	Ala	Ala	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
157	cg43320667	852	GCTCAGGACCAT TCTCTGGCGAA C[G/A]ATGTCTTC GCTGGGCTGGA CCATGA	G	A	Ile	Ile	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
158	cg43320667	908	ATGCGCTGCTTC AGGAGCCCTTT A[A/G]GGTGAGG AACATGTAGGCC ATGTAC	A	G	Leu	Leu	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
159	cg44131042	558	ATCTTTATTCCCA GATCTCCTCTGT C/T]CCCATAGGT TACAGCCACCCC GCCC	C	T	Val	Val	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P80404 AMINO BUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.19) (GAMMA-AMINO-N- BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GABA AMINOTRANSFERASE) - HOMO SAPIENS (HUMAN), 500 aa.	4.20E-268	16
160	cg3001932	230	CAAAACTAAAG GGATGTGGAGA GT[G/C]CGGAAA AGGGGCTACTTT GGGATT	G	C	Val	Val	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P47870 GAMMA-AMINO BUTYRIC-ACID RECEPTOR BETA-2 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 474 aa.	1.90E-256	5 (5q34)
161	cg43299024	2993	TGGCTGTGGCC CTGACCAAGGT GG[G/A]GAGGCC CGAGGGGAGCT GTTCTGGG	G	A	Gly	Gly	SILENT- CODING	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)

162	cg43992911	1660	GAAAAGAAAGTTA C AGATCTTGAAGG G[C/T]CTGAACCT GAAGGTGCAGA GTGGGC	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	7
163	cg43286488	1436	GGTCAGCTTCAAG G CCAGATAGCCAC T[G/A]GGGTCAT GGAGCTGGAGG GCAAAGG	A	Pro	Pro	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12

164	cg43286488	1706	GGCCCCCTAGAA CTTGCCAGTATT G[G/A]CCCCAGG TCTTCCAGACAT AAACAA	A	Gly	Gly	SILENT- CODING	glycoprotein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.[pcis:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12
165	cg43286488	1841	CTGGCTGTCCTC CCCACACCTGGC TTC/AJCCATTGAT GATGGTATTGTT GACCC	A	Gly	Gly	SILENT- CODING	glycoprotein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.[pcis:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12

166	cg43943531	1102	CTCCCTGGACG GGCGTTTCTAC TC[G/A]CTGCTG GATCCCTCTTAT GCTAAGA	G	A	Ser	Ser	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
167	cg43943531	1417	ACATGAAGAATC TGGACATAAGTC G[T/C]CCAGACAA GAAGAGCAAGAA GCAAC	T	C	Arg	Arg	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
168	cg43943531	847	CCTACTGTACTG TTTACTGCCTGG G[C/T]ACTATACT TTCTATGCAGAT CTCCT	C	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
169	cg43943531	916	TCCTTTCATCAG AGCACATGGCAG C[C/G]TTTGGGG TCCTTGGTCTCT GCCAGA	C	G	Ala	Ala	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
170	cg43065490	2042	AAGCAGAGCAGT ATCAACCCCTCA C[G/A]CGTTTCAGT CAGCCTCCAGAA CTCCC	G	A	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
171	cg43065549	1597	AGGGTTATGATG GATGGCAGATTC T[C/G]GAGCCCAA GTGCTCCTAATG GAGGIG	C	G	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
172	cg43065549	1648	GAGTCCTGGGG TCCTGTGATCTG GT[A/G]CCGGTC AGAGCAGTCAAG GAGGGGA	A	G	Val	Val	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

173	cg43065549	1675	CGGTCAGAGCA GTCAAGGAGGG GAC[G/C]CTGGG GCTGACCCCCAG CAGTGTGACG	G	C	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
174	cg43018621	507	CGGACAACCTG GAGCTGAAGAAG CT[G/A]GTATACC TCTACTTGATGA ATTACG	G	A	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa. pcds:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	0	22 (22q12)
175	cg43924995	458	CAAAATGGCAGA TGAATTTACACAG T[AT]CGCTATGA AACTACAAATAA AACTT	A	T	Val	Val	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.2E-222	X (Xq24)
176	cg43301245	1420	GCCCATCAAAGC CATGGGTGCCG AG[A/G]AATGGC GGTACTGACTTG ATGAAAG	A	G	Phe	Phe	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. pcds:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1

177	cg43301245	757	GGTCCAGGGCC CATACCATGGCG CC[C/T]GCCAGC TGCCTGTCCTTC AGGTACT	C	T	Ala	Ala	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1
178	cg43301245	769	ATACCATGGCGC CCGCCAGCTGC CT[G/A]TCCTTCA GGTACTGCACCT TGCTTT	G	A	Asp	Asp	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1
179	cg43059879	580	TTACTTCCCTGC ATTCTGGTAATTT [A/T]GTCCAATTT CCATGTGTCGTG CAGG	A	T	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa.	6.6E-199 (17q23)	17

180	cg43932434	1575	TGGGGTGGATC CGGGGAATCAC CAC[AG]TGCCCT TCTATGAACCCA TACCTGC	A	G	His	His	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.8E-195	11 (11pter)
181	cg43988092	1994	TGAAGTTTCCAG TACTGAAATCCA G[C/T]TCTGATT TTCTGCTCTTGC AAGGC	C	T	Lys	Lys	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4E-192	8
182	cg43918166	2106	AACCATCTTTGC AGTGGTATCTAA T[C/A]AGGGAGTT GATTCATAACG AGGTT	C	A	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.5E-190	5
183	cg44022653	1149	TCTCAGCCTCGG AACAGTTGTGGG T[A/G]CCCAGTG CACACTCATCCA CGTCCT	A	G	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

184	cg43076975	1141	TGAATATGCTAA GGGAGTATCTTA GTCGCTGACG CATTAAAGTG GTATTG	T	C	Ser	Ser	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa.lpcis:SWISSPROT-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa	3.40E-120	5
185	cg43051796	1072	AGGTGAACATCG CAAATCGCTTCC CAGGAGGCCCT CGTTGCCGCGAG CACCCAC	A	G	Cys	Cys	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.lpcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa	4.00E-114	3
186	cg43287997	330	TGGGCCCTCTGCC TCATTATCAGTTG GCTGTGTTGGG GGCAAGATGGTA ATGAAG	C	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.lpcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa	1.30E-113	11 (11q23)

187	cg43959140	705	TTTCCCTGCGGC TATCACAATAATG G[A/G]GTATACCC ATAAGGAGCTCC ATCCA	A	G	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	1.30E-108	
188	cg36834323	312	ACCTGCAGATG CTAAGAATGCTG C[G/C]AAAGATAT GAATGGAAAGTC TTTGC	G	C	Ala	Ala	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
188	cg44018280	1508	CCGTGGCCTGG AGGAGGGAGAG GGA[G/C]AGCAG GAGCAGCAGCA GCCACGAGG	G	C	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.50E-80	11
190	cg44924334	508	CCACCTGCCAGT CTATTGCCCTTC C[C/T]AGCAAGAC CTCTGCCAGTAT AGGCA	C	T	Pro	Pro	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	
191	cg44924334	674	ACCTGTTATTG CTGCATTGTGG G[G/T]GCTGCAG CTACACTGGTTT CCCTGC	G	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	
192	cg41568631	1548	CTGTGGAGTCCA TCAAGAATGGCC T[G/C]GTCTACAT GAAGTACGACAC GGCTT	G	C	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70 (14q11.2)	14
193	cg43918233	1133	CTGCCCTCCAGTG AGAACCCTGAAG G[A/G]JACACTTTC GGATTCCACGG GTAGCG	A	G	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2

194	cg43965366	2066	TCACGTCGAACG TCTCCTTCTTGA AT/C]TCTGCCCTT CGGACCCCGG TGTA	T	C	Glu	Glu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.90E-61	6 (6p25)
195	cg43982558	1326	AGGCTGCAGTG CGCTTCGTGGT TT[C/]CCAGATA AAAAGCATAAGC TGTATG	C	T	Phe	Phe	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
196	cg41603916	259	TCACCTGGCGCT ACCAGCCCGAA GG[G/]GGCAGA GATGCCATTTTCG ATCTTCC	G	A	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q91406 IP1=CNS MYELIN P0-LIKE GLYCOPROTEIN - UNKNOWN, 202 aa.	3.00E-52	1 (1q22)
197	cg43250682	1520	TTCTGACTCCAA AAATCAACCAGA C[G/C]TTTAGCG GGATCATGACTA TGTTGA	G	C	Thr	Thr	SILENT- CODING	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0.00E+00	4
198	cg43250682	2120	AGACCATTTGGCG ATGCCTATTGTG T[G/]GCTGGGG GATTACACAAAG AGAGTG	G	A	Val	Val	SILENT- CODING	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0.00E+00	4
199	cg43956596	1584	GCATTGTCTTCA CCAAGCAGCCG GA[G/]CCGGTG ATCCAGTGAAG GATGCCA	A	G	Glu	Glu	SILENT- CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. pc s:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16

200	cg43956596	1587	TTGTC TTCACCA AGCAGCCGGAA CC[G/A]GTGATTC CAGTGAAGGATG CCACTT	G	A	Pro	Pro	SILENT- CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.pcls:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16
201	cg43956596	718	CAGTCGGCAGA GAGAGCGGGAG CGG[C/A]GGGAA CATGGTGTCTAT GCCTCGTC	C	A	Arg	Arg	SILENT- CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.pcls:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0	16
202	cg43931167	2037	ATGACTTTGGCT GGGGAGTAGTG GT[A/G]AATTTCT CAAAAAAGTCAA ATGTTA	A	G	Val	Val	SILENT- CODING	helicase	Human Gene SWISSPROT-ID:O14232 PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 1117 aa.	3.3E-307	5
203	cg43958815	720	GCTTCTTCCGCT TCTTGTGAGGC GT[C/A]CCAGGC CACGGAGAGCA GGAGGAA	T	C	Val	Val	SILENT- CODING	helicase	Human Gene Similar to SWISSPROT- ID:Q06218 PROBABLE ATP- DEPENDENT RNA HELICASE DBP9 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 594 aa.	3.9E-100	
204	cg43263560	544	ACAAAACCCCTTG CTTTAATTAAAGA [C/T]GGCCCGTGT ATTGGTGGTATC TGT	C	T	Asp	Asp	SILENT- CODING	histone	Human Gene Similar to TREMBLNEW- ID:G2707336 HISTONE ACETYLTRANSFERASE - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 418 aa.	3E-61	3
205	cg43988803	1992	GACATGCTCAGC AGACATCTGCAG TT[C/A]ACGGGC GTCCCCCTGCCCC ACACGG	T	C	Val	Val	SILENT- CODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13

206	cg43332152	981	ACCTGGGCGCC AAGCGCGGGG ACC[G/C]CGCAC CACCATCAAAGC CAAGCAGC	G	C	Pro	SILENT- CODING	homeobo x	Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa.	3.4E-227	17
207	cg41637704	1201	AGGAGCTGCTG GGGCCGCCAGC GCC[G/C]CGAGA CAAGGGCAGCG GACCGCCTG	G	C	Pro	SILENT- CODING	homeobo x	Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.2E-224	7
208	cg43143467	581	CTTCAACCATC TCATTCCCGGG G[G/A]JTCCCTCC CACTGCCATGCC GACCT	G	A	Gly	SILENT- CODING	homeobo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
209	cg43971192	625	TGTTGAAAAGAC CACTCTGTGTAT T[G/G]GTACTTGG TCCAGATTTACA AGTGT	C	G	Thr	SILENT- CODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.9E-144	18
210	cg40291306	693	AGATCAAGATCT GGTTCCAGAACC G[A/C]AGGATGA AGTGAAGAAAG ATTCCA	A	C	Arg	SILENT- CODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q00444 HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11) - HOMO SAPIENS (HUMAN), 222 aa.	8.3E-121	12
211	cg40291306	694	GATCAAGATCTG GTTCCAGAACCG A[A/C]GGATGAA GTGGAAGAAAGA TTCCAA	A	C	Arg	SILENT- CODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q00444 HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11) - HOMO SAPIENS (HUMAN), 222 aa.	8.3E-121	12

212	cg43923497	1741	ACTTCACCTTCT CTGTGGCCAGG CA[CTTTTGATCT TTTCCTCCACCA AGAAGC	C	T	Lys	Lys	SILENT- CODING	hydrolas e	Human Gene SWISSPROT-ID:P45974 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) - HOMO SAPIENS (HUMAN), 858 aa.	0	12
213	cg43922794	2430	TTAAATGCCACC GAACCTATCGGC T[C/G]TTTGAGT GGTCTACCATCA CGGCA	C	G	Leu	Leu	SILENT- CODING	hydrolas e	Human Gene SWISSPROT-ID:Q14694 PROBABLE UBIQUITIN CARBOXYL- TERMINAL HYDROLASE (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) (KIAA0190) - HOMO SAPIENS (HUMAN), 798 aa.	0.00E+00	14
214	cg43285385	618	TTAAGACATTGA AAACTTCTTTAA [C/T]TTTTCATT ATTGTAAATTCT TCA	C	T	Lys	Lys	SILENT- CODING	hydrolas e	Human Gene TREMBLNEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa.	4.80E-173	8
215	cg43925670	1390	TTTTTCTAAGTC GAAAGCAGAAAA G[T/C]TGGAGCTT ATCTCCTTCTTC ACAGG	T	C	Gln	Gln	SILENT- CODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. [pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)]	0.00E+00	1

216	cg43925670	1720	ATATGATGATGA TTTTCTTTCCATT [A/G]AATTTCTCC TTCAAGCTGGTG TTTA	A	G	Phe	Phe	SILENT- CODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pc1s:SPTRMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1
217	cg43082514	921	CCAGCGATGAAG AGAGTGCCGAG GG[G/A]CGGCCA CACTGGCGGAA GAGGAATA	G	A	Gly	Gly	SILENT- CODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188 (4q35.1)	4
218	cg43922672	1212	CTGCTGAAACAT CTGCCCTTGGACA C[A/G]GGGTTCT CGCTCAACCTTT CAGAGC	A	G	Thr	Thr	SILENT- CODING	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
219	cg42887911	402	CCCTGCCACCC TGGCCATGAGTG C[A/G]GGGGCAC TGGAGGCTCTAC AGCTCC	A	G	Ala	Ala	SILENT- CODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P20809 INTERLEUKIN- 11 PRECURSOR (IL-11) (ADIPOGENESIS INHIBITORY FACTOR) (AGIF) - HOMO SAPIENS (HUMAN), 199 aa.	2.5E-103	19
220	cg43929155	434	TCCTATGCAAG CAGTCCATGTCA T[C/T]TACACAGT CAACCTCTACAG CAGTG	C	T	Ile	Ile	SILENT- CODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P21109 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1) - ORYCTOLAGUS CUNICULUS (RABBIT), 355 aa.	4.2E-55	2
221	cg43951261	2559	AACAAGCATTGA TGATGACTATTG T[A/G]AATTGGC TCAGAACTTTGT GGGAA	A	G	Val	Val	SILENT- CODING	isomerase	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0	3 (3p)

222	cg43993971	1428	AGGCAATGATGA ACAGGGAGGAC TC[G/C]GGGTTT AGCTGGGCCAG GGTTTGG	G	C	Pro	Pro	SILENT- CODING	isomerase	Human Gene SWISSPROT-ID:P06744 GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) (NEUROLEUKIN) (NLK) - HOMO SAPIENS (HUMAN), 558 aa.	3.60E-305	19 (19q13.1)
223	cg43930054	738	TCTGGGTTGTGG GTGTGCTGGCTA TTC/TACTGTCCC CTGTACCATCAG GAGGA	C	T	Val	Val	SILENT- CODING	isomerase	Human Gene SWISSPROT-ID:P34949 MANNANOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2.00E-222	15 (15q22)
224	cg43961450	1141	ACTCTGCCCTTAG TCTTCTTTGCAA A/C/TJACATCTGC AAACTTCTTCTTC ATT	C	T	Val	Val	SILENT- CODING	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.---) - RATTUS NORVEGICUS (RAT), 361 aa.	1.80E-117	5
225	cg43961450	1237	CAAGTCCAAGTC CTTTAAGCAGCA G/T/CJGCGTAGA ACTGGGGTTCTA TTGCTC	T	C	Ala	Ala	SILENT- CODING	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.---) - RATTUS NORVEGICUS (RAT), 361 aa.	1.80E-117	5

226	cg43924460	609	TCATAAAGAGTG TTACACCGTGCG C[AT]CCAAAGTA CCACAAAGCCTG CTCCA	A	T	Ala	Ala	SILENT- CODING	isomerase	Human Gene Similar to SWISSNEW- ID:Q27450 PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.jpcls:SWISSPROT-ID:Q27450 PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS- TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.jpcls:SPTREMBL-ID:Q27450 PEPTIDYLPROLYL ISOMERASE (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa	4.20E-71	8 (8p22)
227	cg43145505	253	ACTTGATGCCCC CAAGAATCCTAG T[A/G]GAATGTTT ACTACCAAATGG AATGA	A	G	Val	Val	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.jpcls:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa	0.00E+00	3

228	cg43145505	358	TATTTAAAGAAG CAAGAAATACC C[C/T]CTCCATCA ACTTCTTCAAGA TGAAT	C	T	Pro	Pro	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa. pcds:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3
229	cg43918241	943	TGCTAAAGAGT GTAAAGACCTAA T[C/T]ACACGGAT GCTACAGAGAGA TCCCA	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
230	cg43252989	2330	ATTTTGAGGTTT GGTTTATGATG G[G/T]GTGAACT ACACAAATAGA AGATT	G	T	Gly	Gly	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:O00444 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 970 aa.	0.00E+00	4
231	cg43916734	18295	GCAGGCTATTGT TTATCCCTTCAC G[C/A]GAAGCAG CGAAAGCTATTTC CTTCAA	C	A	Arg	Arg	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
232	cg43257400	2027	TTGCCCTGTACAC AGAGTTCTGCC G[G/C]TCCCTTGT AGGATCCAGTCT AGAAG	G	C	Arg	Arg	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa.	0.00E+00	10
233	cg43329663	2266	CTCGAGAGGCC AACCCAGAGAAA TTT[C/A]ACAGCC GCTTTCGGAATA AGATGT	T	C	Phe	Phe	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:O00542 DIACYLGLYCEROL KINASE ZETA - HOMO SAPIENS (HUMAN), 1117 aa.	0.00E+00	11

234	cg43151490	322	ATCTGACGGTGA GCGTGGACCCAG GT[A/G]CGCGTG GGCCAGACCCAG CACAAAGC	A	G	Val	Val	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P24723 PROTEIN KINASE C, ETA TYPE (EC 2.7.1.-) (NPKC-ETA) (PKC-L) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	14
235	cg44929725	2320	TGGATCTCTTCA TGCACCGGAAAA G[C/T]GATGTCCT TACCACACCCATG GAAAT	C	T	Ser	Ser	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
236	cg44929725	2347	ATGTCCTTACCA CACCATGGAAAT T[T/C]AAAGTTGC CAAACAGCTGGC CAGTG	T	C	Phe	Phe	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
237	cg44929725	2449	AAAACCTCCTCC TGGCCCGTGAG GG[C/A]ATCGAC AGTGAGTGTGGC CCATTCA	C	A	Gly	Gly	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
238	cg44929725	2884	CTGAAGTGGACC CCACACATTTTG A[A/G]AAGCGCTT CCTAAAGAGGAT CCGTG	A	G	Glu	Glu	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
239	cg44929725	3649	CTAACTGTCCAG ATGAGGTTTATC A[A/G]CTTATGAG GAAATGCTGGGA ATTCC	A	G	Gln	Gln	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
240	cg44929725	3658	CAGATGAGGTTT ATCAACTTATGA G[G/A]AAATGCTG GGAATTCCAACC ATCCA	G	A	Arg	Arg	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)

241	cg44918305	1129	TGAGTACTCGCA CAGAAGCATTAG A[A/G]GCCCTTACA GAGTGAAAAATC ACGAA	A	G	Glu	Glu	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	0.00E+00	10 (10q11.2)
242	cg43940596	1642	TCTTCACGCACA AGGGGTGGTTCA T[A/C]GAGACTTG AAACCTAGCAAC ATTCT	A	C	Arg	Arg	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P51812 RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA) (P90-RSK 2) (INSULIN-STIMULATED PROTEIN KINASE 1) (ISPK-1) - HOMO SAPIENS (HUMAN), 740 aa.	0.00E+00	X
243	cg43931272	2078	GTTCTTTCCCAA CCACAAAACACT C[C/T]GGTGGTAA ATACCAATAAGT ACCAG	C	T	Pro	Pro	SILENT- CODING	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
244	cg43930294	1630	TAGCTGGTTGAT GAGAAGCATGCC C[T/C]TGATATC ACTTGTTAACTT GGGAG	T	C	Gln	Gln	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:O00311 CDC7-RELATED KINASE - HOMO SAPIENS (HUMAN), 574 aa.	2.90E-308	1
245	cg43952792	1125	TCCGCCGAGAGT GAAACCACCAA GGT[G/G]GCCTATT CACTTTCTATCC GTGATT	T	G	Gly	Gly	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
246	cg43922705	3970	TCTGCTGGTCCA GGGTATGCAGG AA[G/A]GCTGAGT TGGGGTCCAGG GTGCGCT	G	A	Ala	Ala	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P27987 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)
247	cg43241753	1745	CCTGTGTGTGGC TTGTTTCATTCT [A/G]TGTGTTGAA ACCAGGTTACCA ACAT	A	G	His	His	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9

248	cg43965549	625	GCGCCTTTGGAA AGGTATACCTTGG C[AT]CAAGATAT AAAGACGAAGAA AAGAA	A	T	Ala	Ala	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
249	cg43965549	703	AATTTAAGCCAT CTGATGTGGAA T[C/T]CAGGCTTG CTCCGGGCACGA GAACA	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
250	cg43926820	1479	CATACAGGATGC AACCCAAAGGACC A[G/T]ATGTCACT TTTATTGTTATAA GGCA	G	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P51956 SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 3) (HSPK 36) - HOMO SAPIENS (HUMAN), 459 aa (fragment).	1.40E-251	13
251	cg43069976	469	TGGCTAGTGTA TTACAAAGGGAA C[C/G]AAGGAAA GGCAATACCTTAG ATGAAG	C	G	Thr	Thr	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.[pcis:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1

252	cg43069976	589	GTCATACCGTAT TGCATCGGGATC TGGTAAACACGAGC CAATGTTTTCCT GGATG	G	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.[pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
253	cg43069976	667	TTGGGCTAGCTA GAATATTAAACC ATTGACACGAG GTTTGCACAAA CATTG	T	C	His	His	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.[pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
254	cg43967889	1159	AATTACGGGACC CAAATGTCAAAC TTATCCAAATGG GCGAGACACAC CTGCAC	A	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa.	1.90E-226	3

255	cg43966621	451	AGAGCGGGGAA ATGGGGAGCCC ATA[C/A]CCAAAG CCAGCCAGCGG GGTTCCCC	C	A	Gly	Gly	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.pcls:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.80E-219	17
256	cg38438124	346	CGACCCCGGC AACCTAGGGTCC TC[T/C]GTCCTGG CGAGCAAGACCA AGACCA	T	C	Ser	Ser	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.80E-216	10
257	cg43917871	2435	AGTATTCTCGAG GTCTGTGTGTAT T[A/G]ACATCTGT GTAAACTCTGGC CCTGC	A	G	Val	Val	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
258	cg43924218	902	TTGCAGCAGTAG AGAAGAATGGTG G[C/A]TACAACCA ACTCTGTGATAT CTGGG	C	A	Gly	Gly	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	1E-203	
259	cg43982823	940	TTGTAAAGTCAT TCCTCTTCCAGC T[A/T]CTAAAGG GCTGGGATTCTG TCATA	A	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

260	cg43969473	3923	TCACCTGGCAAG CTCTCGGGGCA CT[C/T]TGTCGGA TAGTGAAATTGA GACCAA	C	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q27467 SIMILARITY TO TYROSINE-PROTEIN KINASE - CAENORHABDITIS ELEGANS, 1280 aa.	2.1E-154	11
261	cg43958362	2164	GGCCACCATGC CGCTCCAGCGC GGC[G/C]CGCTC ACTGCTGGTATT GCCCATGA	G	C	Arg	Arg	SILENT- CODING	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.10E-147	12
262	cg42925992	327	TTGCAGTTGTGC AGCAAGAAATTA T[C/T]ATGATGAA AGACTGTAAACA CCCAA	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene Homologous to SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	5.10E-105	
263	cg44033347	719	GGTGGATGCTG CTGTGCTGGCCC CC[G/A]TCTGCC CAGCTCACCCAGC TCACTGC	G	A	Asp	Asp	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:O00746 NUCLEOSIDE DIPHOSPHATE KINASE, MITOCHONDRIAL PRECURSOR (EC 2.7.4.6) (NDP KINASE, MITOCHONDRIAL) (NDK) (NM23-H4) - HOMO SAPIENS (HUMAN), 187 aa. [pcis:SPTREMBL-ID:O00746 NUCLEOSIDE-DIPHOSPHATE KINASE (EC 2.7.4.6) (NUCLEOSIDE 5'- DIPHOSPHATE PHOSPHOTRANSFERASE) (NDK) - HOMO SAPIENS (HUMAN), 187 aa.	9.10E-99	16

264	cg43966625	337	CCGACCGAGTG CTGAGCACACCC TC[C/T]GTGCAGC TGGTGCAGAGCT GGTATG	C	T	Ser	Ser	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.[pcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407.aa.	3.20E-89	17
265	cg43918784	1346	CTTCTTCTCTGT CTGCAACACACT G[A/G]TCAAGAT TTCACCCCCAGC AGCAT	A	G	Asp	Asp	SILENT- CODING	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
266	cg43933456	286	ATAGTAAGTTT CATCAGTAGCTT C[T/C]TGATAAG GTAATGCACATG TCCTT	T	C	Gln	Gln	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P35169 PHOSPHATIDYLINOSITOL 3- KINASE TOR1 (EC 2.7.1.137) (PI3- KINASE) (PTDINS-3-KINASE) (PI3K) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 2470 aa.	2.10E-57	3
267	cg43105476	550	CCAGGAACTCCA CCACCCGGAGG TG[G/A]CCTTCTT TGGCAGCCCAAGT GCAAGG	G	A	Gly	Gly	SILENT- CODING	kinaseinh ibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
268	cg44931523	926	CCGTCATCTGGG CCACCAGGTCAA A[A/G]GATGCAAA CCCCGCACTGAC GAAGC	A	G	Ser	Ser	SILENT- CODING	kinaserec eptor	Human Gene SWISSPROT-ID:P54753 EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HEK-2) - HOMO SAPIENS (HUMAN), 998 aa.	0.00E+00	3
269	cg43048869	2392	GTAAC TTGGTGT GTAAGGTTTCTG A[C/T]TTCGGACT CTCGCGGGTACT GGAAG	C	T	Asp	Asp	SILENT- CODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29320 EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (HEK) - HOMO SAPIENS (HUMAN), 983 aa.	0	

270	cg43935828	1884	AGGGCCGCCCC CTGCTCATGGTC TT[C/T]GAGTATA TGCGGCACGGG GACCTCA	C	T	Phe	Phe	SILENT- CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140- TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.lpcis:SWISSPROT- ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	
271	cg43935828	1835	ACCGCTTCCTCC GATCCCATGGAC C[C/T]GATGCCAA GCTGCTGGCTG GTGGGG	C	T	Pro	Pro	SILENT- CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140- TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.lpcis:SWISSPROT- ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	

272	cg43935828	2004	CCCTGGGTCTG GGCAGCTGCT GGC[C/T]GTGGC TAGCCAGGTCCG TGCGGGGA	C	T	Ala	Ala	SILENT- CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140- TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.[pcis:SWISSPROT- ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	0
273	cg43991478	1342	CGTCAGCAAGAT TGTGGGGCTGC AG[C/G]CGGGTG AGGTCACGCAG GATGGTGC	C	G	Arg	Arg	SILENT- CODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
274	cg43263845	668	GTAATGAAAAGT TTTCTTAJTTC [G/A]GAGATGGA AGTCACACAGCC CACTT	G	A	Pro	Pro	SILENT- CODING	kinaserec eptor	Human Gene TREMBLNEW-ID:G247985 ACTIVIN RECEPTOR, ACTRIIB=TRANSMEMBRANE PROTEIN SERINE KINASE - XENOPUS LAEVIS, 510 aa.	3.30E-204	2
275	cg43999555	1415	GCGGATCGTGG AGAACCTGGGCA TC[C/T]TGACCGG GCCGCAGCTCTT CTCCCT	C	T	Leu	Leu	SILENT- CODING	kinaserec eptor	Human Gene Similar to SWISSPROT- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa.[pcis:SPTREMBL- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa.	1.20E-99	11
276	cg43975720	5392	CCTCTCCTGCCA GACAGCCCCACG AC[C/T]GGGTCTG ACCCCCCAGGG GACGCCCA	C	T	Thr	Thr	SILENT- CODING 103	kinesin	Human Gene SWISSPROT-ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2

277	cg43987378	967	CAGCCCTGTCAA GCAGCCCAAGCA GA[G/A]GTGGCA TCTCTGCGGCAG GAGACTG	G	A	Glu	Glu	SILENT- CODING	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.50E-254	6
278	cg44009224	123	GCTACAGTTCAC AGCAGCAAAGG GT[A/G]CCATTTC TTCAGCCTCCCG GTCAAA	A	G	Val	Val	SILENT- CODING	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0.00E+00	
279	cg42488873	988	CATGCACGTCTC CAAGGCTGTACC C[C/T]AGCTGCGT CGACAGTGCTTG TATTA	C	T	Leu	Leu	SILENT- CODING	lipase	Human Gene SWISSPROT-ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
280	cg42488873	202	GATTTATCCAC GTTTGTTCAGA G[A/G]AATTAAAC TTTCTGTATTTT CCAA	A	G	Phe	Phe	SILENT- CODING	lipase	Human Gene SWISSPROT-ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
281	cg42686658	452	ACTTTGCCCGCT TTGACCCGCAGG G[C/T]GGGCTGG CCGGCATCGCC GCAATCA	C	T	Gly	Gly	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN- ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134 (6p21.3)	6
282	cg42686658	860	CACCAGATGCCA TGGAGACCCTG GT[C/T]TGTGCCC TGGGCCTGGCC ATCGGCC	C	T	Val	Val	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN- ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.7E-134 (6p21.3)	6
283	cg42928872	389	TGAGCCTAGACC CGCGGCTCTCCA T[C/T]TACAGCAC GGCCGCCCGG TGTTGG	C	T	Ile	Ile	SILENT- CODING	misc_cha nnel	Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0	11

284	cg43311602	5361	CTCGCCCCGCC GGCTACCCAG CAC[A/G]GTCAG CACTGTGGAGG GCCACGGGC	A	G	Thr	Thr	SILENT- CODING	misc_cha nnel	Human Gene SPTREMBL-ID:Q13930 VOLTAGE-DEPENDENT L-TYPE CA CHANNEL ALPHA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 2173 aa.	0	12 (12p13.3)
285	cg43111577	175	TGGAACACAGCA CAGAGATGGAG GC[A/G]GAGGTG GAACCAGAACCG AATCCTG	A	G	Ala	Ala	SILENT- CODING	misc_cha nnel	Human Gene TREMBLNEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa.	0	16 (16q13)
286	cg21657051	5819	AAGGCATGAGG GTGGTTGTGAAT GC[C/T]CTTGTTA GGAGCAATTCCC TCTATC	C	T	Ala	Ala	SILENT- CODING	misc_cha nnel	Human Gene TREMBLNEW- ID:G2665784 VOLTAGE-GATED SODIUM CHANNEL, SUBTYPE III - HOMO SAPIENS (HUMAN), 1366 aa (fragment).	0	
287	cg42684570	1186	CCGAGTAGCCCA GGAGGAGTGTA T[C/T]TTGAAAGA GACCCCTCTCGCC ACTGT	C	T	Lys	Lys	SILENT- CODING	misc_cha nnel	Human Gene SWISSPROT-ID:P46098 5- HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN- GATED ION CHANNEL RECEPTOR) - HOMO SAPIENS (HUMAN), 478 aa.	1.8E-260	11 (11q23.1)
288	cg44021559	2938	TCCTGTCAATTAG GGATGACGTGG GT[A/G]CCATTGT AGATGCCCACTT GCACCA	A	G	Gly	Gly	SILENT- CODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)
289	cg44021559	2989	GCTTGCGGTTCT GCAGGTTTCATGA T[A/G]CTATAGTT GGCGAACTTCCG GTCCC	A	G	Ser	Ser	SILENT- CODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)
290	cg44021559	2992	TGCGGTTCTGCA GGTTCATGATAC T[A/G]TAGTTGGC GAACCTCCGGTC CCCAT	A	G	Tyr	Tyr	SILENT- CODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)

291	cg44929972	1029	AAAAGCTTGAGA TGCATTTCCATA A[G/A]CTTCCAAG CCTCCTCTCTTG TGATG	G	A	Lys	Lys	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
292	cg44929972	1044	ATTCCATAAGC TTCCAAGCCTCC TTC/TCTCTTGTA TGATGTAAACAT GAGAA	C	T	Leu	Leu	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
293	cg44929972	1071	CTTGTGATGATG TAAACATGAGAA TIA/TGCTGCTGG TGAATCTTTGGC ACTTC	A	T	Ile	Ile	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
294	cg44929972	1080	ATGTAACATGA GAATAGCTGCTG GT/C/GAATCTTT GGCACTTCTCTT TGAAT	T	C	Gly	Gly	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
295	cg44929972	1098	CTGCTGGTGAAT CTTTGGCACTTC TIC/G/TTTGAATT GGCCAGAGGAA TAGAGA	C	G	Leu	Leu	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
296	cg44929972	1143	TAGAGAGTGACT TTTTTTATGAAGA [C/T]ATGGAGTCC TTGACGCAGATG CTTA	C	T	Asp	Asp	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
297	cg44929972	1158	TTTATGAAGACA TGGAGTCCCTTGA C[G/C]CAGATGC TTAGGGCCCTTG CAAACAG	G	C	Thr	Thr	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7

298	cg44929972	1167	ACATGGAGTCCT TGACGCAGATGC TTT/CJAGGGCCTT GGCAACACAGATG GAAATA	T	C	Leu	Leu	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
299	cg44929972	1173	AGTCCTTGACGC AGATGCTTAGGG C/C/TJTTGGCAAC AGATGGAAATAA ACACC	C	T	Ala	Ala	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
300	cg44929972	1179	TGACGCAGATGC TTAGGGCCTTGG C/A/TJACAGATGG AAATAAACACCCG GGCCA	A	T	Ala	Ala	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
301	cg44929972	1230	AAGTGGACAAGA GAAAGCAGCGG TC[A/T]GTTTCA GAGATGTCCTGA GGGCAG	A	T	Ser	Ser	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
302	cg44929972	1242	GAAAGCAGCGG TCAGTTTTCAGA GA/T/CJGTCCTGA GGGCAGTGGAG GAACGGG	T	C	Asp	Asp	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
303	cg44929972	1245	AGCAGCGGTCA GTTTTTCAGAGAT GT/C/TJCTGAGG GCAGTGGAGGA ACGGGATT	C	T	Val	Val	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
304	cg43921419	1269	GTGGAGATCCTT TTAGTGCAGATG A/C/TJATACCTTT TCCTGTCTCTTCA GTCCC	C	T	Asp	Asp	SILENT- CODING	nuc_lrec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN); 835 aa.	0	19

305	cg43249083	633	CGCTCTCAGCTG GTGAAGACATGA CIG/CJACCCTGG ACTCCAACAACA ACACAG	G	C	Thr	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P20393 V- ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0	17 (17q11.2)
306	cg43315956	2680	TCAGGAATGACA GGAACAAGAAA AIG/AJAAGGAGA CTTCGAAGCAAG AATGCA	G	A	Lys	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
307	cg43935583	1416	TGGAGGGGGC ATGCCTGGAATG GC[T/C]GGAATG CCTGGACTCAAT GAAATTC	T	C	Ala	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
308	cg43935583	1563	AGAGCAACCCAA AGGTTATGAATC TIC/TJATCAGTAA ATTGTCAGCCAA ATTIG	C	T	Leu	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.30E-195	22
309	cg42933859	233	TACTCTGTATTAA CTCTTCCTTTGA G/AJAGTTTGGAA GGTGAAGCATTT TGAT	G	A	Leu	SILENT- CODING	nucl_rec pt	Human Gene Similar to SPTREMBL- ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.20E-51	17
310	cg44926604	827	CTCACAGCTGCT CAAATGGGAACA G[A/G]TGGGAAG CTGCTGCTTTCT TTTCCC	A	G	His	SILENT- CODING	nuclease	Human Gene SWISSPROT-ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) HOMO SAPIENS (HUMAN), 939 aa.	0.00E+00	3

311	cg44128653	1448	CGTAGGTACAGG CGCTATGAGGCC A[G/A]CTGTATGC AGCAGAGGAGG CCGGTG	G	A	Ser	Ser	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa. pcis:SWISSPROT- ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.40E-203	19
312	cg43952559	211	GAATGTTAACTG ACTTAAGAGCCA TT[C/A]ATTTCAGT TATACAACTAT GGGAG	T	C	Ile	Ile	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
313	cg43952559	235	TTAATTCAGTTAT ACAACCTATGGG [A/G]GCATTACAG CCAGGATTGCCT TCTC	A	G	Gly	Gly	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	

314	cg43952559	251	ACCTATGGGAGC ATTACAGCCAGG ATTCTGCCTTCT CCTGCTATGATT CCAAA	T	C	Leu	Leu	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
315	cg43952559	884	TAACAAAGGAGG CGGAGGCAGAG TTT[A/G]CAACTGA TCGAGAAGCAAG TCCATA	A	G	Leu	Leu	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
316	cg43952559	896	CGGAGGCAGAG TTACAACTGATC GA[G/A]AAGCAA GTCCATAAAGCT CAAATAA	G	A	Glu	Glu	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	

317	cg43952559	914	TGATCGAGAAGC AAGTCCATAAAG C[T/C]CAAATAAA TAGAATAGATCC AGAGA	T	C	Ala	Ala	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
318	cg43943773	407	TATTGAGTTCAT CATTAAAGTCAT C[T/G]ATTTTCAA CCTGAGTGTCGG GAGGG	T	G	Ile	Ile	SILENT- CODING	nuclease nhib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
319	cg43943851	851	TTGTAAGTGTGA ACTGTGCCCGG CT[G/C]CTGAAAG CCGACCACCATG CAACCA	G	C	Leu	Leu	SILENT- CODING	oncogen e	Human Gene SWISSPROT-ID:Q15582 TRANSFORMING GROWTH FACTOR- BETA INDUCED PROTEIN IG-H3 PRECURSOR (BETA IG-H3) (KERATO- EPITHELIN) - HOMO SAPIENS (HUMAN), 683 aa.	0.00E+00	5 (5q31)
320	cg44012756	2265	GGACCAACTGTG ACATCAACAACA A[T/C]GAGTGTGA ATCCAACCCCTTG TGTC	T	C	Asn	Asn	SILENT- CODING	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0.00E+00	
321	cg42827675	215	CAGCCCCGGGC ATGTTCCGAGAC TT[C/T]GGGGAAC CCGGCCCCGAGC TCCGGGA	C	T	Phe	Phe	SILENT- CODING	oncogen e	Human Gene Homologous to SWISSPROT-ID:P15407 FOS-RELATED ANTIGEN 1 - HOMO SAPIENS (HUMAN), 271 aa.	6.40E-146	11

322	cg43964295	4723	TATCACAGTACA GGCCTTGCCAG CC[G]A]TACTGG CACCTGCAGTCA CCTGGGA	G	A	Tyr	Tyr	SILENT- CODING	oncogen e	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1984 aa.	4.80E-120	20
323	cg43916615	130	TGACCATCCAGC TGATCCAGAACC A[C/T]TTTGTGGA CGAATACGACCC CACTA	C	T	His	His	SILENT- CODING	oncogen e	Human Gene Similar to TREMBLNEW- ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa.	3.10E-98	
324	cg42904626	640	AACATAAAGAAA AGATGAGCAAAG A[C/T]GGTAAAAA GAAGAAAAAGAA GTCAA	C	T	Asp	Asp	SILENT- CODING	oncogen e	Human Gene Similar to SWISSPROT- ID:P01118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.1E-97	12
325	cg44029157	533	GCTTCCTGCTGG TGTTCCGCCATTA ATT[C]GACCGGC AGAGTTTCAACG AGGTGG	T	C	Asn	Asn	SILENT- CODING	oncogen e	Human Gene Similar to SWISSPROT- ID:P17082 RAS-RELATED PROTEIN R- RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.1E-66	
326	cg43975131	4247	TCCTTCTTCTTCA GGCGCTCGATG GC[C/A]CGGCTC TGGCCTTTGTTG GCTTICT	C	A	Arg	Arg	SILENT- CODING	oncogen e	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.8E-64 (17p13.3)	17
327	cg43307658	1322	CCGGCTTCGAG CAGGCCTACCCT GA[T/C]CCCGGT CCCGAGGCGGC GCAGGCCCC	T	C	Asp	Asp	SILENT- CODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15

328	cg43307658	1514	GCGCGCAGCAG GGCCGCCTCAG CGT[G/A]GGCAG CGTGTACCGGC CCAACCAGA	G	A	Val	Val	SILENT- CODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15
329	cg44028217	1031	GCACCAGCACCT GGCCCTTCAGCC C[C/T]GCATAGAA GTTGAAGCCACC TTTAA	C	T	Ala	Ala	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
330	cg44028217	471	GGTAGATGCTGC TGCTGCACAGCT C[C/T]GACTCCC GGTACTTGGTCA CTGCCA	C	T	Ser	Ser	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
331	cg44028217	638	GGGGGCTGGTA AAGAGCAGGTAC TT[A/G]GGCAGCT TCCTTTTGAAGC GGAAGG	A	G	Pro	Pro	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)

332	cg44028217	725	GAGTTGGCTGGA CCACGCGGTGT CTT[C]GGGCTC CAGGGGTTGGT GATGTTTT	T	C	Pro	Pro	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
333	cg43271573	1320	GGGCTGTTCTGA GTCCTGAAAGGT GT[A/G]AATAAGT TACCACCACCAA GTGTCA	A	G	Val	Val	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:Q01740 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) - HOMO SAPIENS (HUMAN), 531 aa.	5.30E-293	1 (1q23)
334	cg43051423	618	ATCGCAGGTAGT GATAGCCTGAGG ATT[A/J]CCCCCAGT GCCAGCCTTGCT GCCTA	T	A	Gly	Gly	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
335	cg43051423	633	AGCCTGAGGATC CCCCAGTGCCA GC[C/T]TTGCTGC CTAGCATCCTGT GCACCA	C	T	Lys	Lys	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4

336	cg43051423	642	ATCCCCCAGTGC CAGCCTTGCTGC C[T/C]AGCATCCT GTGCACCATGCA CACAT	T	C	Leu	Leu	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
337	cg43051423	648	CAGTGCCAGCCT TGCTGCCTAGCA T[C/T]CTGTGCAC CATGCACACATG GTTAT	C	T	Arg	Arg	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
338	cg43972840	190	ACCAAATGAGAA TGGCTGACCTCT C[G/A]GAGCTCC TGAAGGAAGGG ACCAAGG	G	A	Ser	Ser	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.60E-168 (16p13.3)	16
339	cg43254736	905	AGCAGTTGGTGT GCAGGTAGTTGA A[A/G]TCGGACAT GCCTCCCGTGAA GCTGT	A	G	Asp	Asp	SILENT- CODING	peptidase	Human Gene Similar to SPTREMBL-ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.10E-67	
340	cg41626506	1029	TGCTGTCACAAG ACTCAAAGTCTT C[G/A]GGGAATTT GCCGACTTGGAA GGCAT	G	A	Pro	Pro	SILENT- CODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00 (3q26.3)	3
341	cg41626506	1176	TGTTCTCCCACC AAAACCAAGTCAC C[G/A]TCCCGCA GAGCCTTCATCT GCTTCC	G	A	Asp	Asp	SILENT- CODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00 (3q26.3)	3

342	cg40084915	1911	GGACGTCCTGCG TGCGGTTCTTGT CIGAJCGGTTCC GGGGCAACAGG GCGATGC	G	A	Arg	Arg	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa.	0.00E+00	1
343	cg43956369	4272	CAGTCTGGGA GGTCCAGCCACT GG[G/A]ACTGCA GGATCAAATGAT CTTATAC	G	A	Val	Val	SILENT- CODING	phosphat ase	Human Gene SWISSNEW-ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R- PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa. pcls:SWISSPROT- ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa.	0.00E+00	6
344	cg43917453	3092	CGAGAACCTCCA CGTCAGCGAAC GC[A/G]CTGCTG GGCACCTGCAG GAGGCGGG	A	G	Ser	Ser	SILENT- CODING	phosphat ase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
345	cg43920534	4634	TTTTGTTCTTTT GCAACTCTTCTA G[A]ATATCCCA AATGTCTTCATC TGCT	G	A	Leu	Leu	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
346	cg43920534	4641	TCTTTTGCAACT CTTCTAGATATC C[C/T]AAAATGTC TTCATCTGCTAC ATCAA	C	T	Leu	Leu	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
347	cg43920534	4749	TCCAACATGCTT CTTCTTTACCCC A[G/A]TGAGCTG CAGCATGAAGAG GTGTCC	G	A	His	His	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12

348	cg43920534	4785	CATGAAGAGGTG TCCAGCCATCAT A[A/G]TCTTTAAT ATTAACATCATA GCCTG	A	G	Asp	Asp	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
349	cg43920534	4836	CCTGTATTAAAA GTTTTAAACTTC TTCTGTATACCCCT TTGGCCGCTGCC ACGT	T	C	Thr	Thr	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
350	cg43920534	4842	TTAAAAGTTTAA AACTTCTGTATA C/GJCCTTTGGCC GCTGCCACGTG GAGTG	C	G	Gly	Gly	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
351	cg43920534	4851	TTAAAACCTTCTGT ATACCCCTTTGGC C/AJGCTGCCACG TGGAGTGCTGTG CCTC	C	A	Ala	Ala	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
352	cg43920534	4857	CTTCTGTATACC CTTTGGCCGCTG C/C/AJACGTGGA GTGCTGTGCCTC CGGATT	C	A	Val	Val	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
353	cg43920534	4863	TATACCCCTTTGG CCGCTGCCACGT G/G/AJAGTGCTG TGCCTCCGGATT TTGCAT	G	A	Leu	Leu	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12

354	cg43920534	4872	TGGCCGCTGCC ACGTGGAGTGCT GT[G/A]CCTCCG GATTTGTCATGC CGGACAT	G	A	Gly	Gly	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
355	cg43920534	4878	CTGCCACGTGGA GTGCTGTGCCTC C[G/A]GATTTTGC ATGCCGGACATC ATTTA	G	A	Ser	Ser	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
356	cg43321833	2271	CTAACACTGTGG AACCAGAGAAGC A[A/G]GGGGAGA ACACCATGAAGA TGACTG	A	G	Gln	Gln	SILENT- CODING	phosphatase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0.00E+00	20
357	cg43326090	1070	CATCATCTACAT TGGAGAGCTTCA C[AT]CGCGTGG CATCATAGGGCA ATATA	A	T	Arg	Arg	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:P23467 PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.1.3.48) (R- PTP- BETA) - HOMO SAPIENS (HUMAN), 1997 aa.	0.00E+00 (12q15)	12
358	cg42548845	1611	TGAAAAAGCTCA TCGAAGAGAAGG A[C/T]TTTCAAAT GCTGTATGCATA TGATC	C	T	Asp	Asp	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	0.00E+00	
359	cg43918944	997	TCCGGACACTTC CTCCAAGTGATA A[C/T]CCAGACTT TGACCCCGGAAGA GGATG	C	T	Asn	Asn	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
360	cg43918944	1003	CACTTCCTCCAA GTGATAACCCAG A[C/T]TTTGACCC GGAAGAGGATG AGCCCA	C	T	Asp	Asp	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1

361	cg43918944	1009	CTCCAAGTGATA ACCCAGACTTTG A[C/T]CCGGAAG AGGATGAGCCCA CACTTG	C	T	Asp	Asp	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
362	cg43918944	1012	CAAGTGATAACC CAGACTTTGACC C[G/A]GAAGAGG ATGAGCCACAC TTGAGG	G	A	Pro	Pro	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
363	cg43918944	1024	CAGACTTTGACC CGGAAGAGGAT GA[G/A]CCCCACA CTTGAGGCCTCT TGGCCTC	G	A	Glu	Glu	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
364	cg43918944	1030	TTGACCCGGAAG AGGATGAGCCCA C[A/G]CTTGAGG CCTCTTGGCCTC ACATAC	A	G	Thr	Thr	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
365	cg43918944	1084	TGGTGTATGAAT TCCTCTTGAGAT T[C/T]TTGGAGAG TCCTGATTTCCT GCCCCA	C	T	Phe	Phe	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
366	cg43918944	1108	TCCTGGAGAGTC CTGATTTCAGC C[C/T]AGCATTGC AAAGCGATACAT TGACC	C	T	Pro	Pro	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
367	cg43918944	976	AAATGATCAGTG CTACATCTTCC G[G/T]ACACTTCC TCCAAGTGATAA CCCAG	G	T	Arg	Arg	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1

368	cg43988504	819	CTTCTGTCTGGC TGATACCTGCCT C[T/C]TGCTGATG GACAAGAGGAAA GACCC	T	C	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
369	cg43988504	900	AGAAATGAGGAA GTTTCGGATGGG G[C/T]TGATCCAG ACAGCCGACCA GCTGCG	C	T	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
370	cg43933809	4446	CAAATAATCTCA GTAAATCTGTAT A[T/C]TGTCCATG AATATCTCCACA AATTT	T	C	Gln	Gln	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS.MUSCULUS (MOUSE), 327 aa.	1.60E-181	2 (2p23)
371	cg43269274	1510	CAGCCTCACAGT GGACCAGGACC TT[G/T]CCTCCCT TTCCCTGACAC AGTCAA	G	T	Gly	Gly	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.20E-151	10
372	cg43269274	1674	ACATTCAGCAGG GCTGTGATGTGC A[A/G]GTTGGCG AGGAACCTCGCAC TTGGAT	A	G	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.20E-151	10

373	cg44021995	2412	TTTTAAGTAAAGT AGTGGACAGCCT [G/A]GCCCCATC CATTACTAATGTT TTAG	A	Leu	Leu	SILENT- CODING	phosphor ylase	Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.[pcls:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.	0.00E+00	16
374	cg42688448	1787	GAGGAGCACCT GTGGGGGTTGC AGG[A/G]CGAGG CGCCATGGTAGT CTGAGGCT	G	Arg	Arg	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
375	cg42688448	1790	GAGCACCTGTG GGGGTTGCAGG ACG[A/G]GGCGC CATGGTAGTCTG AGGCTGGG	G	Pro	Pro	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
376	cg42688448	1793	CACCTGTGGG GTTGCAGGACGA GG[C/T]GCCATG GTAGTCTGAGGC TGGGCAT	T	Ala	Ala	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
377	cg42688448	1826	TAGTCTGAGGCT GGGCATGGGCA TG[G/C]GCCCTGC ATCTGGGCCAAG GCCTGCT	C	Ala	Ala	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
378	cg42688448	1856	GCATCTGGGCCA AGGCCTGCTGA GG[A/G]ATCATT ACAACTGCCCAT TCTCAC	G	Ile	Ile	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20

379	cg42688448	1940	AGTTCTGGATGT TGGTCGGGTTCT G[A/C]GGCGGCT GCGGCAAGCGC GGGGCCA	A	C	Pro	Pro	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
380	cg42688448	1954	GTCGGGTTCTGA GGCGGCTGCGG CA[A/G]GCGCGG GGCCAGCACGG TGGGCGTC	A	G	Leu	Leu	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
381	cg43968623	801	TCTTGAAGATG AACTGCAGCGTA T[A/C]AAACTAAA AGGCACCATTTGA AGTGT	A	C	Ile	Ile	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.[pcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7.00E-199	
382	cg43311989	248	ACTTCGAATAAA GTTGTTCCAATG A[G/A]GACTGCAT AGTTTCCAAATA ACCAG	G	A	Ser	Ser	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00419 MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 372 aa.	1.90E-197	
383	cg43993893	502	ACTCATTGATTG TGAAACCCCTTTT C[T/C]AGGGCAT GAGCCCTCATAT TCTTAT	T	C	Leu	Leu	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.[pcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178	8 (8p11.2)
384	cg43993893	679	CCATGAACCTTG TCTCACCCCTTTG A[C/A]AGGGTATC TGTGATAAAATG AACCT	C	A	Leu	Leu	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.[pcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178	8 (8p11.2)

385	cg43993893	877	AATCCACTTTTT AACTTCATTTAG T/AJACAATATCTT GCATTTGTAACA TCT	T	A	Val	Val	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. pcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178	8 (8p11.2)
386	cg43916712	4150	TGTGAGCAATGA ATTCATCATGAA G[G/AJACTGAGG AATTGGCATCAA TCTGAA	G	A	Val	Val	SILENT- CODING	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.20E-148	
387	cg42876552	418	CTTCTGCAAT CAATAGGCACAG ATT/GIATGCGACC TGTTTTAGGATG AACAC	T	G	Ile	Ile	SILENT- CODING	polymera se	Human Gene Similar to SWISSPROT- ID:Q24317 DNA PRIMASE SMALL SUBUNIT (EC 2.7.7.-) (DNA PRIMASE 50 KD SUBUNIT) (DNA POLYMERASE SUBUNIT A) (DPR150) - DROSOPHILA MELANOGASTER (FRUIT FLY), 438 aa.	2.20E-88	12 (12q13)
388	cg43948227	366	TCGAATTTTACA GTTTCTTACTG C[A/GJTCATCAAT GTCAGAAATCTG TTCCT	A	G	Asp	Asp	SILENT- CODING	polymera se	Human Gene Similar to SWISSNEW- ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa. pcis:SWISSPROT-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5
389	cg42534568	612	AGCGCGTCCACA TCAACATCTCCG G[G/CJCTGCGCT TTGAGACGCAGC TGGGCA	G	C	Gly	Gly	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)

390	cg42937321	1388	ATATGCACCCAG TGACCATAGGG G[C/G]AAGATTGT GGGATCTCTCTG TGCCA	C	G	Gly	Gly	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
391	cg42937321	353	AGCGCGTGGTC ATCAACATCTCC GG[G/C]CTGCGC TTCGAGACGCAG CTGAAGA	G	C	Gly	Gly	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
392	cg43331104	878	CCTTCTTCATCG TGGAACGCTGT G[T/C]ATCATCTG GTTCTCCTTCGA GCTGG	T	C	Cys	Cys	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:Q09470 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1) - HOMO SAPIENS (HUMAN), 495 aa.	5.60E-266	12
393	cg43992375	3210	GATTCACCTGGAT TTTGGCAGACCC A[A/G]CTTGGGG CTCGGGATGTCT GCACAG	A	G	Leu	Leu	SILENT- CODING	potassiu m_chann el	Human Gene SPTREMBL-ID:Q16547 POTASSIUM CHANNEL BETA3 SUBUNIT - HOMO SAPIENS (HUMAN), 408 aa.	1.30E-218	3
394	cg43951368	505	TTCGAAATGCAA TTATGAGTTATG T[G/C]TTGACATC CAGATCACATTT GATTG	G	C	Val	Val	SILENT- CODING	prostagla ndin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa. pcls:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)

395	cg43986296	1743	ACTCATCCCCGA CATCCCTGATGA C/A/CJAGCCTGTA GGTCCCTCGGG CTCTCT	A	C	Leu	Leu	SILENT- CODING	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
396	cg43982119	1306	GCTTGGTTTTTT CTTTTGACTGG T/CJCGATCCAGG CAGATGGTATTT TCAA	T	C	Arg	Arg	SILENT- CODING	protease	Human Gene SWISSPROT-ID:P20807 CALPAIN P94, LARGE (CATALYTIC) SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE- SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT) - HOMO SAPIENS (HUMAN), 821 aa.	5.70E-161	15
397	cg43306871	1105	GCTCGCCCTGAA GAAGCAGCAGG TG[G/A]TCATCCC CTACTCGAGCCC ACAGTG	G	A	Asp	Asp	SILENT- CODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. pcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
398	cg43923853	2273	CAGACCGAGATG TCATTCCAGTGC T[T/C]TTATGAA ATTCTTATTATTA ATTA	T	C	Lys	Lys	SILENT- CODING	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa. pcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

399	cg43074055	916	CCCTCTACGTGG ACTGGATCCGTT C[C]TACGCTGC GCCGTGTGGAG GCCAAGG	C	T	Ser	Ser	SILENT- CODING	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.70E-138	19 (19p13.3)
400	cg43967243	387	TCTCTGCTTCTG TAAGAATCCTGA ATT/CJT TAGGATT TTCAACTGTCAC TACTC	T	C	Lys	Lys	SILENT- CODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa. pcls:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130	

401	cg43967243	489	ATGTAATTGCAG TTTCCACTGTCT GTTCTCAAATGT CCAATCAAATTT CTTCT	T	C	Glu	Glu	SILENT- CODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa. pcis:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130	
402	cg43930253	972	CCACATATATAA ACCATGTCGTTT CCTTGTGGCTG GGTGGGGCATC AGTGATG	C	T	Ser	Ser	SILENT- CODING	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
403	cg42914280	589	GCAAGCCCAGG TGTTGGAGTTCCT GACTTGTGGTC ACTTCAGAACCT TTCCTG	C	T	Asp	Asp	SILENT- CODING	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.30E-63	11 (11q23)

404	cg43920929	1459	GATTGTCAATCA TATCCCTGGTT C[A/G]TTTTTAAC CCATGCATTGAT GGAAT	A	G	Asn	Asn	SILENT- CODING	protease nhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
405	cg43920929	1705	TTACGCCGTATC TCATCACCATGG C[G/A]AGCTGCTT CTTGGTCCTGCC GTCCG	G	A	Leu	Leu	SILENT- CODING	protease nhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
406	cg43268468	512	GCAGGGACTTG GTGACTTCGCCT TC[G/A]TAACTCA GCTTCAGCTTGG GGACAG	G	A	Tyr	Tyr	SILENT- CODING	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188 (17p13.3)	17
407	cg43059041	1182	TCACCATCTCTG GAGTCTATGACC TTT[C/G]GAGATGT GCTGGAGGAAAT GGGCA	T	C	Leu	Leu	SILENT- CODING	protease nhib	Human Gene Similar to SWISSPROT- ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83 (14q32.1)	14
408	cg43059041	1440	ACTTCACCTGGA GCAGCCTTTTCC TT[G/A]GCGAGGG TTATGAACCCAG TGTAAG	G	A	Leu	Leu	SILENT- CODING	protease nhib	Human Gene Similar to SWISSPROT- ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83 (14q32.1)	14
409	cg43969711	1750	AGAGAAATCCC TTTCTTTGGGAT C[C/T]TTTATGTA AGTGTCATAAAG AAGAC	C	T	Lys	Lys	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208 2 (2p25)	2 (2p25)
410	cg43969711	1984	AGTGCTGAATGT CCTTGAGAGGT C[C/A]ACCTCCTC GGCGGTCCAAA GGAAG	C	A	Val	Val	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208 2 (2p25)	2 (2p25)

411	cg43969711	2158	GCTCCGTGGC TCCTGGAAGATC CTT/CJCTCGCG GTCCTGCTGGCC AGGACGC	T	C	Arg	Arg	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)
412	cg43941472	701	TCATTGAGTGTG CCGACTCTGCC ATT/CJGGCCTGAA GGCCACATCAT CTCTG	T	C	His	His	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
413	cg43987538	1820	CTGATCGCAATT TCAGGACTTCTG GTC/TCCACCAA TTCAAAACTCT AACAG	C	T	Gly	Gly	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.1E-171	1 (1p31)
414	cg43286949	355	AATATCTGTTTC GTTTAGACCAG GTC/TCCCTTTTC TTCAATCCATGA CAGTG	C	T	Gly	Gly	SILENT- CODING	reductas e	Human Gene SWISSNEW-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa. pcls:SWISSPROT-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7
415	cg43336298	1175	CCATCTCTACAT ATAACAGAACCG GTC/CJCCACTTCC CCCAGGCCCCAC CCCCAG	T	C	Gly	Gly	SILENT- CODING	reductas e	Human Gene Homologous to TREMBLNEW-ID:G2947100 15- OXOPROSTAGLANDIN 13- REDUCTASE - SUS SCROFA (PIG), 329 aa.	6.70E-146	
416	cg43948290	715	TAATAGGTTTGT GCTTGTGGTTAA C/A/GJGGCATGTT GATAAACATCCA TTCAG	A	G	Thr	Thr	SILENT- CODING	reductas e	Human Gene Homologous to SWISSPROT-ID:P18405 3-OXO-5- ALPHA-STEROID 4-DEHYDROGENASE 1 (EC 1.3.99.5) (STEROID 5-ALPHA- REDUCTASE 1) (SR TYPE 1) - HOMO SAPIENS (HUMAN), 259 aa.	2.90E-141	5 (5p15)

417	cg42717608	109	CGCAGCTTAATG TGGCCTTTTCCC G[G/T]GAGCAGG CCACAAAGGTCT ATGTCC	G	T	Arg	Arg	SILENT- CODING	reductase	Human Gene Similar to SWISSNEW- ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa. pcls:SWISSPROT-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa.	1.80E-51	
418	cg43257152	622	CTACCAAGACTT TGAGATCACTA C[A/G]AGAAAAAC TCCTTGTGGTGA AGGTT	A	G	Thr	Thr	SILENT- CODING	ribosomal prot	Human Gene Similar to SWISSPROT- ID:P17075 40S RIBOSOMAL PROTEIN S20 - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 119 aa.	8.2E-59	3
419	cg44937448	365	TCCTGTTACCA ACCGCACAAAGG A[G/A]GAGGTGA ATGAGTGGTTCA CGAAAT	G	A	Glu	Glu	SILENT- CODING	ribosomal prot	Human Gene Similar to SPTREMBL- ID:Q19302 SIMILAR TO 60S ACIDIC RIBOSOMAL PROTEIN PO - CAENORHABDITIS ELEGANS, 220 aa.	5.3E-55	7
420	cg43255045	5515	GCGAGGAGGAA CAGCTACGCCAG GA[A/G]AGGGAA GAACAGCAGCTG CGCCCCC	A	G	Glu	Glu	SILENT- CODING	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1
421	cg43927378	843	TCCTGGGTGCTG GCCCTGTGCTG GA[G/A]GCTTTTG GAAATGCCAAGA CAGCCC	G	A	Glu	Glu	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
422	cg44033566	3341	AGGCCTGGCTCT CCATCACCCAGA A[A/G]GCTGTGG CCTCTGAGGACA TGCCCG	A	G	Lys	Lys	SILENT- CODING	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. pcls:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)

423	cg43131005	8940	ACAGATATCTCT TTAAGGAAGTTG C[A/G]GGGCCAA CAGAAATGTGTG ACCAGA	A	G	Ala	Ala	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P46939 UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) - HOMO SAPIENS (HUMAN), 3433 aa.	0	
424	cg43131005	8946	ATCTCTTTAAGG AAGTTGCAGGGC C[A/G]ACAGAAAT GTGTGACCAGAG GCAGC	A	G	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P46939 UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) - HOMO SAPIENS (HUMAN), 3433 aa.	0	
425	cg43249606	108	ACACACCTGGAA GCCATTGAGAGC A[G/A]CTGGAGAT GGAGTGGCAGC TGGAGT	G	A	Ser	Ser	SILENT- CODING	struct	Human Gene SWISSNEW-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa. pcds:SWISSPROT-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.	0	
426	cg44918439	1208	AAAAGGAAAAGG AAAGAATAGAAC G[C/T]GTGAAGG AAGAGCTAATGG AACGTC	C	T	Arg	Arg	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
427	cg44918439	1508	CCAAGAAGAAA AGGAAGAGGAA GC[T/A]ACTGAGT GGCAACACAAAG CTTTTG	T	A	Ala	Ala	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
428	cg43980812	870	GAAGCTGGGCC CGGCATGTAGAA CA[C/T]ACAAAGC AGCCCACGTGAA AGACGC	C	T	Val	Val	SILENT- CODING	struct	Human Gene SWISSNEW-ID:Q15654 THYROID RECEPTOR INTERACTING PROTEIN 6 (TRIP6) (OPA- INTERACTING PROTEIN 1) (ZYXIN RELATED PROTEIN 1) (ZRP-1) - HOMO SAPIENS (HUMAN), 476 aa.	2.9E-272	7

429	cg43987609	1752	CAGTTCCTTTCA AATCTCTTTGCA A[G/A]CGACGTC CAAAGTCCCTGA ACATGG	G	A	Arg	Arg	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.1E-226	2
430	cg43987609	1785	CAAAGTCCCTGA ACATGGTTGAAC C[T/A]CCAGAGA GGACAAATATTCT TG TAGA	T	A	Gly	Gly	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.1E-226	2
431	cg11751474	312	ACGACACCCATC AGCACCAACCACC A[C/T]GGTGACC CCAAACCCCAACA CCCACCT	C	T	His	His	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q99322 MUCIN CORE POLYPEPTIDE, TRACHEAL - HOMO SAPIENS (HUMAN), 295 aa (fragment).	3.6E-189	
432	cg43916919	421	CAGATATCAGCA GTTCAAGGGCAA A[T/G]GGGCTGG AGTCAGCCACCT TGGTCA	T	G	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa. pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.30E-188	2 (2cen)
433	cg43304066	2468	TTTGCTTCCGAG CTTCTTCCCCCG C[G/A]GAGCTGA GGTCCCTTAGGC AACCTG	G	A	Ser	Ser	SILENT- CODING	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.20E-186	2
434	cg43304066	2495	AGCTGAGGTTCC TTAGGCAACCTG T[C/T]GTGTTACG CAGAACTAGTGA AGTCT	C	T	Thr	Thr	SILENT- CODING	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.20E-186	2
435	cg43948677	478	TCATGAGTAACC AGCAGTACTACC A[A/G]GCCCTGA GCAGCAGCTCCA TCATGA	A	G	Gln	Gln	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)

436	cg43949677	802	TCAAGGAGAACAC AGGTGTTGAAGA C[C/A]CTGAATGT GGAATCCAACTT CATT	C	A	Thr	Thr	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
437	cg43949677	865	TTCTGCGCCTGG TAGAAGCCCTCC C[C/A]CACAAACAC TTCTCTGGTCGA GCTGA	C	A	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
438	cg43962437	1215	ACGGCGATGCA GGCTACGGGCA GGG[G/C]CCCGG CGGTACGGGC CCCAGGATT	G	C	Gly	Gly	SILENT- CODING	struct	Human Gene SWISSNEW-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcIs:SWISSPROT-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcIs:TREMBLNEW-ID:G2707601 SYNAPTOPHYSIN - HOMO SAPIENS (HUMAN), 313 aa.	4.80E-173	X (Xp11.2 3)
439	cg43956325	1173	CCTTAACAATCA GCTGCCGCTGT GC[A/G]TTTGACC TCTCAGTCAGAA TGCTGA	A	G	Asn	Asn	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN II) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
440	cg43956325	1181	ATCAGCTGCCGC TGTCATTGAC C[T/G]CTCAGTCA GAATGCTGATGA GCATT	T	G	Arg	Arg	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)

441	cg43956325	1185	GCTGCCGCTGT GCATTTGACCTC TCACGTCAGAA TGCTGATGAGCA TTTTCT	A	C	Thr	Thr	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
442	cg43956325	1212	TCAGAATGCTGA TGAGCAATTTCT CIA/GITCAGTTCC AATTCCTCTGAT TGCTT	A	G	Asp	Asp	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
443	cg43985529	889	GCTCCATGGCC GTCTGCAAGGG CGC/C/GJGGCTC CTGGGCTGGGC TTACGAGAC	C	G	Pro	Pro	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
444	cg43985529	895	TGGCCGCTCTGCA AGGGCGCCGGC TC/C/TJGGGCTG GGCTTACGAGAC TGTTTT	C	T	Gln	Gln	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
445	cg43274709	941	GAAGATTAGAAG TGAGATTCCAAG G/G/AJGAATGGG GGACAATATGTG ATGACG	G	A	Gly	Gly	SILENT- CODING	struct	Human Gene Homologous to SPTREMBL-ID:Q28910 MUCIN - BOS TAURUS (BOVINE), 600 aa (fragment).	3.90E-106	12
446	cg43051155	1016	CGTGCCGAAGCT CAGACCCCATGA C/C/GTGCCATT GCCCTCCTTGTC AAAGA	A	C	Thr	Thr	SILENT- CODING	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17

447	cg42731508	1386	ACGGCTTCGTCA GCGCCGCCGAG CT[G/A]CGACAC GTCATGACCCGG CTGGGGG	G	A	Leu	Leu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2
448	cg44014373	559	ATTCATTGTTCT GCCGCTCCAGTT C[G/A]TGGCGTA GCTGCGTCAGTT CCTCCT	G	A	His	His	SILENT- CODING	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.10E-70	17
449	cg43936426	1293	GCTCCAGGTTCC GGGCAGGGCC GA[G/A]GGGACC TCTTCCAACTGG TTCTTCT	G	A	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
450	cg43933305	1781	ACACCTGGTTCCG TGTTGGCCCTTCA C[G/A]CGGAAGG AGTCGTTCTCCC CCGTCT	G	A	Arg	Arg	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
451	cg42522566	256	TAGCAGGGGT CGGTTTGGCCAG GT[G/C]CACAGG TGACAGAGAGG TCTACAG	G	C	Val	Val	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	
452	cg42522566	286	GGTGTACAGAGA GGTCTACAGGCC TTT[C]GCACTGGC AGCCAAGATCAT CAAAG	T	C	Leu	Leu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	
453	cg42522566	295	AGAGGTCTACAG GCCTTGCACTGG C[AT]GCCAAGAT CATCAAAGTGAA GAACG	A	T	Ala	Ala	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	

454	cg43977322	2051	CCACATCGATGC TCTCGGCAAGG C[A/G]CTCGCCT CGGCCCGGAGG CCTGGCT	A	G	Ser	Ser	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
455	cg43918310	227	TGAGTTCCAGC AGCAGAAGCAG CC[C/T]TGCATCC CACCCCTCAGC TTCAGC	C	T	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50	1 (1q21)
456	cg43918310	362	CTGAGCCCTGCC ACCCAAAGTGC C[T/C]GAGCCCT GCCAGCCCAAG GTTCCAG	T	C	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50	1 (1q21)
457	cg43248320	2084	TGGTGGCTTCC TGCACTCCTGGA C[C/G]AACCTCC GGCTGCAGACA CTGCCCC	C	G	Thr	Thr	SILENT- CODING	sulfotran- sferase	Human Gene SWISSPROT-ID:P52848 HEPARAN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARAN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N-DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 882 aa.	0.00E+00	5 (5q32)
458	cg43999676	536	TGGGTATACAG CACTCAGTGAAA C[G/C]GAGAGTC CAGGTTATTCT CCTCCC	G	C	Thr	Thr	SILENT- CODING	sulfotran- sferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
459	cg43987111	1817	AGGAGTCTGAGA ACTTCGTGTATT T[G/C]CCCACAA GGCAATAGAG CAGGTCT	G	C	Gly	Gly	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP-- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	18 (1p34.1)

460	cg43971304	1192	TCTCCAACAAGG GTGCTGACGTCT TTC/TCTGGAGG CATTGGCTCGGC TCAACT	C	T	Phe	Phe	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
461	cg43971304	385	TGGGGCCGTAC ACGGAGCAGGG CGT[G/C]AGGAC CCAGGTGGAAC TCTGGAGG	G	C	Val	Val	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
462	cg43948262	1222	GTCCTTCCTGCT GCAACCATGAGA A[G/A]ACCCTGG GGATCCTCCAGG TCTGGG	G	A	Val	Val	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa.	0.00E+00	21 (21q22.1)
463	cg43918661	587	CTCTTTCTGGTC TTTGCTTTTGCAT [G/A]ATGTCCTGG AAGTTCTTCAGC AGTC	G	A	Ile	Ile	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	7.50E-173	3 (3p21.1)

464	cg43953338	1430	ATACTTTGATGG GTCTTCGTTACT G[C/T]AAGGAGA GAGGAGCTTTAA CTGTGG	C	T	Cys	Cys	SILENT- CODING	synthase	Human Gene Homologous to SWISSPROT-ID:P44708 GLUCOSAMINE--FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE- 6- PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L- GLUTAMINE-D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE 609.aa	3.10E-107	2 (2p13)
465	cg42721903	326	ACATCACGAA GGGAAGAATTCT C[T/C]CGCTGA CGGCCAACCTCA TGAATT	T	C	Ser	Ser	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:Q06647 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.40E-79	
466	cg42721903	389	ATGGTCGCCCTAG GCAACACCCAG GG[C/T]GTCATCT CTGCCCTTCTCCA CCATCA	C	T	Gly	Gly	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:Q06647 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.40E-79	
467	cg43933068	695	ATTTGATCAGAT GACCATTGAGGA C[T/C]TGAATGAA GCTTTCCCGAGAA ACCAA	T	C	Leu	Leu	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BÖS TAURUS (BOVINE), 160 aa.	1.90E-75	12

468	cg43968419	606	AGCATCGGCTGCT GCCTGGTGGCC AC[T/C]GATGGG GCCCTTTCCATG GATGGCG	C	Thr	Thr	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P53556 8-AMINO-7- OXONONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO-8-AMINO- PELARGONIC ACID SYNTHETASE) (7- KAP SYNTHETASE) (L-ALANINE-- PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa. pcis:SWISSPROT- ID:P53556 8-AMINO-7- OXONONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO-8-AMINO- PELARGONIC ACID SYNTHETASE) (7- KAP SYNTHETASE) (L-ALANINE-- PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa.	9.90E-70	
469	cg43064068	1466	GAGAGGTGGTG AAGGCATTTGTG GT[C/A]CTGGCCT CGCAGTTCCTGT CCCATG	A	Val	Val	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. pcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	
470	cg44017251	1301	ACACACAGCGG CTGGAGTGCATC GA[C/T]AATGACG AGTGCGCCGAT GAGGAAC	T	Asp	Asp	SILENT- CODING	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
471	cg43925970	1694	CTATGCACAGAG CACATAAGGTGA A[G/A]GTGGTGA CTCCCAGAGAAG CGACCT	A	Thr	Thr	SILENT- CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9

472	cg43925970	1937	TGATGCCGGTCC CGAAGATCACCA C[A/G]GACAGAC ACATGACAGCAT AGGCTC	A	G	Ser	Ser	SILENT- CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
473	cg43925970	1952	AGATCACACAG ACAGACACATGA C[A/C]GCATAGG CTCCATAGGACT CCTGGG	A	C	Ala	Ala	SILENT- CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
474	cg43925970	1955	TCACCACAGACA GACACATGACAG C[A/G]TAGGCTC CATAGGACTCCT GGGTCA	A	G	Tyr	Tyr	SILENT- CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
475	cg36988276	638	TTCACAAGATTC ATTCTCTCCAAA A[A/G]GTTTACT TGACATTCAAGA TAACA	A	G	Lys	Lys	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0.00E+00 2 (2p21)	
476	cg43275892	1359	GAACCAGCAGCT ACTAGGGAGAAG T[C/T]TGCAAGAT GTCAAGGGCCAA GAAGT	C	T	Leu	Leu	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:Q99572 P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.	0.00E+00	
477	cg40358719	1284	TGGCCGTCCTCT ACTGCTTCCTCA A[C/T]GGGGAGG TGCAGCTGGAG GTTCAGA	C	T	Asn	Asn	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P47872 SECRETIN RECEPTOR PRECURSOR (SCT-R) - HOMO SAPIENS (HUMAN), 440 aa.	3.00E-242 (2q14.1)	2
478	cg41084924	1298	CCCACCACGGTC TCCACAGCACTC C[C/T]GACAGCC CCGCCAAACCAG AGAAGA	C	T	Pro	Pro	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11

479	cg41084924	1422	CCTCCCTCAAGA CCATGAGCCGTA G[G/A]AAGCTCTC CCAGCAGAAGG AGAAGA	G	A	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
480	cg43264978	1175	CCAAGCTCATCG ATGCCTCCAGAG TTC/G]TCAGAGAC GGAGTACTCTGC CTTGG	C	G	Val	Val	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
481	cg43264978	1193	CCAGAGTCTCAG AGACGGAGTACT C[T/C]GCCCTTGA GCAGAACACCAA ATGAT	T	C	Ser	Ser	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
482	cg43264978	140	CCCGCCTCAGAA CGATGGATCTGC A[C/T]CTCTTCGA CTACTCAGAGCC AGGA	C	T	His	His	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
483	cg43264978	164	ACCTCTTCGACT ACTCAGAGCCAG G[G/C]AACTTCTC GGACATCAGCTG GCCAT	G	C	Gly	Gly	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
484	cg3001696	1274	GCCAGACCCC AGCAGCTTCAGC CG[G/C]CCCCGC GAAGCCACGGC CCGCGAGC	G	C	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.10E-195 (1p36.1)	1
485	cg43967090	790	GGGCTAAATATT TTATGGTTTATT [C/T]ATTACTGT GTTCTCATGCTG TGTT	C	T	Phe	Phe	SILENT- CODING	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.10E-195	2

486	cg43326635	770	ACTTCAACTTCTTG TGTTGGGTGCT [G/C]CCCCCGCT TCTCCTCATGGT CCTCA	G	C	Leu	Leu	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P30542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
487	cg40245117	1286	CATGCCAATTG TTTCCGTCATGA G[A/G]ATGGACTA CATGGTATACTT CAGCT	A	G	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P33765 ADENOSINE A3 RECEPTOR - HOMO SAPIENS (HUMAN), 318 aa.	1.50E-167	1 (1p21)
488	cg21411454	920	TCTACTGCAAGT TCCACAACTTCT T[C/T]CCCATCGC CGCTGTCTTCGC CAGTA	C	T	Phe	Phe	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
489	cg42666032	1372	TGCTGGCGTC CACGAAGTGGTC TT[C/T]GCCTTCG TGACGGACGAG CAGGCC	C	T	Phe	Phe	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT- ID:P30083 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP- R-2) - RATTUS NORVEGICUS (RAT), 459 aa.	2.40E-75	17 (17q25)
490	cg38841808	111	CCAGCTGGCAG CTGGCACTGTGG GC[A/C]CCAGCC TACCTGGCCCTG GTGCTGG	A	C	Ala	Ala	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT- ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-67	
491	cg1408914	683	AGGGGAAGTTTC TCTCAGTGTTTT A[C/T]ACAAATGA GGTACCCCATGCT GAACC	C	T	Tyr	Tyr	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	
492	cg1408914	675	TCTCAGTGTTTT ACACAAATGAGG T[A/T]CCCATGCT GAACCCCTTCAT CTACT	A	T	Val	Val	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	

493	cg1408914	87	CCCCCAAAATGC TGATGAGCTTTA TTC/TTCAGAGAG GAACATCATCTC CTTTC	C	T	Ile	Ile	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	
494	cg43336100	168	CGGATGATTATG ATCTCATGTATG T[A/G]AATTGGA CAACGAAATAGA CAATG	A	G	Val	Val	SILENT- CODING	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
495	cg21138682	220	TTTTGCTGTGTA TCCTCATAGAAG GT/CJTGGAACA GATAGAAGATGA AAGGAA	T	C	Leu	Leu	SILENT- CODING	tnf	Human Gene Homologous to SWISSNEW-ID:P29965 CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39) (CD154 ANTIGEN) - HOMO SAPIENS (HUMAN), 261 aa. pcsl:SWISSPROT-ID:P29965 CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39) (CD154 ANTIGEN) - HOMO SAPIENS (HUMAN), 261 aa.	3.60E-136	X (Xq26)
496	cg43335558	1143	TGCTGGTCCAG CAAATGAAGTG A/C/TCCCACTGA GACTCTGAGACA GTGCT	C	T	Asp	Asp	SILENT- CODING	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
497	cg44027791	1440	TCCTGCCACAGT CGGGGATGTGG CA/A/CJACGTGCT TCTTCTTGCCCT GCTCTC	A	C	Val	Val	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17

498	cg43934374	1459	TAGGAGCCCATG AAGGCTTGTCCTC C[A/G]ACACCTTT CATGAACTCAAA TCTGA	A	G	Pro	Pro	SILENT- CODING	transcript factor	Human Gene SWISSNEW-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa. pcis:SWISSPROT-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	15 (15q21)
499	cg43921342	2556	TGGGATTCAGGT TCCGCTCTCGCA C[C/T]TGCTGCTC CAGCCCCAGGAT GACCT	C	T	Gln	Gln	SILENT- CODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa. pcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.	0.00E+00	
500	cg44130900	1140	ATTTCGTGACATT TGATCCTATAGC T[C]AAAAATGGCA AAACTGTAAAG TAAG	T	C	Ala	Ala	SILENT- CODING	transcript factor	HOMO SAPIENS (HUMAN), 654 aa. Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
501	cg43321351	580	GCTCTGTCAGGC TCTCGGGGTG GC[A/G]ATGGTG ATGGTGTCGGC GGCAGCCG	A	G	Ile	Ile	SILENT- CODING	transcript factor	Human Gene SPTREMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa.	1.00E-290	
502	cg43336856	861	CCTGGTAAGG GGCACCATTGGC GGT[C]CCCTGC CCATACGGGG CATAGCAC	T	C	Gly	Gly	SILENT- CODING	transcript factor	Human Gene TREMBLNEW- ID:G2895870 ZINC FINGER TRANSCRIPTION FACTOR (ZNF207) - HOMO SAPIENS (HUMAN), 478 aa.	1.90E-265	

503	cg43129605	399	GGCCCGCGCTC GGCCGCCCGCC GGT[G/A]AAGCG GAGGCTGGACC TGGAAACTG	G	A	Val	Val	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
504	cg43984259	1159	TGTTCCGGACG AACTGCTGCTGC T[A/G]CTGTTGCT GCTGCTGCTGCT GCTGC	A	G	Ser	Ser	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F- 4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211 (16q22.1)	16
505	cg43984259	1693	CTCCAGCAAAGC ATCTGCAGATGT C[C/T]TCATGAGT GACGTAGGCCAA ACAGC	C	T	Glu	Glu	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F- 4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211 (16q22.1)	16
506	cg44028769	343	CCTTCTTGTCCTC CCGAGCCTGTCA C[G/A]ATGTATTT GTTATTTCTGGA GATGT	G	A	Ile	Ile	SILENT- CODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q02482 TRANSCRIPTION FACTOR UNC-37 - CAENORHABDITIS ELEGANS, 612 aa.	4.60E-119	1
507	cg43918209	1268	GGTTGGAAAG GCGCCCTCCGC TTG[C/G]GCCGG AGGGGGCTGCA GGCGATCGG	C	G	Ala	Ala	SILENT- CODING	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
508	cg43918942	2589	CTGATGACCTCC TTCACAGTCCTC C[G/T]GAAGTCAT GCATTCTGGCTG CAACC	G	T	Arg	Arg	SILENT- CODING	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
509	cg43918942	2617	AGTCATGCATTC TGGCTGCAACCA G[A/G]AGCGCTG CTCCACAGAGGC CAGAGG	A	G	Leu	Leu	SILENT- CODING	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

510	cg43918942	2629	TGGCTGCAACCA GAAGCGCTGCTC C[A/G]CAGAGGC CAGAGGGGGCGC CGGCCTG	A	G	Cys	Cys	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
511	cg43918942	2638	CCAGAAGCGCT GCTCCACAGAG GCC[A/C]GAGGG GCGCCGGCCTG TGTCATCC	A	C	Ser	Ser	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
512	cg43918942	2665	AGGGCGCCGG CCTGTGTGCATC CA[A/G]TCCCGCT TCATCCTCTGCA GAAGCC	A	G	Asp	Asp	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
513	cg43918942	2683	GCATCCAATCCC GCTTCATCTCT G[C/T]AGAAGCCT CAGGGCAGTCAT GGATA	C	T	Leu	Leu	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
514	cg43918942	2686	TCCAATCCCGCT TCATCCTCTGCA G[A/G]AGCCTCA GGCAGTCATG GATACCT	A	G	Leu	Leu	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
515	cg43918942	2707	GCAGAAGCCTCA GGCAGTCATG GA[T/C]ACCTCAT GGTCTTCTCCC CAAATT	T	C	Val	Val	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
516	cg43918942	2713	GCCTCAGGGCA GTCAATGGATACC TC[A/G]TGGTTCT TCTCCCCAAATT CCAGTA	A	G	His	His	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

517	cg43918942	2728	TGGATACCTCAT GGTTCTTCTCCC CIA/GIAATTCCAG TAGATGCGCAAA TCGTG	A	G	Phe	Phe	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
518	cg43918942	2749	CCCCAAATTCCA GTAGATGCGCAA A/T/GJCGTGGAAT ATACAGGCACGG GTCTA	T	G	Arg	Arg	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
519	cg43051067	1325	CAAACTGCACA TCCACCAGCGAG T/A/TJACACACAG AGAGAGGCCCTA CAAGT	A	T	Val	Val	SILENT- CODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcis:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.30E-91	
520	cg43129841	1228	AAATGGTGGCAG CAACAGGTTCAA C/C/TJGGTGGCTT TTTGGAAAGGTGT CGTGA	C	T	Pro	Pro	SILENT- CODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	2.10E-83	1 (1q32)
521	cg43255753	1095	CCGAGGCCGAG AGCAAAGAGGA GCA/T/CJGGCCC CGAGGCCTGCG ACGCGGCCCA	T	C	His	His	SILENT- CODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	4.70E-63	
522	cg42532030	319	ATAAATGTGATG AGTGTGGGAAAG C/C/TJTCAGTCA GAGCTCAGATCT TATTA	C	T	Ala	Ala	SILENT- CODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.90E-57	

523	cg43946772	1709	ATCAATATTTAAT ATACTGGCTACCI A/C]GTTCTAATC AGGAAAAAAAT CTTG	A	C	Thr	Thr	SILENT- CODING	transfere se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
524	cg43948635	2125	CTATTTTGTAGC CCAGCTCCGTCA G[G/]GCCCTCAG ACAGAGCCCTGC AGTTGG	G	T	Ala	Ala	SILENT- CODING	transfere se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
525	cg43948635	2164	CCCTGCAGTTGG CCACCACCTGGT G[T/C]TGATAAAC TTTAAATTCCAG AGTCA	T	C	Gln	Gln	SILENT- CODING	transfere se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
526	cg43948635	2203	ATTCCAGAGTCA TAGCTTGCTTCA G[T/G]GCCACAG CAACCCCAGCAA TGGCGT	T	G	Ala	Ala	SILENT- CODING	transfere se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
527	cg43948635	2248	TGGCGTGGTTGT GGGGACCTCCC TG[C/A]AGGCCA GGGAACACAGC AGAATTGA	C	A	Leu	Leu	SILENT- CODING	transfere se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
528	cg43948635	2269	CCTGCAGGCCA GGGAACACAGC AGA[A/G]TTGATA AGAGACTCCAGG TTGTACA	A	G	Asn	Asn	SILENT- CODING	transfere se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
529	cg43948635	2275	GGCCAGGGAAC ACAGCAGAATTG AT[A/G]AGAGACT CCAGGTTGTACA GAATCT	A	G	Leu	Leu	SILENT- CODING	transfere se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17

530	cg43948635	2370	AAGATCATGCCA GCTCGGCAGCC TC[G/T]CAGGGT CTTGTGAGTGGT GGTGGTC	G	T	Arg	Arg	SILENT- CODING	transfe se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
531	cg43948635	2986	CCAAACTGCTC GGCTGGCGAAAT T[T/C]TCCGAGGC AATCAGCTCCAA TCCAA	T	C	Glu	Glu	SILENT- CODING	transfe se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
532	cg43995237	830	TTACTTGATGCA ACTGACTTGTA T[A/T]GCCAGAAA TCCTGTGCAACA ATAGA	A	T	Ala	Ala	SILENT- CODING	transfe se	Human Gene SWISSPROT-ID:P53611 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL- GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1
533	cg42879858	531	CACACGCTGTGGC CTATTTTGTTTTA [C/T]ACATTGAAC AGCAATGTTTCAT TCTG	C	T	Tyr	Tyr	SILENT- CODING	transfe se	Human Gene Homologous to SWISSPROT-ID:Q93070 ECTO-ADP- RIBOSYLTRANSFERASE 4 (EC 2.4.2.31) (NAD(P)(+)-ARGININE ADP- RIBOSYLTRANSFERASE 4) (MONO(ADP-RIBOSYL) TRANSFERASE 4) - HOMO SAPIENS (HUMAN), 267 aa (fragment).	4.60E-143	
534	cg43933127	2359	GATTTTCTGCAA TTTGTCTCTGTAA G[G/A]AATGGAA CATTGGCTGAAT TGTGAA	G	A	Phe	Phe	SILENT- CODING	transport	Human Gene SWISSPROT-ID:P41541 GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP) - BOS TAURUS (BOVINE), 961 aa.	0.00E+00	4

535	cg43919796	1566	CAGAAATTGCTAA C AGCGCATCCTGG A/C/TJAGCAACAA GAGAGTACAAGA AGCTG	T	Asp	Asp	SILENT- CODING	transport	Human Gene SWISSNEW-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) (MIP) - HOMO SAPIENS (HUMAN), 890 aa.lpcis:SWISSPROT-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	5
536	cg43053829	1294	TGCTCAGGTTGC C CACCAGCCTCTG TTC/AJACTTCGTG GGATAACCCAAG TTGCA	A	Val	Val	SILENT- CODING	transport	Human Gene SWISSPROT-ID:Q92887 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - HOMO SAPIENS (HUMAN), 1545 aa.lpcis:SPTREMBL-ID:Q92887 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	10
537	cg43998978	1880	GGTCTGCACGC C CCTTTCTGGTGG CC[C/T]TGTGCAC ATTGCGCGTCTA CGTGAC	T	Leu	Leu	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16

538	cg42719351	1242	CAGGATCCCTGG TGCTGCTGTGCA CTTCCTGCTTAT CCTCCTCGTCAA GATGC	T	C	Thr	Thr	SILENT- CODING	transport	Human Gene SWISSPROT-ID:Q06495 RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2) - HOMO SAPIENS (HUMAN), 639 aa.	0.00E+00	5 (5q35)
539	cg43935986	1447	TCGTAAGGAGG GTGCTGCACTTG GG[G/T]GTGCAG ATGCTGATGCTG AGCTGTG	G	T	Gly	Gly	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
540	cg43935986	2101	TATACACAGATG TAGGGGAGAAG GG[A/G]AGCCAG CTGGCTGCGGG ACAGAAAC	A	G	Gly	Gly	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
541	cg43935986	2380	GACAGGACCTCT ATCCCGCCTGG T[G/T]CAGCAGC GGCTGATGGACT GAGGCC	G	T	Val	Val	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
542	cg44008864	597	CAATGAGGTTGG CTGGAGAATCAA A[T/C]TTAGCTAC TACTCCTTTGTC CAGGA	T	C	Lys	Lys	SILENT- CODING	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. pcls:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0.00E+00	

543	cg43300953	371	TGGCGGGGACC CCGGAGCACCG CTGTTTCGAGT GCCGGACGCGG CGAACCTGA	T	C	Cys	Cys	SILENT- CODING	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.60E-261	5
544	cg43300953	425	GCGCCTGGCGC AACAAACAGTGTC CC[G/A]CTGCGG CTGCGGGACGG CCGCGGAGG	G	A	Pro	Pro	SILENT- CODING	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.60E-261	5
545	cg43984039	3102	GGGAGCCCAAGC ACTGCTCCTCCC AC[G/A]GCCAGC ATGAGGCGGACG CGTCAGCT	G	A	Ala	Ala	SILENT- CODING	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
546	cg44011204	825	TGCTTCTCGACT CCGTACGGTCCA C[G/A]TAATTTTG GAGGAGTCCTG CCCCCA	G	A	Tyr	Tyr	SILENT- CODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. pcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
547	cg43924839	1431	CCCACTGTAATT TGCTGAGTGTC G[G/A]TTTAACAT TAAACAGTGCA TAAAG	G	A	Asn	Asn	SILENT- CODING	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
548	cg43298674	600	AAACAAAGTAGG GGGCAATGATGC TTG/C CCCACTCT GGAGGCCCGTGG ATGTGA	G	C	Gly	Gly	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	5.2E-64	5

549	cg42726186	827	CAGTTGGTTCAT CCAACAGGAAAA TTC/TTGAGGATC TCCTAAATGGC AATCC	C	T	Gln	Gln	SILENT- CODING	transport	Human Gene Similar to SPTREMBL- ID:Q92473 ABC-C TRANSPORTER - HOMO SAPIENS (HUMAN), 1704 aa.	2.5E-60	17
550	cg43269525	3119	TATGAGCTCTTG GCAGCTTTTCAG G/A/CJGTACCCC ACTGTTCAACTG TAAATG	A	C	Thr	Thr	SILENT- CODING	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN-PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.5E-163	15
551	cg43291895	321	ATCTATACAACT GGGAGGTGGCC ATC/TJTCGGGC CCCCCAACACCT ACTACG	C	T	Ile	Ile	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.5E-129	
552	cg43120117	1162	TTGTAGATCATA ATAACCGAACAA C/G/CJGAGTTGA CAGACCCAAGGT TACACC	G	C	Thr	Thr	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7.00E-121	
553	cg44005525	795	TCCACTGTCTGG CCATTCTGTGTCAT G/C/TJCTGCTCT GTTGGTCATATA CTGAG	C	T	Glu	Glu	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
554	cg43921266	1300	CCCCCGAGCTG CTGCAGTGGA GCC[G/A]TGGTG GTGATGGAGCA GGTCATCTC	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0.00E+00	1

555	cg43929067	1882	CCTCCGGGGT GAGGAATCTGAA GA[G/C]GACTGG GTTGGAGGCAG CACAAAGAC	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0.00E+00	1
556	cg43944666	1082	TCTAGGGGTTTC CTAAACCAAAAG A[G/A]TCTACAAC TGGGTTGCTGAA AGCCA	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0.00E+00	1
557	cg43947011	1749	TCFTCTCCAATG TGGCCAGGAGAT CT[C/T]CCACCTG GTTCCGTACAGA CTCAT	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0.00E+00	1
558	cg43948542	3513	ATCCTGCATATG CAAAATGGGTAC A[G/A]TCACACAG AGACCTGCCCAT CAAGC	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0.00E+00	1
559	cg43969426	2856	AGAAGATCTTCG ATGGGTCCCTAC A[G/A]CCACAAGA TGTTATGTGTAG CATAG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0.00E+00	1
560	cg43273361	1765	TCAAGAGCAGCT CCTGAGCCCTTC C[A/G]AGAGCAA AGACAGGAATGA GACCCC	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P79101 CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR PROTEIN - BOS TAURUS (BOVINE), 684 aa.	0.00E+00	2

561	cg43961763	550	CCCTTCCCTTT CTGCCCTTTCTT G[G/A]TTGAGGTA TTCCAGCACTTT CATT	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETOGRANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa.	0.00E+00	2
562	cg44911887	797	CAAGATCTGGAA AAAAGCAAAAA A[A/G]AAACTTT AGCTGAAATCAA CCAAA	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0.00E+00	2
563	cg43925942	2262	ACATATTTGATAA ACTTAAAGAGGC [T/C]GTTAAGGAA GAAAGTATTAA CGAC	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0.00E+00	3
564	cg43931104	1483	AGGATGAAGAG GACACTTGTCTG GA[T/C]TGCATAC TGCACACAGGAT CCATCG	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75329 ATAXIN-7 - HOMO SAPIENS (HUMAN), 892 aa.	0.00E+00	3
565	cg43939697	947	GATACCAAGGTC CTACCAAGATGA C[A/G]AAAGAAGA GTAAATGCCCT CAAGT	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0.00E+00	3
566	cg43940975	304	CCTGATGGCTGT CTGGATCCACGG A[G/A]AAATATCC AAGACGCTCAA CTGGA	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0.00E+00	3
567	cg43948629	1640	TGCCTGTGACCC TGCCCAACATCG C[A/G]TCTTTCAC TGGCAAGGGAG GCCCC	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15031 PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0.00E+00	3

568	cg43948629	3577	CCTGTCCTCCCC AACCCAGCTGG A[C/T]GTGCCTCC CAGGCCTGCTGT GGTTC	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15031 PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0.00E+00	3
569	cg43978862	955	AGTCCTTGACAG TGAACATTCATCA T[A/G]CAGCTGAA TGTCATGCCAC AGCTG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43020 COAT PROTEIN GAMMA-COP - HOMO SAPIENS (HUMAN), 874 aa.	0.00E+00	3
570	cg43930961	2098	CGGTGGAACCG CTTGGGACTGAT A[G/A]GGGCGA GGCGGGGTCA GACTCGT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0.00E+00	4
571	cg43935402	9617	CTCCTCCGGATC CCCAACTTTTGG TT[C/T]CAGAATC CAGCCAGAGGA CAGACC	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0.00E+00	4
572	cg43994452	954	CGATCTTCACGT GCCGCCCTGGTG GG[C/T]GAGAGC TGGGCCCATGCA GTTGAGGC	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0.00E+00	4
573	cg43933355	1161	TGTATGAGCGCA GCATAGACCCTGG G[A/G]CGGCCCA CTCTCCTGTCGT CAAAGT	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0.00E+00	5
574	cg43964609	678	TGACCACTAGTA AGCTGGAGCTCT C[C/T]TGGTAGCC AAAGATAAAGCC TGCAT	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35443 THROMBOSPONDIN 4 PRECURSOR - Homo sapiens (Human), 961 aa.	0.00E+00	5

575	cg43981461	3634	TGTATCTGAAA TGCTAATTACCT G[AC]GAACACC AAGAACTCTTGT GGAACA	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43314 KIAA0433 - HOMO SAPIENS (HUMAN), 1243 aa.	0.00E+00	5
576	cg43999670	3571	AAGTGGAATGG CTCAGAGGAGTG A[AG]GAGAATGT GCTAGCACTGAA GAGCG	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12766 HYPOTHETICAL PROTEIN KIAA0194 - Homo sapiens (Human), 1435 aa (fragment).	0.00E+00	5
577	cg43918386	304	GACTGGAAGGAT GGTGGCTGTGCT C[AG]TTACACGG TCGGCAAGGCAT TGTC	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14511 ENHANCER OF FILMENTATION 1 - HOMO SAPIENS (HUMAN), 834 aa.	0.00E+00	6
578	cg43925091	2303	CTAGAACAGAGG TGGAGGAGGCG CC[G/T]GCGGTC CTCTGCCATGTC CCGGCTC	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa.	0.00E+00	6
579	cg43932558	1823	TCACCCCTGATGG GATTCATGTCGG G[C/T]CGACTAG GCTTGGAACCG CTTTCA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14670 MRNA (KIAA0082) FOR ORF (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 607 aa (fragment).	0.00E+00	6
580	cg43968933	1726	AGAAAACTGCTA AATCAAAAAA A[AG]AAAACTTT AAAAAAAACCC TACAC	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46275 SEC63 PROTEIN - HOMO SAPIENS (HUMAN), 759 aa.	0.00E+00	6
581	cg43971946	4582	CCTCCTCTTCTT CATCGATCTCAA ATT[CT]GGGTTT TAATCTTGGCAT TGGCC	T	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92794 MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN - Homo sapiens (Human), 2004 aa.	0.00E+00	8

582	cg43916922	5946	AGTCCTGCAGCA GACGAGCTTCCC G[A/G]AATTTGTA CTCCTTGATGTC ATCCC	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75181 KIAA0699 PROTEIN - HOMO SAPIENS (HUMAN), 847 aa (fragment).	0.00E+00	9
583	cg43921541	1233	CATGGTAGGCAT CCAGGAGCCCTT G[C/T]CGGTCTC CAGAGTCGTAAA TTGCAT	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA10753 TIP ASSOCIATING PROTEIN - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	11
584	cg43966967	2002	CTGCCGGCCCA GCCTCCTTCTGC TG[C/T]CACATGT TCTGGTGCGAGC CCAATG	C	T	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0.00E+00	11
585	cg43329920	1900	AGAGCCGGGCC CTCGGGGGTCC TCC[A/T]GAATAC CTGGGACAAAGA CACAGGC	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
586	cg43329920	1903	GCCGGGCCCTC GGGGTCTCTCC AGA[A/G]TACCTG GGACAAAGACAC AGGCTGG	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
587	cg43329920	1925	AGAAATACCTGGG ACAAAGACACAG G[C/T]TGGAGGA CGAGGAGGACG AGGAAGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
588	cg43334182	5043	GAGGCAAGACTT GTGGAGCTTGAG G[T/C]TGACTCAC TGGCTGTGCAGT AGTGG	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15052 KIAA0344 - HOMO SAPIENS (HUMAN), 1246 aa.	0.00E+00	12

589	cg43916884	404	GCTGATGATGGT CCTTAGGTTTCA G[G/A]GTGGCCT GAGTCTTGGATG GGGATA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0.00E+00	12
590	cg43918356	2336	CGCTACGTCCTA TATTTTGCAAAT [T/C]AGTTTATCA AACTCAACAGTC AAAT	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75176 KIAA0692.PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
591	cg43918566	1480	AGCGTGGCATG GAGCGGGAAC GGA[G/A]AACATC ATCCAGGAGACA GAGAAAG	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0.00E+00	12
592	cg43918566	808	TCCGGCCCCCA CCCAGTGCTGCA CC[G/A]CAGGCC ATCCTCTGTCAG CCTTCCC	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0.00E+00	12
593	cg43950437	955	GCTTGGCCCCAC GTCGCAGCTTGC C[C/T]ACAACTGA CAAAAAAGCACT GAAGA	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0.00E+00	12
594	cg43969319	1996	GATTACCAGATT TAATTGAAGAAA A[C/T]CATGTTGT AAATAAGACAGA CTTGA	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15398 HYPOTHETICAL PROTEIN KIAA0008 - Homo sapiens (Human), 765 aa.	0.00E+00	14
595	cg44018598	1379	ATTACTTGAATT GTCTAGGACAGG [A/G]AGATCTTCA CTATCACTGCTT TGTC	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14

596	cg44018598	953	AAGGTAGAGAAA ATGTTTATCACC T[A/G]CATTCTAC AGCAAGTACATT TTGTG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14
597	cg44018598	986	CAGCAAGTACAT TTTGTTGGGGGAG A[C/T]GATGATGA GGGACTCATTCC AGTGT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14
598	cg44022133	3061	AATGGCCCCAGT CCAATCCCAAAT TT[C]CTTTGTGC TGACTATGCCGA GCAAG	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0.00E+00	14
599	cg43981471	3033	CCCAGCCTCCTG AGGGCCCTGGC CT[C/T]CCGAGG AGATCACCCCTC ATTGTA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15082 KIAA0377 - HOMO SAPIENS (HUMAN), 1406 aa.	0.00E+00	15
600	cg43926221	5853	GCACCGAGAAA GTCCGGTTGTATC TG[C/T]TGAATT GTCTGTTTTTATT AGTAC	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15025 KIAA0308 - HOMO SAPIENS (HUMAN), 1297 aa (fragment).	0.00E+00	16
601	cg43945577	1886	TCACCTTCCTCTG AATACCTTCCTA C[G/A]TTATGGGT CAAGCTTTACAA AAGCG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0.00E+00	16
602	cg43945577	1988	TCCATTTCCTCC CACTGCTCAGAG A[T/C]GGCGAGA ACTATGTTGTGC TTCTGG	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0.00E+00	16

603	cg43955093	2884	GGGGCTGTGGG GGCATCCGCC AGGTC/GTCCCT CCATCAGAGGG GCTATCAT	T	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0.00E+00	16
604	cg43983241	362	AGTGTGACACAA TATTCACCTTTGT [G/C]GAAAAAAT GTTGCTACTTGG AAAT	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0.00E+00	18
605	cg43983241	395	ATGTTGCTACTT GGAATCAATA C[A/C]TTCTATT TGCTGGGAAAA TTACT	A	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0.00E+00	18
606	cg42702030	2347	TACAGTGGGG CACAAAGAGCTG CA[G/A]GGCCGC CTGCAGCTGTT GGCCAGG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92619 MYELOBLAST KIAA0223 - HOMO SAPIENS (HUMAN), 1165 aa (fragment).	0.00E+00	19
607	cg43297500	1921	GGGCCTTCCAGA CAGTCGTGCTGG ATT/CICCTGAAGG GGATGCCCCAGAT CGATC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49747 CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP) - Homo sapiens (Human), 757 aa.	0.00E+00	19
608	cg43927434	3540	AGCAGGCCTCCT GTAGCTCGCTAA TIGTTACCCGTGA CTTTACCATCCA CTGCA	G	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	19
609	cg43927434	606	GAGGGGGCCGG GGTGCTGGGGC CGG[C/G]GCCAA GGTCAGGGGCT CCAGATCAT	C	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	19

610	cg43991657	193	CCAGGGCAGCC GCTGCAGCAGC AGA[C/G]GAGCG GGAAGGTGTGG CCACAGCTT	C	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0.00E+00	19
611	cg43991657	208	CAGCAGCAGAC GAGCGGGAAGG TGT[G/A]GCCACA GCTTGGCTCAAG GGCGTGG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0.00E+00	19
612	cg43919691	1039	TCTTCATTCACT CAACTGCTGCCT [G/A]ACCAGGGC AAGCTCATCGCT GIGTT	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0.00E+00	20
613	cg43936220	1966	TCTGCGTGCTCA TCTCCCGGCTCG C[A/G]GCCCTCGA AGGGCTTTAGCG CACGGC	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75132 KIAA0637 PROTEIN - HOMO SAPIENS (HUMAN), 1171 aa.	0.00E+00	22
614	cg43973809	1170	TCGTGGCTGTGG TCTTCCAGGATG A[G/A]AACACTCC TTTCGTGCCCGA CATGA	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0.00E+00 (1p36.1)	1
615	cg17663981	207	AAGATGGCTCTG GGGATCCCGAG AA[C/T]CCGGGC ACAGCGAGAGC CTGGTGCC	C	T	Ash	Ash	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00 (10p11.2 3)	10
616	cg17663981	210	ATGGCTCTGGG GATCCCGAGAAG CC[G/C]GGCACA GCGAGAGCCTG GTGCCAAG	G	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00 (10p11.2 3)	10

617	cg17663981	220	GGATCCCCGAGAA CCCGGGCACAG CG[A/C]GAGCCT GGTGCCCAAGTG GCCCAAAA	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
618	cg17663981	240	CAGCGAGAGCC TGGTGCCCAAGTG GC[C/T]CAAAAGT TCACGGGGGGC ATCGGAA	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
619	cg17663981	243	CGAGAGCCTGG TGCCAAGTGGCC CA[A/G]AAGTTCA CGGGCGGCATC GGAAACA	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
620	cg17663981	372	GGAAGGCCGCC TGACCTGCGAC CA[A/G]AAACCCT GCAGCTGCCCC AAAGGG	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
621	cg17663981	375	AGGCCGCCCTGC ACCTGCGACCAA AA[A/G]CCCTGCA GCTGCCCCCAAAG GGGATG	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
622	cg43968854	6834	TATGCACTGACA AGCCACGACTC A[T/C]GAGAAAAC TACCAAAATAGC CTGCA	T	C	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0.00E+00	10 (10q25)

623	cg43968854	9441	AAGAGGAACACA AATTACAAGACT C[G/A]GTCCTG AAATAAGGGAA TATCCC	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0.00E+00	10 (10q25)
624	cg43979900	2597	TGGCAAAATTGTT GTGACACATTGA A[A/G]TAAGGAAG AAATGGCCGTAT GCACT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0.00E+00	14 (14q24.3)
625	cg43979900	2816	CCACGTAGTGCC CACTCCATGGCT C[T/C]TGGCCG TCATCAACCCCG ATCTCC	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0.00E+00	14 (14q24.3)
626	cg44014448	3469	TCCAGAAAGATT TGGTGAAGGAAG C[C/T]ATCAACTC CTATATCAGAGG GGACG	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53675 CLATHRIN HEAVY CHAIN 2 (CLH-22) - Homo sapiens (Human), 1640 aa.	0.00E+00	17 (17q11)
627	cg44928323	3760	CAAGAGCTACAT TTATGGAAGTTC T[G/C]ACAAAAT CCTTCAACAAGG CACAG	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0.00E+00	17 (17q11.2)

628	cg43973129	1228	AGCGCTATAGGG GCAGAGGAAGT GA[G/A]GAATACA GGGCTCCAAGA CCTCAGA	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETOGANIN I PRECURSOR (SGI) (CHROMOGANIN B) - Homo sapiens (Human), 677 aa.	0.00E+00	20 (20pter)
629	cg43955813	1995	GTCATGATGAAA TTTCCAGATGTT C[G/A]CTGAGTG AGCCATTGGAAA GTGATG	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0.00E+00	4 (4q12)
630	cg44923983	576	GGAATTACAATT TTGGTGGAGAAT T[C/T]GTAGAAGC CATGATTTCGTCA ACTTA	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q09161 80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80) - Homo sapiens (Human), 790 aa.	0.00E+00	9 (9q22.3)
631	cg25268354	1419	TCATCACCTCCT GCACGTACAACA C[G/A]GAAAGACC GGGAGCTGGCC ACAGTGG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P09172 DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-HYDROXYLASE) (DBH) - Homo sapiens (Human), 603 aa.	0.00E+00	9 (9q34)
632	cg43921948	1765	AAGATCCAGAG AGAGAAACCCAC T[A/T]ACTCCAGC ATCCGAGCCCC GGTTTT	A	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0.00E+00	X
633	cg43032555	677	GCTTCTCGGCT TCTGACTGGTCC A[A/G]GATCTTCT GCCGCTCAAGC CGACCG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
634	cg43032555	699	CCAAGATCTTCT GCCGCTCAAGC CG[A/G]CCGGGG GCTTCCTGTTCC AGTCTCT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	

635	cg43032555	714	GCTCAAGCCGAC CGCGGCTTCCT GTTCTCCAGTCT CTGAGCCTCATG CTTGG	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
636	cg43032555	765	CCGCCGCTTCCT GGGAGTTGGTG GTATGATCTCGA TGGCCAGCTGAA CGCTGC	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
637	cg43032555	783	TGGTGGTAATCT CGATGGCCAGCT GATGACGCTGC GCTGAAGGGCAT CCCGGG	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
638	cg43032555	792	TCTCGATGGCCA GCTGAACGCTGC GCTTTGAAGGG CATCCCGGGTCC TCTGAT	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
639	cg43032555	795	CGATGGCCAGCT GAACGCTGCGCT GATCJAGGGCAT CCCGGGTCTCT GATCCA	A	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
640	cg43032555	801	CCAGCTGAACGC TGCGCTGAAGG GCATGTTCCCGG GTCCTCTGATCC ACAGGCT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
641	cg43032555	840	GATCCACAGGCT CCACTGACTGCA CATGTTCCACACT GCTGACTACCCAG CCCGT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	

642	cg43032555	855	CTGACTGCACAT CCACACTGCTGA CTT/CJACCAGCC CGTTTGGGGAA AGACAG	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
643	cg43032555	873	TGCTGACTACCA GCCCGTTTGGG G[A/G]AAGACAG CCTGGTCCCGG GGCCTGG	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
644	cg43054046	2616	TACTGGGTGTGA AAGCTGTTTGG CTT/CJGAAAGTTA TGAAAAAATACA CAAAG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48200 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 2 (IRE-BP 2) (IRON REGULATORY PROTEIN 2) (IRP2) - Homo sapiens (Human), 963 aa.	0.00E+00	
645	cg43277456	832	ACTTCGAGGCCT ATGTGCAGTACC G[C/T]GAGTACAT GGGCTTCATCCA GGCCA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0.00E+00	
646	cg43303383	232	TGGCCGAATTC CTTCGGCTCGTG G[A/T]GCTGGGG CTGCTCCTGACC TTGGCG	A	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0.00E+00	
647	cg43926470	2502	AGAGCCTCTTCT CCACAGCCTTCT C[C/T]GAGTCCCT GGCTGCAGAGAT CAGCT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75154 KIAA0665 PROTEIN - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	
648	cg43971555	583	AGGTGAACCTCGT GGCGCCCGGTG TC[G/A]GCAGTA GCGTCCGGGGC TTAGGCG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0.00E+00	

649	cg43971555	904	GGAAGCGGACA TAGGGGCAGCC AAC[G/A]TCCAGC ACAACCTCCTGG CTAAGCC	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0.00E+00	
650	cg43972478	2073	CTATGTTAGGCT GGCTTTCTATCA A[C/A]GCGTGAA GGGATGGGCAA GATGCCA	C	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43264 HZW10 - HOMO SAPIENS (HUMAN), 779 aa.	0.00E+00	
651	cg43986766	1862	GCACCTCCATGG TGTAGGCCGCC CG[A/G]CAGATGT CACAGCCGTACA TGGGCT	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O08961 ZINC FINGER PROTEIN 104 (ROAZ) - RATTUS NORVEGICUS (RAT), 1186 aa.	0	
652	cg44932392	840	TGCTAAAGTTCA TATTTAATGAAAA [C/T]GAAGATTCT GCATCAATATCT TCCT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
653	cg43956210	1507	ATAAAGTGAAC CTCTTGATTTTG G[C/A]GGTACTCA GAAACAGAAACA ACTTT	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
654	cg43982721	1732	CGTCCTGCCCAG GCAAGATCTCCG T[C/G]CCTCCTGT GCGCAACCTACA TCAGT	C	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROXYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	
655	cg43955051	494	GTTCTGACTTAA AGCAAAAATACA C[G/A]GCATAGAT TGCAACAGCAAA GAAGT	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD10823 SQUALENE EPOXIDASE (EC 1.14.99.7) - HOMO SAPIENS (HUMAN), 574 aa.	1.9E-305	8

656	cg43951838	1686	TAGCCACCGCCT TGTCACAGACGA C[G/C]GTCATCC GCTCCTCTATCC CGTTGA	G	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
657	cg42682985	315	CTGATCCTGGCT GAAGAGGTTCCA G[C/T]GACACTTG AATAGTAAGTTTT GTTT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene REMTREMBL- ACC:D1020806 (LAMBDA) DNA FOR IMMUNOGLOBULIN LIGHT CHAIN - HOMO SAPIENS (HUMAN), 541 aa (fragment).	2.00E-301	22
658	cg43917155	474	CAGTCCTTAAGA AAAGGGAGTATG G[A/C]TCAAAGTA CACTCAGAATAA TTTCA	A	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2.00E-301	
659	cg43255486	1152	TCAAGCCCAACA AGCTTCGAAATG G[C/A]CACAAAGG GGCTTCGGATCT TCTGCA	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.70E-294	17
660	cg43255486	1686	TCATCCTGCCGA GCGAGGAGGAG GG[C/T]CGCCTG TACTTCAGCATG GATGATG	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.70E-294	17
661	cg43926493	1341	CGCTGCTGAAGT GGACCGAGTACA C[G/A]CCAGATC CTAACCATGGCT TCTATG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27715 CGI-06 PROTEIN - HOMO SAPIENS (HUMAN), 574 aa.	1.40E-293	20

662	cg43316305	1345	TGTTGGGCTCCT GTTGCTCACACA A[G/A]GAGCGCC TGAGTATCCTCC GGGCAG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75708 HIRIP3 PROTEIN - HOMO SAPIENS (HUMAN), 551 aa (fragment).	8.70E-292	
663	cg42903434	103	AGGGCTGCAGC CACGGTCTCCAG AT[A/G]TTGCCCA GCCTGTCCAGCT GCAGAG	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P51690 ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	2.30E-291	
664	cg42903434	67	CCCTAAGGCACC AGCAGAGGGG AA[C/T]GGGCCA CAGCAGGGCTG CAGCCACG	C	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P51690 ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	2.3E-291	
665	cg43949262	837	GCTGCTCTCTCA CCACTGCAAGCT C[C/T]GCGTCCC ACGCAGTGTAC TGAGCA	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
666	cg43995003	1790	TTTGTGGAATGA CATCAAATGGT T[C/T]ACCAATTGC AGACCCAGATGA TAGAG	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
667	cg43926814	645	AACCAAAAGGAT CTTCCTCAAAC G[A/C]ACTGGTC CTTCTCGGCCTC TCTGTC	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
668	cg44028870	446	AGAAAATAAAAA TGTCGACCTCGT C[C/T]TTGAGGC GCCAGATGAAGA ACATCG	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83017 KIAA1065 PROTEIN - HOMO SAPIENS (HUMAN), 641 aa.	5.6E-288	

669	cg40918088	1907	CAAAAGCCACAGT AGGGCCGGATC ATT[TA]ACAGTGG AGGATCACTACC CGCAAG	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.8E-287	X (Xq28)
670	cg43129343	1526	TGGTCGAAGGTC AGGGCGAGAAG AA[C/T]GTGACCT TCTGGGGGAGA CCGCJGC	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
671	cg43931056	1275	TGGCCATGGAGT GACATGGACTTG A[T/C]CATCAAGT AATTCTGTAAAC CTTCG	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa.	4.5E-286	12
672	cg43968641	3598	CGATGGCCAGG CCATCGATGAAA TT[AG]TGGAGG CCGTCGCTCAGA GTGATCA	G	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
673	cg43949830	1018	TTGAGATGTAGC ACTCACATGCTT T[G/A]TTTCCTAA ATAATTTATAACC TCAG	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
674	cg43949830	793	TTTTCATGTCTAT TTTTTCCTTTTGA T[C]CCTCCAGCA AGTAGATTGATA TTTT	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16

675	cg44002920	1169	TCTGCAGCAGCA GTGAATCAGATA C[A/G]TTGGGATT TTTCAAATACTG GCACA	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
676	cg44002920	644	CAAAAGTTTCTC AGTGCTGCTTTC C[C/T]GCACTGTC ATAGAAATCTCT GATCC	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
677	cg43922691	1088	TGGCTGGAAGT TAATTCCTGTGC A[C/T]CAAGTGAG AGGTTTGAAAGA GAAGA	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
678	cg43922691	416	ACGAGGACGCG TTGCTGCGGGGT CT[G/A]CGAGGC CCGAGGGTTCAA GAACAIG	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
679	cg43922691	788	CCACATCAACTT CTCTTCCAAGAG G[C/A]ATCTTGAA GATGAAGAAGCTG CCAGC	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.50E-278	17

680	cg43984386	374	CGCGGAGGGTC ACCAACGTGGG GTC[T/C]CTGTTG CTCACCCCGCAG GAGAACG	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00401 N-WASP - HOMO SAPIENS (HUMAN), 505 aa.	5.90E-277	
681	cg42935995	1294	CAATCTTCTGGC TCAGGTAGATTA GIC/TTCCTCTGT CCGTCGCATACT CTGGA	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1.00E-274	
682	cg43929467	717	AAACTTGGTGG AGTTCACAGATG A[A/G]GAGGGAT ATGGTCGTTATC TCGATC	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.30E-274	1
683	cg43947753	641	TCCCGAGCGT GTAGGAGCAGT GCG[A/G]TCGTG GTCCCTCCCTAT GCAGCCTG	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.10E-274	12
684	cg43333012	1838	TGTTCAATGAGCT TTGGAAAAGCTG CT[C/A]AATAAGCC CTCAATCCGAGT TCGGG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)
685	cg43333012	1861	GCTAATAAGCCC TCAATCCGAGTT C[G/T]GGTCATTT CCACAAAACGTGC GAGAA	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)
686	cg43333012	407	CAGCTCCCTCTT CTTGGTATTACA A[A/G]ATTTCATA CTTATCCACTAG GAAAG	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)

687	cg43926574	872	AAGATCTAAGAC ATTTAATAGTATC [A/G]AGAAGTACA CAGGCACCACTA ATAA	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.10E-268	7
688	cg42869211	1895	TGCACTGAAAAG CTTGATTCCTAC A[T/C]TGGAAAA ACCAAAAGCACC AGCAA	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15397 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 508 aa.	7.00E-267	9
689	cg43031103	1702	CCCTCCCCTTGG TTGAGGAGACAG C[A/G]GGGGCTG GTGTGAGGTGCA GCACCC	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.30E-266	
690	cg43313186	495	TCTCATTCCAA GATCTTCAAGGG A[T/C]TGGCAGCT GACCAGACAGA GGCCCT	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.30E-265 (20q11.2)	20
691	cg43922182	1285	CTTCCCGCGGG AGCCGCGGCC AAG[T/C]TGCACC ACAGCCTCAGCT TCTCGGG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.10E-261	2
692	cg43922182	1476	CCTCCGCGGCC TCCACGCCCTCG GG[C/G]GCCCGG ACATGCTGCGCC TCCGCGG	C	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.10E-261	2
693	cg27359628	196	GAGACAGCGTG CCACACAACAC CC[T/C]ACCAAGT TCAAGGTGACAA ATGTGG	T	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.30E-260	

694	cg43980777	999	ATAATTTTCTGAA ATCCATGGGCTC [T/A]GGTACAATC TGGGGTTCGTGA GCAAG	T	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.20E-259	2
695	cg43980777	882	CATGCTTGCTTC TCAGTGCCCCCGC TTC[T]GAGGCTTC TGCGGGCGCCT CC[T]CCT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.20E-259	2
696	cg43986498	1090	CGGAGGAGGAG CTGGAGCGGCT GGA[G/A]GAGGC CTGCGACATGGC GCTGGAGC	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.30E-255	19
697	cg43986498	1664	CCGGAAGCAGG CCAACCGTATGA GC[A/T]NCGGAG AGATCGAGGAG GACGCCTA	A	T	???	???	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.30E-255	19
698	cg39711096	941	ACGTGGAGGTG GACATGTCGGGA GA[C/T]TTGGGGT GGCTGTTGAACC TCTTCC	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
699	cg39711096	953	ACATGTCGGGAG ACTTGGGGTGG CT[G/C]TTGAACC TCTTCCACAACC AGATTG	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
700	cg42101957	279	TTTATGTAATAA TGCGTTTCGGTC [G/A]TTGTTAAGA TGTTGTGCCAAA TGAC	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04279 SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA- INHIBIN-92; ALPHA-INHIBIN-31] - Homo sapiens (Human), 462 aa.	5.50E-251	20 (20q12)

701	cg44910581	1321	CAACTGCCTGTC CAAGTGTGCGC C[G/A]CAACACTT GGACCTCGTCCT AGTTT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.80E-251	
702	cg44910581	2649	AACTGGACAAAG CATTAGCTTGTT TTT/CJCGAAATGC TATCAGGGTCAA TCCTA	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.80E-251	
703	cg43950250	675	GTTCTCTACTT CGGGTGGGAAG TC[G/A]GGGTTCT GGAATTGCTGCA TGAGTT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P11926 ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC) - Homo sapiens (Human), 461 aa.	7.00E-251	2 (2p25)
704	cg43962278	371	AGAGGGTGAGG GTCTGGAGGACT CC[T/A]GTGGTG CAGGCCATCTCC CGGATAG	T	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD01211 ASPARTYL AMINOPEPTIDASE - HOMO SAPIENS (HUMAN), 472 aa.	1.50E-250	2
705	cg44027341	957	GCACTGGTTTCC GCCTCCGACCTG T[A/G]GCTGGCC TGCTTTCCTCTC GGGATT	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00439 PHENYLALANINE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4- MONOOXYGENASE) - Homo sapiens (Human), 452 aa.	1.60E-246	12
706	cg43996564	739	AGAGGGCACCC CGCAGGCTCAG GGG[C/G]CCACC ACCAGGCGTGA GCTGGATGG	C	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.90E-245	3
707	cg43980318	600	GCCCAGTTTATT CGTCCAAAGCTG C[AT]GGGAGTG GACTCAGGATGT GCGACC	A	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.60E-244	1 (1cen)

708	cg43985156	1497	CTCTCAAGTTCA TGCTGACGAATC TTT/GJAAGTGGG GTCTTGCTTGGG TGTCCT	T	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.80E-243	17
709	cg42897932	675	ATTATATCTCTG GGATCCAGACTA TTT/CJGGACATAG GGTAATTGTATC TGATG	T	C	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA32662 KIAA0017 PROTEIN - HOMO SAPIENS (HUMAN), 1217 aa.	8.20E-241	16
710	cg43936335	747	AAAGGGAATGA GGAGGAGTAGT GGATTTTGC GA GCAGGTTCTCGG AGGGACC	A	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74919 KIAA0896 PROTEIN - HOMO SAPIENS (HUMAN), 1230 aa (fragment).	8.50E-239	8
711	cg44013460	1019	TCACTGAGTTGA AAAAGCTGGACT TTC/GJCCAGCTC CAATTGGACCCA GCAGCA	C	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
712	cg44013460	1040	ACTTCCCAGCTC CAATTGGACCCA GTC/GJAGCAGAA TTCGTATTTGTT GAACCA	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
713	cg44013460	1043	TCCAGCTCCAA TTGGACCCAGCA GTC/GJAGAATTC GTATTTGTTGAA CCAGGG	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
714	cg43948360	2144	CCACACCTGTCA GATCGGGCGAG CT[G/C]CGGAAC GGTCAGCCCA GGACTGGA	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.10E-234	22

715	cg43962127	363	CCAAGAAAGA TGTTGTTGAAC G[C/T]GTTGCACA AAGTTTCTTGAC CTCTT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.10E-233	7
716	cg43962127	678	TAAACTGGGGT CTTTCTCAGACC C[G/A]GACATCCT CTTGTTGATGTT AAACT	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.10E-233	7
717	cg43940483	1031	AGAAATGGCTG AGCGCTGGAAC C[A/G]GGCCCTC CTCCGCTCAGAC TCAGCT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.10E-232	
718	cg43933074	206	CCGACCTCAACC GCAAGGACAAGT TTT[C]CCCGCCAT CACCCACCTCAA GTTC	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.20E-228	19
719	cg43984330	868	CGAGACCCCGC TTCTCCCGGTTG TC[A/G]CTGAGCA GTGGGGTTATGG TGTACA	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P32121 BETA-ARRESTIN 2 - Homo sapiens (Human), 409 aa.	8.50E-223	17
720	cg43999712	467	CCCTGGCAGTG GCCGCTGTGCTA TA[C/T]CACAAGA TGAACAGCGGG AAGCAGG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
721	cg43994204	1151	GCATCGCCACAT CCCTGGATGGCT T[C/T]GACGTCGC GTCCGTGCAGCA GCAGC	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.40E-221	19

722	cg43994204	1157	CCACATCCCTGG ATGGCTTCGACG TTC/TGCGTCCGT GCAGCAGCAGC GGCAGG	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.40E-221	19
723	cg43960557	1813	TGAAATCAAGGG CCTGGTAGACGA GT/C/GAGTAGA GGTATTCCACCT TCCTAC	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.70E-220	22
724	cg43251548	1238	ATAGTCAGGTTG ATTGGACTTAGG AT/CJCCAAATGA ACCTCGATACTG CATT	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment).	2.70E-217	
725	cg43068795	633	CTCCTTCTTCT CCTTCCTCTGTT C/C/TJCGTTCCCTC TTTCATATCTCTA AGTA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB51071 HYPOTHETICAL 295.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 2701 aa.	2.80E-215	1
726	cg43990581	767	ACCCGTACCTCC CGCTCGTCACCG AT/CJGAGGACA GCTGGTACAGCA AGTGGC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60651 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa.	1.60E-214	17
727	cg43083763	776	CCCTGAACGCCA CTCCAGGGACCT C/A/GJCTCATCTC CTTCAGTGACAA GGCCA	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P21549 SERINE-PYRUVATE AMINOTRANSFERASE (EC 2.6.1.51) (SPT) (ALANINE- GLYOXYLATE AMINOTRANSFERASE) (EC 2.6.1.44) (AGT) - Homo sapiens (Human), 392 aa.	1.10E-211 2 (2q36)	
728	cg43984681	666	ACCCAGCCTTCA TCCGGGCCCTGG GT/GTJGGCGGG GTCCGGCAACTAC AAGTTAG	G	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.30E-210 (19q13)	19

729	cg44927668	1463	ATCAGGCTGCGT TTTTGAGTCAAG C/C/TTCACAGAT GTACGACTCCTC TTTGA	C	T	Ala	Ala	SILENT- CODING	UNCLAS- SIFIED	Human Gene TREMBLNEW- ACC:CAB48885 DJ462023.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 406 aa.	2.10E-210	1
730	cg43948416	2020	TTT TAGGACGAC CCCGTAAGAAAT TTT/CJTGCAATGCT ATTAAGTGCATC CATAG	T	C	Gln	Gln	SILENT- CODING	UNCLAS- SIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.70E-206	11
731	cg43959472	1584	TCTTGAGCCACA CGATGCCGCAG GT[A/G]CGCGTG AAGGGTTCTCG TTGATCT	A	G	Arg	Arg	SILENT- CODING	UNCLAS- SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.40E-203	15
732	cg43921081	528	ACAAGAGAAGAG AATTATCACCG GTT/CJGATGTTGA ACCAACAGATGC GGAAT	T	C	Gly	Gly	SILENT- CODING	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:Q99733 NUCLEOSOME ASSEMBLY PROTEIN 1- LIKE 4 (NUCLEOSOME ASSEMBLY PROTEIN 2) (NAP2) - Homo sapiens (Human), 375 aa.	3.10E-202	11
733	cg44128902	965	AGATGGAGTCAG CAGATCAGGCC GT/T/CJGCTGAG CTCAACGGGACC CAGGTGG	T	C	Val	Val	SILENT- CODING	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201 (1p36.2)	1
734	cg44128902	761	GGGATCGAGAC CGAGACCGAGA GGGTT/GJCCTTTC CGCAGGTCGGA TTCAATTCC	T	G	Gly	Gly	SILENT- CODING	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201 (1p36.2)	1
735	cg44128902	797	GGTCGGATTTCAT TCCCTGAACGGC GTA/T]GCCCCCTA GGAAGGGAATA CTCTCT	A	T	Arg	Arg	SILENT- CODING	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201 (1p36.2)	1

736	cg43289239	822	TCACCACCTGC CCCATGTGCAGA A[A/G]TACCTGAA GTCCGTACGCTA CATTG	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15059 KIAA0351 - HOMO SAPIENS (HUMAN), 557 aa.	1.50E-199	9
737	cg43320965	1607	GTGATACAAGGC AGAGCCTGCAG CA[A/G]TCCATGC CTCCCTGTGAGC CACCAT	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD30184 HYPOTHETICAL 43.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 391 aa.	5.30E-198	14
738	cg43944615	2020	CATAGCTGTAGT TTTTGCTGAGAT A[C/T]GTTGCCAA AGTTGGCTTCAC CTTTT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa.	1.30E-192	
739	cg43935935	777	TCCAGTCAGAA TCCATTTCTAAC [T/C]TGATCCAGC TCAGTTGGGATG TACT	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60735 GA17 PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	1.70E-192	X
740	cg43964795	2166	CCACGAGTAGT CTTCCCGGATAA T[G/A]TGCTCCAC ACGGATCCGAG CTCGTT	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.80E-192	16
741	cg43980381	460	ACACCTCAGGA CCAAGAAGAACA C[T/A]GCCATTGT CAAGCGCTGGA GCGACC	T	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.60E-191	9
742	cg43996402	1312	GTGCAACCCAC TGTTTCTCATCT C[C/G]GCTATTAG CTCCGAGGGGT GCATCG	C	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.60E-189	2

743	cg43933608	390	CCTTGAGTTTCA GGAGGGGCTGT AA[G/A]GTGAAGA AGCATGAAACTC AGTCTC	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.50E-189	8
744	cg43249389	924	GCTTCAACCGGT CCCGGGAGTATC A[G/A]CTCAACGA CTCTGCCAAATA CTACC	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.40E-188	15
745	cg43947129	1282	TTCTATTTGGG GCTCCACTGGAC A[A/C]ACGTAGAA TCCTTGAGAAAT ATCAA	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3.00E-188	
746	cg43927276	1007	CAGCCTATGGAG GCCTCAATGAGA A[A/G]TCTTTTGT AGATGGCTTGAA TTTTA	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P50616 TOB PROTEIN (TRANSDUCER OF ERBB-2) - Homo sapiens (Human), 345 aa.	3.10E-186	17
747	cg43957632	893	TGCCTCCCCCGC CCAACATGTTCA T[G/A]GTGCTGTC CAGGTGGTTCTC CACCA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
748	cg43957632	1081	GCTCGGAGCCC GGGTGGGATA GCA[G/C]CGCAG CCCCTGGCCGC AGCGCGGGG	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	

749	cg43950796	369	AGTAGTACCGCT GCCAGCCCTGTG GT/CJGTCCGCT CTTCCTCAGGAG CAGGGA	T	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
750	cg44001387	770	GCTGTCTGGTTG TGCTCCCAGGCA C/A/GJACACAAGG GCTCCCTGAAGC CCCACG	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14832 PEROXISOMAL PHYTANOL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) - Homo sapiens (Human), 338 aa.	8.4E-184	10
751	cg43917229	245	GCCCACTTGCAA CCAGGAGAGCAT T/C/TJCTAAAGAA GAAAGGCTGA CAGATG	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75381 PEROXISOMAL MEMBRANE ANCHOR PROTEIN HSPX14P - HOMO SAPIENS (HUMAN), 377 aa.	1.6E-180	1
752	cg43981031	525	CTGCTATCCCTT TATGAGAGGGAG A/C/TJAAGGTCTG AAGTTTGTTCCTC CAAAG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34057 CGI-62 PROTEIN - HOMO SAPIENS (HUMAN), 325 aa.	1E-178	
753	cg43919917	1068	ATGACTCAGAGC AGGTGCCCCAG GC/A/CJCTCCGC CGGCTCCGCC GCGCACCC	A	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60808 BK833B7.1 - HOMO SAPIENS (HUMAN), 339 aa.	3.5E-178	22
754	cg43989723	426	AGCTGCGGGC CGGAGCGAGGC TGA/G/AJATCCG GGTCTTCCTCCA GCAGCTCA	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
755	cg43931789	116	CGGCAGCGTCG CTGGAGCTGTG GCT/G/CJAACAAA GCCACAGACCCA AGCATGT	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14564 HYPOTHETICAL 67.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	2E-175	16

756	cg43967532	3684	TCATGGCGATGC AGACGTCCCCCT C[G/C]GGGAAC TGTCACACTTAA GCATCT	G	C	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.30E-174	8
757	cg43967532	3843	AGAGCGAGCAG AGGAAGACCTG GGT[G/C]CCGGC GTGGCAGTTCTT GTTGAGCA	G	C	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.30E-174	8
758	cg43250735	1560	TGATGATGTGGC TCTGGAACCTGT T[G/A]AAGTAGAT AGAACCGTTGTA GACCA	G	A	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q62609 NEURONAL OLFACTOMEDIN- RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B426B) - Rattus norvegicus (Rat), 485 aa.	1.20E-173	9
759	cg43918085	877	CACCCATGGGAC CATCTGACCCAG G[A/G]CCCCATTG GAAAATTAGGTC TGTTAG	A	G	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.90E-173	
760	cg43927536	1855	GAGCTGGTGTG GTAACCTCTGGTT AC[A/G]AATTGG AAGAACTGGCAT ATGCAG	A	G	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60667 ANTI-FAS-INDUCED APOPTOSIS - HOMO SAPIENS (HUMAN), 390 aa.	3.80E-172	
761	cg43923012	1198	CTAACTCTACCA CTGCATTCCAC C[A/G]TAAAGACT GTACATGTCATC TGCAA	A	G	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.10E-171	X
762	cg43941339	1200	TGGAGTCCTGGC TGTCACACATGGT C[A/G]TCATCATC TTCATCATCCAT ATCAT	A	G	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10451 OSTEOPONTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPONTIN) - Homo sapiens (Human), 314 aa.	8.20E-170 4 (4q21)	

763	cg43251632	646	TAAGTTGTTGT GTGTCACTGTGA C[G/A]GCTCCCA CGGTTGTTTCCT TTGGCA	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38537 TRANSPORTIN-SR - HOMO SAPIENS (HUMAN), 975 aa.	2.50E-169	
764	cg44032718	435	GGGAGGCACCT GCCACCCAGGC CTC[G/A]TCTACT ACTCAGCTGACT GATACCC	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.70E-169	X
765	cg44032718	807	CAGGTGGCCGA AGGGTCTCAAAG GC[T/C]CTAATGG CCTCAATGGCCC GCAGGG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.70E-169	X
766	cg43959938	1549	TGCATCCAGCAC ACTTCTTGCCCA C[A/G]AAGTTCTT GTAGCAATCCAC GCAGT	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa.	5.20E-168	X
767	cg43329903	874	TCCGGATCCTCC CAGCCCAGAGC CG[A/G]GCCCTC GGAGGCCCTCC AGAATACC	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
768	cg43329903	883	TCCAGCCCAGA GCCGAGCCCTC GG[A/G]GGCCCT CCAGAATACCTG GGACAAA	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
769	cg43329903	892	AGAGCCGAGCC CTCGAGGCCCC TCC[A/T]GAATAC CTGGGACAAAGA CACAGGC	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12

770	cg43329903	895	GCCGAGCCCTC GGAGGCCCTCC AGA[A/G]TACCTG GGACAAAGACAC AGGCTGG	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
771	cg43329903	917	AGAATACCTGGG ACAAAGACACAG G[C/T]TGGAGGA CGAGGAGGACG AGGAAGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
772	cg43329903	952	AGGAGGACGAG GAAGAGGCTGAA GG[C/T]GGGGG CTGGCCAGCCTT CGCCAAT	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
773	cg43949591	1809	TAAGAACACCTA TCCTGACTTCAT C[A/G]AGATCTTT TAAAAACCCATT AAAAA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
774	cg43949591	1812	GAACACCTATCC TGACTTCATCAA G[A/G]TCTTTTAA AAACCCATTAAA AATCG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
775	cg43949591	1824	TGACTTCATCAA GATCTTTTAAAA [C/T]CCATTAAAA ATCGGAACCAGG TCIG	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
776	cg43924431	1015	TTTCATTTTCATT CTCTTGAGCATT C/TGTGTTCTATAT TATTAGCTACTT CAC	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.20E-166	5

777	cg43951985	856	TGATTCAGCAT CATGGCAGGTAT TTT/CJACCACATC TGTCACATTCTT ATAGG	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.50E-164	22
778	cg43949202	1179	TTGACTTCTCTTT TTCCAGTTCTTCI G/AJGCAAGGCCA CAGGTGCAGTTC TTAC	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75207 HYPOTHETICAL 33.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 312 aa.	6.30E-163	16
779	cg43986422	891	CCTTTGTGTCCT TTCTTTTATTGAG [A/G]TCTTCAAAC TGGCATTGAATA TAGG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P04898 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-1 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) - Homo sapiens (Human), and Bos taurus (Bovine), 353 aa.	6.30E-163	7 (7q21)
780	cg44015739	526	CATCACTGTCCG TGAGACCTATCC A[A/G]CGCGTGA AGGGTTCGTGT GTTGTA	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03969 HEPATIC LECTIN H2, VARIANT (ASIALOGLYCOPROTEIN RECEPTOR H2) - HOMO SAPIENS (HUMAN), 287 aa.	2.80E-160	17 (17p)
781	cg43986534	766	ACTTCTGCTACG AATCCCGCTTCC C[G/C]CGGGTGG CCACCACCCCCAC CGCCCC	G	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75900 METALLOPROTEASE MMP21/22A - HOMO SAPIENS (HUMAN), 390 aa.	4.70E-160	
782	cg42720055	609	GAGGAGTGGCA GTATTCATTGGG CA[A/G]CCCCACA GAGGTCGTGAAA GTCAGAC	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P25874 MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN 1 (UCP 1) - Homo sapiens (Human), 307 aa.	1.60E-157	
783	cg43287561	637	CAATCTGGCCTT TCTGCCGGGTTT C[C/A]GGATTAC TTTCTTCCTGGG AACAA	C	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)

784	cg43287561	661	CCGGATTCACTT TCTTCCTGGGAA C/A/G/AACCCTCT ATTGACCAGGAT GGTGA	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
785	cg43287561	673	TCTTCCTGGGAA CAAACCTCTAT T/G/T/JACCAGGAT GGTGA	G	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
786	cg43287561	693	CTATTGACCAGG ATGGTGACTCCC A/A/G/GTCAAG CAATGGAAAGGA GTAA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
787	cg43287561	697	TGACCAGGATGG TGACTCCCAAGT C/A/G/GAGCAAT GGAAAGGAGTAA CAACAT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
788	cg43287561	703	GGATGGTGACTC CCAAGTCAGAGC A/A/G/TGGAAAG GAGTAACAACAT AGGCC	A	G	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
789	cg43287561	709	TGACTCCCAAGT CAGAGCAATGGA A/A/G/GGAGTAA CAACATAGGCC CACTT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
790	cg43287561	715	CCAAGTCAGAGC AATGGAAAGGAG T/A/G/AACAACATA GGCCCCACTTTC AGTTG	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)

791	cg43287561	733	AAGGAGTAACAA CATAGGCCCCAC TTTCCTCAGTTGA GGATAATCTGCC AGCAT	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
792	cg43287561	769	ATAATCTGCCAG CATCACGTGCCT CTTCCTGGACAG GGTCCACCATGG TCCGAG	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
793	cg43287561	793	CTCGGACAGGG TCCACCATGGTC CGATGCGGCATT ATGTACAGCTCC TTGGAAT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156	9 (9q34)
794	cg43254730	1641	GTGGCTCATTCC AGAAGCTGAAC CTAGJAGGAGCA GCTGGTTTCTCC TGGACA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.80E-156	22
795	cg43298828	424	TGATCTCAGCCT TCTGGATCTCCC CTAGJTTACATA CGGAGAGACTCT CAGAG	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.10E-155	17
796	cg43060941	358	CTGCTGCTGTGT CCAGGCTCTCTT TTTCCTGCTTCTC CACTATTTTATCT TTCA	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment).	4.90E-153	
797	cg43919239	407	CATGCATGGCTG CAGCATAGAACC TTCATGCCACTTC CTCGTTGGGGTT GCCCT	C	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR, (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	

798	cg43917036	2502	TCGGGAAATGT AGTACCAGTTGT T[G/C]GGCAGAC GGAAATGCGGT AATGCT	G	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13239 PUTATIVE SRC-LIKE ADAPTER PROTEIN (SLAP) - HOMO SAPIENS (HUMAN), 276 aa.	1.30E-148	8
799	cg43927534	538	CCCGCTCCTGG GGGAGGTAGTC ATG[G/A]CTGTG GGGCCCTGAGG TAGAGGGGC	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa.	9.00E-148	1
800	cg43985786	1352	GGTCTGTTTGA TGAAGTGGAAC C[A/G]AACAGCTC CCTCAGGCACAG AAGCA	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
801	cg43950886	894	TGTCCCTTCAGT ATTTTCATCCCTG C[A/G]CTGTCCTA GCACCCCTGTCGC TGGAG	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60921 HUS1+-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	8.1E-147	
802	cg43971525	829	CTGGTGAGGCC ATTTTCTCTCGC TTT[C/T]CCTGTT CAGCCTCCGGA CCAATCA	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11
803	cg43999829	685	GCCTGCTGTCAC CAGGGCGGAGG CT[G/C]ATCAGCA TCGAGATCAACC CCGACT	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143 (22q11.2)	22

804	cg43308029	1020	ACAGTTACCGCG TGTAACAATG C[C/A]GGCCCCA AGGATGAGGAC CAGGACT	C	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43819 CDNA HOMOLOGOUS TO YEAST SCO1 & SCO2 GENES AND C.ELEGANS C01F1.2 GENE - HOMO SAPIENS (HUMAN), 266 aa.	6.7E-143	22
805	cg43024858	413	GCGAGAGCAGC GACTTCGAATGC AA[T/C]CAGATGC TAGAGGCGCAG GAGGAGC	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60438 HT PROTEIN - CRICETULUS GRISEUS (CHINESE HAMSTER), 348 aa.	2.3E-142	22
806	cg43309726	616	ACTGTAAGAAGG ACCTGCTCCGCC G[G/C]GACGTGC TGTAACAAGG GCCGGC	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83064 KIAA1112 PROTEIN - HOMO SAPIENS (HUMAN), 694 aa (fragment).	5E-136	
807	cg43309726	623	GAAGGACCTGCT CCGCCGGGACG TG[C/T]TGACTA CAAGGGCCGGC TGGACAT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83064 KIAA1112 PROTEIN - HOMO SAPIENS (HUMAN), 694 aa (fragment).	5E-136	
808	cg43994220	323	TCGGGGTGTAG CCAGAGTCGGCT TC[G/A]GTGGTG AGGTCAGCGCCT CGGGCCA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
809	cg43948495	1189	TCCTACTCCTCC GTTCTCATATG G[G/T]GAATGGG TTGTCCTCCAC GGTCAC	G	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
810	cg43942432	811	TGTAAGCAGGGC GATGCTCTGCCG G[C/T]CCAGGGA CAACAGCCTTTC TCTTGC	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa.	5.30E-134	2

811	cg42910848	319	CGCAACACTAGA GACGTCTTCTGG CTT/CJGCCATCAG GGGACTCGGAG GTAGGG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132	
812	cg42910848	484	TGAAGATCTTTT CATAGTACTCGA TTC/TJAGCAGTTC AGTGAACATGTT CAGGG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132	
813	cg43918679	330	TGACGCGGAAG ATGGTTCTGACC CG[G/A]GCCAAG GCCTCGGAGCT GCACAGCG	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3.00E-131	21
814	cg43918152	356	AAAGTAATGGTC CAACAGACAGTT A[C/T]GCAGCCAT TTCAGAAAGTGGA TCGAT	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
815	cg43918152	362	ATGGTCCAACAG ACAGTTACGCAG C[C/T]ATTTTCAGA AGTGGATCGATT GCAGT	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
816	cg43918152	431	GTAATGGAGAG AAGAACAACGCG A[G/A]CGCTTGG AAGCCCTCGATG CCAATT	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
817	cg43918152	446	AACAAACGGAGC GCTTGAAGCCC TTC/TJGATGCCAA TTCTCGGAAGCA AGAAG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)

818	cg43918152	503	GGAAAGAAAAGG CAATAAGGAGC T[G/A]GAAGAGT GGTATGCGAGG CAGGAGC	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
819	cg43918152	509	AAAAGGCAATAA AGGAGCTGGAA GA[G/A]TGGTATG CGAGGCAGGAC GAGCAGC	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
820	cg43918152	518	TAAAGGAGCTGG AAGAGTGGTATG C[G/A]AGGCAGG ACGAGCAGCTAC AGAAGA	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
821	cg43918152	521	AGGAGCTGGAA GAGTGGTATGCG AG[G/A]CAGGAC GAGCAGCTACAG AAGACAA	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
822	cg43918152	542	CGAGGCAGGAC GAGCAGCTACAG AA[G/A]ACAAAGG CAAACAACAGGG TGGCAG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
823	cg43918152	548	AGGACGAGCAG CTACAGAAAGACA AA[G/A]GCAAACA ACAGGGTGGCA GATGAAG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
824	cg43928955	182	ACTCTTATGTGA AGTCTACCAAGC TT[C]GTGCTCAA GGGAACCAAGG CGAAGA	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.30E-129	

825	cg43917824	584	CAGTGGTGGTGT TCAGATTTTCC A[A/G]GAATTACC AGGCTCAGATCC GGTGT	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.30E-128	16
826	cg43917824	674	TCGGCCGGGAG AGGCACTCGTGT GATT[C]GCGCTG AATCGCTGGCTG GGAGAAC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.30E-128	16
827	cg44128041	132	GGCAGTATGAGAT ACAGCGAAGGG GGT[C]TGGATG GAGGACTATGAC TACGTTG	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.80E-128	
828	cg43926784	1062	ATACAAGCCATT CATAAACCTCAT C[G/A]CTGATGCA GAGTGTGTCATA TTTGA	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB44334 CYSTEINE CONJUGATE BETA-LYASE - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 419 aa.	6.70E-127	
829	cg43995142	894	ACAGTGAGATGGC CTGGGAAGTAAA C[C/A]CCCTCAAA AATATCTTTGTAA GCCA	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:O60660 ASH2L1 - HOMO SAPIENS (HUMAN), 628 aa.	8.00E-127	
830	cg43975901	682	CAGTTAAAGGCG TCACAGGACATG A[A/G]GTCTGCAA TTATTCTGGAAT GTTC	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30288 GOODPASTURE ANTIGEN-BINDING PROTEIN (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 624 aa.	2.60E-125	
831	cg43307940	788	GATCAAGTCCCT CACCTATACGGC A[A/T]ATTCTGTT GTTGTTCACTAA CAATG	A	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.10E-125	15

832	cg44028574	1607	AGGCCGAGTTCA GCCTTCTGCAGG A[A/G]CATCTGG GTGAGGGTCCA GCGAATG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4.00E-122	20
833	cg43958446	421	CGGGGCCATCT CAGATGGTCTCA TC[A/G]TCGCTCA TGTCCTCAGATCT CAGCAG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43069 HYPOTHETICAL 73.5 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 650 aa.	3.10E-120	
834	cg44002087	380	AATTCACAACG AAATCAATATGA A[C/A]GAAAAGGT GAAAAGGCACCA AAGCT	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60712 HYPOTHETICAL 26.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 236 aa.	2.90E-119	
835	cg29350504	989	CTGTAATAGATT CCTCACTGCTTG A[A/C]AGGCTTTC TATGGTCTCCCT TGCAA	A	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa.	4.70E-119	4 (4q21.1)
836	cg43067745	180	TCCCTACCTTAG AAGAAGGGAGG TG[G/A]TAGATGA AATGAACTGTAT GAAGAG	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	
837	cg43067745	210	TGAAATGAACTG TATGAAGAGCCA CT[C]AGCCCTGG CCACACACACAGA AGAAGG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	
838	cg43067745	225	GAAGAGCCACTA GCCTGGCCAC AC[A/G]CAGAAAG AAGGACTGGCC CGTCTTCT	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	

839	cg43919033	1463	CCGTGGGTTCCCG CGAGGCTCTGTG G[C/T]GTGGGCA TGCAGGCGTAGT TCCATT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
840	cg43919033	1511	ATTGTCTGTGTCAG AACCTTCCTTCT T[G/A]CTGAAGAT GCTCCTCACGGC CACTA	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
841	cg43919033	1577	GACACTGGTAGC TGAAGCCTTGCC G[G/A]TTCAAATT CACCCACCCATC ATCGC	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
842	cg43948724	1702	CATCTCATGAGT GTGCCCCATGG GT[C/T]CCCTCCC CTCTCAGCATT CCTTGT	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.90E-114	16 (16q21)
843	cg43036790	144	CTGTAACATCTT CCTCTTCCCAT C[G/A]GGGTGA ATCTATTGAAAT GTATAC	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.50E-110	
844	cg43325007	854	ACGGGTCCAC CTGGGTTTCAGG GAT[G/A]TAGCCC TTCTCTACAGCC AGCGGGC	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
845	cg42907145	903	GGCACTTCTCGG ACTCTCCAACT T[C/T]GCAGTGAA TTTGAAGGGTT GCTGG	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50461 LIM DOMAIN PROTEIN, CARDIAC (MUSCLE LIM PROTEIN) (CYSTEINE-RICH PROTEIN 3) (CRP3) (LIM-ONLY PROTEIN 4) - Homo sapiens (Human), 194 aa.	1.10E-108	11

846	cg43296554	173	CGGTACACGGTC GTCTCTCTCCTG C[C/T]CTCATCAG TGGCCTTCTCTC TTGGG	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15527 SURFEIT LOCUS PROTEIN 2 - Homo sapiens (Human), 256 aa.	6.40E-108	9
847	cg43997383	293	TCGAGGACCTGT CTGAAGACTTGG A[A/G]TGGAAT TATCTATGTGGG CTCTG	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43363 HYPOTHETICAL 23.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	8.00E-108	
848	cg43941085	500	GGGCCTGGGTTT GCTCCAGTTTC C[G/T]GGCTACC GAGGATTTTCAGT ATGTGC	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P53673 BETA CRYSTALLIN A4 - Homo sapiens (Human), 195 aa.	8.10E-108 (22q11.2)	22
849	cg43947512	425	TCAACAGGTTAG GAGAGTTGATCC TTC/TACCTCTGA GAGCAGCCGCT ATCAGT	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.10E-107	17
850	cg43947512	570	TCATAGAATCAG GATAGAAACAT G[C/A]NTCGGA AAGGCTGAGACA AAAGAG	A	???	???	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.10E-107	17
851	cg43979124	1071	CTCATCAAAGGA ATGCACTAGGAT TTC/TJGCGCGG GGTCTTTCTGGT TCCTGT	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	2.10E-107	
852	cg43945125	680	AGGACTTGTGT GGTACGTGCCTC G[C/G]GCCAGCA TGCCCTTGGGAG CCTCCT	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52566 RHO GDP- DISSOCIATION INHIBITOR 2 (RHO GDI 2) (RHO-GDI BETA) (LY-GDI) - Homo sapiens (Human), 201 aa.	2.70E-107	12

853	cg42854459	287	AGGGTAACCGCA AGTACTTGGTGA C[A/G]TTATGGAG GTTTATGGCATA CAGAG	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41342 HEPARANASE - HOMO SAPIENS (HUMAN), 543 aa.	3.50E-107	
854	cg42923937	543	CCAGGTCCAGG GGGTAGGTCAGT GA[A/T]GCCGGCT GTCGTTCCAGCC AGTGCGC	A	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43378 R29893_1 - HOMO SAPIENS (HUMAN), 216 aa (fragment).	4.40E-107	
855	cg42365149	259	TGGCGAACCA GCCAGGACTGC GC[G/A]CCGCCG GCCCGGCCGCCG GCACACCT	G	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA77398 TEN-M3 - MUS MUSCULUS (MOUSE), 2715 aa.	1.70E-105	
856	cg43991689	688	GGGCTTCGGTGT TGAACACGTAGG C[A/G]TCCAGGC TGAGCAGGTTTG GGTCAT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD45504 ENDOPLASMIC RETICULUM ALPHA- MANNOSIDASE I (EC 3.2.1.113) - HOMO SAPIENS (HUMAN), 663 aa.	2.50E-104	
857	cg43963123	1595	AGAACTTGACCG TGATCACAGTTC T[A/G]CCACCCTG GACCCCTCTCGGT GGCCT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.70E-104	17
858	cg43972159	1519	TGGCCGCCATCA CCTTCTTGATGT C[A/G]TCCTTGGC CCGGCTACGGG TCCTCGG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102 (12q24.1)	7
859	cg43943283	1114	ATGTGAGCGAAT TGGGCCCTTGTA C[A/G]CAAGGAG GCAAAGTTATT GGGGAA	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76994 INTRONIC PROTEIN 259 - DROSOPHILA MELANOGASTER (FRUIT FLY), 259 aa.	1.10E-101	5

860	cg43980312	2517	CTTCGGGCTGGGT CCATTTTCCTTTC [T/A]GAGTCAGAG AGGTGAACCTTTC TCTT	A	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.90E-101	8 (8q22)
861	cg42028329	109	CGGCGGCCAAG GAGAACCCGTG CAG[A/G]AAATTC CAGGCCAACATC TTCAACA	G	Arg	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
862	cg42028329	220	TGACGCAGGCAA AACCATTATG G[T/C]GGCTGGC TGCTCCTGGCTC CAGATG	C	Gly	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
863	cg42028329	223	CGCAGGCAAAAC CCATTATGGTG G[C/T]TGGCTGCT CCTGGCTCCAGA TGGCA	T	Gly	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
864	cg42028329	247	GCTGGCTGCTCC TGGCTCCAGATG G[C/G]ACCGACT TTGACAAACCCAG TACACC	G	Gly	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
865	cg42028329	268	ATGGCACCGACT TTGACAAACCCAG T[A/G]CACCGGT CTCGGAAATGGC AGCGAC	G	Val	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
866	cg42646578	422	ACCGATCACGGT TTTCAAAGTCTC T[G/A]TGAGCATA TCTTGCATAAGT CTTGT	A	His	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD31085 KU70-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	2.40E-99	

867	cg43925352	207	AGGAGTTGCAGC GGCGGCTGAAG CG[C/T]CTCTACC CGCCCGTGGAC GAACAAG	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.70E-97	6
868	cg43961552	454	TCATGTTGGCGA GCTATTTCCCTTAT [C/A]TCCATGTTT GGAGGAGTCAT GGTCT	C	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O75915 JVA PROTEIN - HOMO SAPIENS (HUMAN), 188 aa.	2.80E-96	3
869	cg43935925	597	GAGTACTCTCCA GAGGCTGGAGG TT[C/T]GTGCGGA GTTTGTACATGT GGTTGA	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.60E-96	16
870	cg43971745	1560	GAGGGTCCTCA GGCTCAGGGGT CTG[C/C]CCGCC AGGTGGGGAT GGGAGTGAG	G	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2.00E-95	1
871	cg43922566	874	CACCAGGTGCCT CTGCAACAATGA A[A/G]TACTCTGG CCAGTGGGCGA GGTATT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40190 N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT - HOMO SAPIENS (HUMAN), 178 aa.	3.40E-93	20
872	cg43968495	1510	CCAAGTCTACCT CTGGGGGGGACG CC[T/C]GGCTCA GCCCCCGCAGA CCIGCCCA	T	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.40E-92	3
873	cg43955549	1295	GACTATGAGCAA AGGAACAGTTTC C[A/C]ACATATTG ACATTTTCCCA GAAG	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82983 KIAA1031 PROTEIN - HOMO SAPIENS (HUMAN), 940 aa (fragment).	1.70E-91	16

874	cg43978148	805	TAAACAACCTCC TGCACAGTCTGC A[A/G]CTTCTGA GGCCTGTTCTGA AATAA	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4.00E-90	16
875	cg42341305	100	AACAGACTTTGC CAGATGAATATT C[G/C]AGTACAG ACACACCGTATC CCGGCA	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
876	cg42341305	124	CGAGTACAGACA CACC GTATCCCG G[C/T]AGCCTACC TCCAGAACTCCG GGTGA	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
877	cg42341305	130	CAGACACACCGT ATCCCGGCAGC CT[A/G]CCTCCAG AACTCCGGGTGA AGGCAG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
878	cg42463588	275	TTATTAATTCAA GGCATCTCTGAC [A/G]TATGCTGAA GCTCAGTTGAGA ATTG	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76852 KIAA1008 PROTEIN - HOMO SAPIENS (HUMAN), 928 aa.	8.20E-90	
879	cg43924895	200	AGGTTGGAGATC TCATCTATGGCC A[G/A]TTTGTGGT TGCTAATAAAGA CATGG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34097 CGI-102 PROTEIN - HOMO SAPIENS (HUMAN), 220 aa.	1.30E-89	9
880	cg43969092	638	GGCCGGCCATC AGCACGCCCTTC AC[G/C]CGTTCCT CCTCCTCACTGC ACTCGT	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74913 KIAA0890 PROTEIN - HOMO SAPIENS (HUMAN), 1194 aa.	6.30E-89	

881	cg43955651	521	CACACTCTCTGT GCATCGGCTTGC G[C/T]GTGTCGG GGTGGAAAGGAG TTGAACG	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.10E-87	2
882	cg43970868	507	TCTGGCTCTGGG ATATTCTGGCCT C[C/T]GACTTCAC ACCGGATGAGA GAGCTA	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa.	9.80E-87	12
883	cg43068353	456	AAATCCTTCTTT GGTTGACTTAA[T/C]TCTGTATTAG AAGAACCCCTTG TGG	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1.00E-86	2
884	cg43250258	123	AAATGATAGCAT CCAATAATGTCC C[G/A]ATACTTTC TTCTTGGAAGA GAGTT	G	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34116 CGI-121 PROTEIN - HOMO SAPIENS (HUMAN), 175 aa.	2.60E-86	2
885	cg43934734	1040	GTATGGAAATCT CATCCGGCTCCC C[C/T]TGGTACTC CGGCAGGTCAAT TTTCT	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.10E-84	20
886	cg43934734	617	GTCAAGCTGCCA AACTGCCAAAGT A[C/T]TCCTGCAG CTCCAGCAGGG CCCGGA	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.10E-84	20
887	cg43986941	388	TTGCACTAAAAG GATCTGTAGCTT TT[C]CCAGCTGA GAATGGAGTTCA GAATA	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16044 PREPRO-MELANIN- CONCENTRATING HORMONE - HOMO SAPIENS (HUMAN), 165 aa.	3.10E-83	12 (12q23)

888	cg43989507	273	GCAGGAGTGGA AACCAGTAGCTG TC[G/A]TCGGGC CACATGTCCTTG AAGGGGA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36639 7,8-DIHYDRO-8- OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) - Homo sapiens (Human), 156 aa.	3.90E-83	7 (7p22)
889	cg43970119	426	CCATTAGTAGGC AAATGTGCTCTG C[G/A]AATTCTCG GATGGCACCAC GGCCAC	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa.	1.00E-82	12
890	cg43120215	1007	GGCAGCACTTG GACAGGATGCTG AA[G/C]CCGGCT GCAATGAAGATG AC	G	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa.	1.30E-82	7
891	cg44007579	95	GCTACCGCAGC CGCTGGTTCGTG TT[C/T]GACGCGC GCCGCTGCTACC TTTACT	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83007 KIAA1055 PROTEIN - HOMO SAPIENS (HUMAN), 868 aa (fragment).	2.20E-82	
892	cg43322319	622	ATGCCCTACAAGA CTATGAAAGAGG A[C/T]GAAAAAAG ATACAAATGAAAG AATT	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41267 HYPOTHETICAL 66.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 609 aa.	1.20E-81	
893	cg43917139	113	CTTGGCTGGTGG CCGGCTTGGGT T[C/T]GCTTGAC ATTCAGCACATA ATCAT	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76671 CARBONIC ANHYDRASE VB - HOMO SAPIENS (HUMAN), 317 aa.	2.50E-81	X
894	cg43321624	660	AATAACGTGGAT TATGAGGGGCCT C[G/A]GTCACAG CCTGCAGTTCGT AGGGGA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60377 P1.11659_5 - HOMO SAPIENS (HUMAN), 188 aa (fragment).	1.10E-80	9

895	cg42903844	671	TGGTGCCTGTCA GCAAGCCCGGT GC[A/C]CTTCGTC GCTCCCTGTCCC GCTCCA	A	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O15273 TELETHONIN - Homo sapiens (Human), 167 aa.	1.40E-80	17
896	cg43969140	425	CAAAGATGGACA CCAGCGAATCAT CT[C]AGTAATAA GTCTGTCTCCTT CCCAA	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
897	cg43969140	515	CCGCCTTGTGG GCTCGGCCCA CTC[G/T]CCAGTC ACAAAGGCATCA TTAACAC	G	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
898	cg43969140	605	CCTCAGCCTGCT CCACAAACCCTG G[C/G]AGGTGTG TCTTGGAAACATC CAGGGG	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
899	cg44024149	417	ATTCCACAGAA TGATCAAGTTGA C[G/C]ACAGGAA AGGAAGCCGCA CTCAGTT	G	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)
900	cg44024149	453	AAGCCGCACTCA GTTATGGCTTCT A[C/T]GGCTGCC ACTGTGGCGTG GGTGGCA	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)

901	cg43969316	338	GCTCGAGCTACA GTGGACTACTTG A[G/A]CGACATCA TATTCACACCAA AAATG	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
902	cg43969316	371	ATATTCACACCA AAAATGTAGAAC A[C/T]ATAATTGA TAGTTTACGGGA TGAAG	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
903	cg43969316	374	TTCACACCAAAA ATGTAGAACACA T[A/T]ATTGATAG TTTACGGGATGA AGGGA	A	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
904	cg43969316	377	ACACCAAAAATG TAGAACACATAA T[T/A]GATAGTTT ACGGGATGAAG GGATTG	T	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
905	cg43969316	443	AGCGAGGGAG TACGATGAAGAG AC[A/T]GTTCGAT GGCAGACGCT GTCATAG	A	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
906	cg43969316	458	ATGAAGAGACAG TTCGATGGGCAG A[C/T]GCTGTCAT AGCTGCGGGAG GTGATG	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
907	cg43327305	199	CACCTGCCCTTAA AATTTAAGGTTG A[A/G]AATTTCTT CTGTATGGGATC CCCAT	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46606 PHOSPHATIDIC ACID- PREFERRING PHOSPHOLIPASE A1 - BOS TAURUS (BOVINE), 875 aa.	6.10E-78	

908	cg43973026	689	ACAAGGTACTAG CTATGACCAACC G[A/G]AACTTGTC ACCCAAGTCTAC AGGGT	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P52434 DNA-DIRECTED RNA POLYMERASES I, II, AND III 17.1 KD POLYPEPTIDE (EC 2.7.7.6) (RPB17) (RPB8) - Homo sapiens (Human), 150 aa.	1.00E-75	15
909	cg43931888	295	CCTGGCCACCC CAACGCCGAAC GC[C/G]TCCAGG GAGGCCACCT GGGAACCC	C	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16192 ORF3 5' OF PD-ECGF/TP - HOMO SAPIENS (HUMAN), 157 aa.	1.00E-75	22
910	cg42897014	515	TGCGCTCCTGCG GCCGGGCCCGG GC[G/A]TCGGT GGCAGCGCCAG GAGGCAGA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.70E-75	11 (11q13)
911	cg43155233	81	AGGATGCATTAA ATACAACTGAGA A[C/T]AAATTGCT TGATGCATATAC TCAGA	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46427 HYPOTHETICAL 88.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 785 aa (fragment).	5.60E-75	
912	cg44012742	226	CCCCCATCCAGA ACATCTCATCCA A[T/C]GTGCTAGA GGAGTCCGCCAT CTCCG	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.80E-74	
913	cg36728314	198	TTGGAGTGTGG CAGTGGGAGGG AC[G/A]TCGATCC GAAGCTCTTTCT GGCTGG	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	1.30E-73	
914	cg43932428	588	CAATGGCCCGCT CGATTTTGCCAA G[C/A]ACCTGGT ATTGGGTATGGC CCGTC	C	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.50E-72	

915	cg43934599	837	AGAGGGAAAAG CCAGCAAGACCC A[G/A]AAGCTTTT CCATAGGCTTAG AGAGG	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34127 CGI-132 PROTEIN - HOMO SAPIENS (HUMAN), 137 aa.	3.70E-71	10
916	cg43045396	269	AGGAGCAAGCC AGCTGCCCTTCAC TC[T/C]CGGACAT AAATTCTGGTGC AGACCA	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
917	cg43045396	386	GGCCGTCCCTTC CAAGAAGAGTTT G[C/G]GTGCAGT GGATCTTGTTCT CATTCT	C	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
918	cg43045396	503	TGAAGTTGATCT CAGTGGTGCGC AC[C/G]GTGGTG GATGCTTGATG TAGAACT	C	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
919	cg43045396	617	GCATGGCGTTCA CACCCAGTGCCT T[C/G]AGCAGCT CGTCGAAATTCT CGCTGC	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
920	cg42696021	431	GCTTCACACAGT GGCTGTGCCGC CT[T/G]CACAAATG AAGTGAACCGGA AGCTGG	T	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
921	cg42696021	449	GCCGCCCTTCACA ATGAAGTGAACC G[G/C]AAGCTGG GCAAGCCTGATT TTGACT	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	

922	cg42696021	467	TGAACCGGAAGC TGGGCAAGCCT GA[T/C]TTTGACT GCTCAAGAGTTG ATGAGC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
923	cg42696021	470	ACCGGAAGCTG GGCAAGCCTGAT TTT[C/G]ACTGCT CAAGAGTTGATG AGCGAT	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
924	cg42696021	485	AGCCTGATTTTG ACTGCTCAAGAG TTT[G/G]ATGAGC GATGGCGTGAC GGCTGGA	T	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
925	cg42696021	494	TTGACTGCTCAA GAGTTGATGAGC G[A/C]TGCGGTG ACGGCTGGAAG GACGGCT	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
926	cg42696021	500	GCTCAAGAGTTG ATGAGCGATGGC GTT[C/G]ACGGCT GGAAGGACGGC TCCTGTG	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
927	cg42921698	532	AGACCACTCCG ACGTGTCCAGCC G[G/T]GGGTTGA AATGCAGGGCG GCATCGG	G	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19
928	cg42921698	547	TGTCCAGCCGG GGGTTGAAATGC AG[G/C]GCGGCA TCGGAGCCCTG CTCCTCCC	G	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19

929	cg42921698	664	TGCCAGGGCGG ATGCCCTCGGG CAG[C/T]GAGGA CTTGTGGGGGA CGTGGACA	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19
930	cg42721336	1100	CCAGCTCCTGTG CTGGCCTCTTCA T[C/T]GCCCTACA CATCGGCTTCGA CTGGC	C	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P34629 PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-) - Caenorhabditis elegans, 491 aa.	3.30E-69	
931	cg43930848	573	TACGGGCGCGC GTGGCGCACTCC GCA[A/G]CGCGT TCAGGACCCCG GCGGGGCA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa.	7.90E-69	7 (7q21)
932	cg43323149	526	GCCTGACTAGTG TGCTGAGCACCA G[C/T]GGAAGCC CTACAGACGGAC TCAGCG	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
933	cg43323149	541	TGAGCACCAGC GGAAGCCCTACA GA[C/T]GGACTCA GCGTCATGCAAG GGCCCT	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
934	cg43323149	547	CCAGCGGAAGC CCTACAGACGGA CT[C/T]AGCGTCA TGCAAGGGCCCT ACAGCG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
935	cg43323149	550	GCGGAAGCCCT ACAGACGGACTC AG[C/T]GTCATGC AAGGGCCCTACA GCGAAA	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1

936	cg43323149	553	GAAGCCCTACAG ACGGACTCAGC GT[C/T]ATGCAAG GGCCCTACAGC GAAACAG	C	T	Val	Val	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
937	cg43323149	577	TCATGCAAGGC CCTACAGCGAA C[A/G]GCCAGCT TTGCTGCCCTTT CAGGGG	A	G	Thr	Thr	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
938	cg43323149	589	CCTACAGCGAA CAGCCAGCTTTG C[T/A]GCCCTTTC AGGGGGCACAC TGAGTG	T	A	Ala	Ala	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
939	cg43323149	595	GCGAAACAGCCA GCTTTGCTGCCC T[T/C]TCAGGGG GCACACTGAGTG GTGGCA	T	C	Leu	Leu	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
940	cg43323149	607	GCTTTGCTGCCC TTTCAGGGGGCA C[A/G]CTGAGTG GTGGCATTCTCT CCAGTG	A	G	Thr	Thr	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
941	cg43323149	616	CCCTTTCAGGGT GCACACTGAGTG G[T/C]GGCATTCT CTCCAGTGGCAA GGGAA	T	C	Gly	Gly	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
942	cg43323149	646	TTCTCTCCAGTG GCAAGGGAAT A[C/T]AGCCGGTT AGAAGTTCAAGC CGATG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1

943	cg43323149	650	CTCCAGTGGCAA GGGAAAATACAG C[C/A]GGTTAGAA GTTCAAGCCGAT GTCCA	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
944	cg42017985	338	ACAATCTATGCA GTGAAAGAGCTT A[C/T]GATCCTAA GCACCTCCATAA TAGGG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P56180 PUTATIVE PROTEIN- TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - Homo sapiens (Human), 551 aa.	1.80E-68	
945	cg43942922	234	CCACATCTCAGG CCACTAGGGG AG[A/G]ACAAATA GGTCCTCTGTCA AGACCC	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
946	cg43942922	345	TCACCTCTGAGC CCACATCTCAGG C[C/T]ACTAGGG GAAGAAAAATA GGTCCT	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
947	cg43942922	366	AGCCCACTAGG GGAAGAAAAAAT AG[G/A]TCCTCTG TCAAGACCCCTG AAACAG	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
948	cg43271511	252	ATGACGGCACTG TCAGAAAGGAAT C[C/T]GGCATTCC GTCAGGCAAAAT TGAGG	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD15557 T-CELL RECEPTOR GAMMA CHAIN, TRGV9 - HOMO SAPIENS (HUMAN), 137 aa.	3.40E-68	7 (7p15)
949	cg42831353	788	GCACCGCGGCG GTGGTGAGGAC ACA[G/A]GCTGC GGTGTAAGCCC GCGTCACCG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.30E-67	22

950	cg43973869	385	TGGCGGCACAA CTGCGGCTGATA CC[C/T]TGGGTG GAAAAGATCAGA ATGACAG	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD36983 MAP KINASE PHOSPHATASE-LIKE PROTEIN MK- STYX - HOMO SAPIENS (HUMAN), 313 aa.	3.10E-67	7
951	cg43999983	413	CTTCCAAATTAG CTTCAGTTTTC GT[A/J]GAGCAAC CATTAAATCCTAT ATAAA	T	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43446 HYPOTHETICAL 34.0 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 299 aa.	1.00E-66	
952	cg43080742	266	AGACGGTGGCC TCGCTGTGGCC GGC[G/C]CTGCA GGAAGTGGCCC GGTGTGGGA	G	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P53603 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Pig), 541 aa.	2.20E-66	21
953	cg43927424	304	CGCAGTATTTC GAGAAAAGTATA C[T/A]CTTCAGCT GAAGTACCCGCA CCCTC	T	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.90E-65	
954	cg43919145	1731	CCTCAACAGACT GCCTTTGTTCAC T[G/A]TCTGGAGA AGATAGCAAAGG AGTAG	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment).	3.20E-65	1
955	cg42381630	261	CGACCTATTATT GGCCTAGACCAA G[G/A]CGCTATGT ACAGCCTCCTGA AATGA	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	

956	cg42381630	267	ATTATTGGCCTA GACCAAGGCGC TA[T/C]GTACAGC CTCCTGAAATGA TTGGGC	T	C	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
957	cg43132517	529	TCCATCTTCAGA CACCCCCCGTC T[C/T]TCTGCACA GGGAGTTGGCC TTCCAG	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.60E-63	
958	cg43132517	556	CTGCACAGGGA GTTGGCCTTCCA GT[A/G]GGTGTT GCTCTTCTGTCT TGACGTC	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.60E-63	
959	cg43950549	237	AGAAACCGGATG ATGCACAGTATT A[C/T]TGTCAAAG AGCTTATTGTCA CATTG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.40E-62	
960	cg43950549	432	GACAAAAATTAG ATAGTCAGATA C[C/T]AATTTCAG TGACTGGATTAA AAGGT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2, ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.40E-62	
961	cg43969918	863	TTGCGGCCACTT GGCCCTTGAGAA T[G/A]GCAGCTTT TCCTCGGCCAGC CCCTG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P43331 SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) - Homo sapiens (Human), 126 aa.	2.90E-62	22
962	cg43950850	526	CCGTCGCGATC GGCCTCCGCCG GAT[C/T]AGGTTA TCAATCAGGCCG GAGCAGT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (Cl-B14.5B) - Homo sapiens (Human), 119 aa.	7.80E-62	11

963	cg42672206	593	GCCCTGAGACCA CTAACCTTGAT TTCJTTTACAGG CTCAGAGACCAT GGAAC	T	C	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O55129 MICROTUBULE- ASSOCIATED PROTEIN 6 (STOP PROTEIN) - MUS MUSCULUS (MOUSE), 906 aa.	1.30E-61	
964	cg44926530	1939	CTGCACAGGTCA CAATATATTTATA [G/A]GCTTTTCCC AACTTAACCAGG TGTG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.10E-61	X
965	cg43918476	2024	TGAGCATGACCC GATCTTGAACCT C[A/G]CTGTACTG CAGGTTAACTAC CTTGT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa.	6.30E-61	2
966	cg43285334	682	CGGTGACCCGG GCGTCAGTGTC CC[G/A]TAACAG AGTAGGCCAGCA GTGATC	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.90E-60	1
967	cg42313635	272	GGGTGAGCAGC AAACAGGAGGTG AC[A/G]CAGATT CTGCAGCTCTGA GTGTC	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:G598237 T CELL RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 134 aa (fragment).	8.00E-60	
968	cg43985327	429	TCGCGCAGGCC AGACAGCGGTG CAG[A/G]CCGCC CCCTGGCAGGT CGGGGTCTGA	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.10E-59	1
969	cg43939569	691	GCATCCTCAGCT CGGAGATGAATT C[G/T]CTTCCGGA TCAAGAAGTAGA ACTGA	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.50E-59	17

970	cg43924537	521	ATCCATTGGCTT TATCCACAGCCT GIC/AJAGGACTC GCTGGATGCTCT CCTTGT	C	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1,20E-58	
971	cg43920127	340	AAAGATGCAGTT CATAATGTTCTC CIC/AJGATTCAGG AACTCTTATGCT GTGTC	C	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q75273 R26984_1 - HOMO SAPIENS (HUMAN), 508 aa (fragment).	3.10E-58	15
972	cg40968986	217	CGCGCCTCCTG CTGGCTGCACTG GTIG/CJGAGGAC TATGTGCAGATG AAGGCCA	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
973	cg40968986	262	AGGCCAGTGAG CTGGAGCAGGA GCA[AV]GAGAG AGAGGGCTCCA GAATCATTTG	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
974	cg40968986	304	GAATCATTTGCC AGAAGAGAGCCT GTICJGACACTG CCACCTGTGTGA CTCATC	T	C	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
975	cg40968986	361	CAGGCTTGCTGA GCAGATCAGGG GGT/CJGTGGTG AAGAACAACTTT GTGCCCA	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
976	cg40968986	379	CAGGGGTGTG GTGAAGAACAAC TTT/CJGTGCCCA CCAATGTGGTT CCAAAG	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)

977	cg42165815	217	GGATCCTGGCCTA CGGAGAAAGCGG TC[A/G]TAGAAAG GAGAGCGCAAC AGGTAGT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD22466 PEROXISOMAL BIOGENESIS FACTOR 16 - HOMO SAPIENS (HUMAN), 336 aa.	3.50E-57	
978	cg43052776	294	AGGGTGGGAGA TTCCTGATGGGA AC[G/A]AATTCTC CAGACAGCAGA GATGGTG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43247 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 323 aa (fragment).	3.60E-57	
979	cg4399272	459	AGAAAGCGGTG ACTCCAGCTCCT CC[C/T]ATAAAGA GGTGGGAGCTG TCCTCGG	C	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa.	3.20E-56	19
980	cg43300763	922	CTCGGCGAAG AGCATCTTTGAA TA[C/T]CACCGCA TAGAGCTGGACC CCAGCA	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18500 HYPOTHETICAL PROTEIN C36E8.3 - CAENORHABDITIS ELEGANS, 476 aa.	3.20E-56	
981	cg43319008	251	TTAAATTATATAG CAGCATCACCAA [C/T]CAACAGAG GAGATACCTTGA GAAGC	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA20786 KIAA0328 PROTEIN - HOMO SAPIENS (HUMAN), 1661 aa (fragment).	9.20E-56	2
982	cg43869932	1229	CGTTCTGCACCG TCTCCTTCCGAG C[A/G]TTGAATTT CTTCCCCCTTGTA GATGT	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20124 SIMILAR TO S. CEREVISIAE YJU2 PROTEIN - CAENORHABDITIS ELEGANS, 323 aa.	1.10E-55	
983	cg43935092	99	TGGAGCGGTGC CAGCAGCAGGC GAA[C/T]GAGGT GACGGAAATTAT GCGTAACA	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD26992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa.	1.80E-55	2

984	cg43942680	699	CGGAGGAGAGC GCCCTCAATCAC GT[G/C]CAGCAC CCGAGCGACGA AGCCGAGG	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38498 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 127 aa.	1.80E-55	10
985	cg43269198	536	GCTGGCAGTCTA CCACGCTGATTT G[G/A]AACTCGCT GGAAGGCAACAT TTCAA	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41301 DJ596C15.1.1 (NOVEL PROTEIN) (ISOFORM 1) - HOMO SAPIENS (HUMAN), 162 aa (fragment).	1.80E-55	20
986	cg43917388	701	GGATGTCCACAT TGACCACGTGCA C[A/G]GGCTGGC AGGTCTCCTGTT CTCTGG	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q22453 SIMILARTO LDL RECEPTOR-RELATED PROTEIN. NCBI GI: 1055166 - CAENORHABDITIS ELEGANS, 1357 aa.	2.30E-55	1
987	cg43917989	775	TGGGCATGCTTG CTGGGGCCGCC AC[G/T]GGTGCT GCTCTTGGCTCA CTTATGT	G	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
988	cg43917989	793	CCGCCACGGGT GCTGCTCTTGGC TC[A/G]CTTATGT GGTCGCCCTTGCT GGTTCT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
989	cg43917989	796	CCACGGGTGCT GCTCTTGGCTCA CTT[C]ATGTGGT CGCCTTGCTGGT TCTGAG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
990	cg43917989	808	CTCTTGGCTCAC TTATGTGGTCGC CT[C]TGCTGGTT CTGAGCCCTGG GGCTCG	T	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11

991	cg41664708	357	AGCAATCGACCA ATACAGCTGTGA C[C/T]CTGACTGG CTAGTAGTCTCT GGCAC	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P47892 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2.00E-54	1
992	cg43332460	324	GGAACATCTGCG TCAGCTCCGTGT C[T/C]CCAAACTC CTGGGGGAGGT GGTAGA	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	5.40E-54	
993	cg42855650	520	CCGGGCCCTC ATAGGAGAGGAA GC[T/C]CGGGAG GTGCCAGGCG GCAGGAAG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O00230 CORTISTATIN PRECURSOR [CONTAINS: CORTISTATIN-29; CORTISTATIN-17] - Homo sapiens (Human), 105 aa.	7.90E-53	
994	cg42903443	49	TCACCGCCAGGA GGACGCATTCTG GC[G/C]GAACCC AGAGCCAGCGAT GCGCACA	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45012 573K1.15 (MM17M1-6 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY) (OLFACTORY RECEPTOR LIKE) PROTEIN)) - MUS MUSCULUS (MOUSE), 309 aa (fragment).	1.90E-51	
995	cg44027270	229	CAGAGTCCATTA CTTTCTCTCTGT [A/G]AATTTCAC GTTGTTGTCTTT CTG	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14737 TFAR19 - HOMO SAPIENS (HUMAN), 125 aa.	2.20E-50	
996	cg44027270	499	GTTGGGCCGCAT CACCAGGATCCT G[T/G]CGGCTAA ACTTGGGTCATA ACAAC	T	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14737 TFAR19 - HOMO SAPIENS (HUMAN), 125 aa.	2.20E-50	
997	cg41568177	226	CATTCTTGTCCT TTTCTCAAAGA C[A/G]TCGGCGA GGTAATTGTGC CCTTT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P31151 S100 CALCIUM-BINDING PROTEIN A7 (PSORIASIN) - Homo sapiens (Human), 100 aa.	4.50E-50	1 (1q21)

998	cg44010855	651	CCTGGAACGAGAC AGCGCAGGGTC TA[C/T]GAAGAAT AGGGTGAAAAAC CTCAGA	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.80E-50	5
999	cg44917490	446	TCTGGGCTCGG CTGAAGGGGTG AAG[G/A]GGGCC GGGTCAGGGTC GTTCCCTCCA	G	A			SILENT- NONCODI NG	amyloid	Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa.	0.00E+00	19
1000	cg43921977	3515	CAGCCGCGGAC CGTAGCTGGCAG TA[C/T]CCGCTCC TGCCGCCGCTC CGCCTCA	C	T			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
1001	cg43921977	442	GGAATTCGTGAC AAGTTCAAAAGG A[G/A]AACTTCCT TTGTTTAAATGCA GCTG	G	A			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
1002	cg42840476	5048	TGTAATCCCAGC TCCTTGGAGGC T[A/G]AGACAGG AGGATTCCTTGA GCCCTG	A	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:O14727 APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1) - HOMO SAPIENS (HUMAN), 1194 aa.	0.00E+00	
1003	cg43970780	245	GGCAGGAGATAA ACCATCCAGCAG A[T/G]TTTTCTGT GTAAAAACATTT ATTTT	T	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSNEW-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.lpcis:SWISSPROT-ID:Q92785 ZINC- FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.	2.30E-212	11

1004	cg44001801	997	AGTAAATATCCC CTTGGCTGTGT TTT[<i>gap</i>]GTCAAA CATTGGGATTCT TTTTGCC	T	<i>gap</i>			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1005	cg44001801	1041	TTTTGCCAAGTG CAAACATGACTC TTA[G]CCACTGTT ACCACCAATTGC AGTGG	A	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1006	cg44001801	1050	GTGCAAAACATGA CTCTACCACTGT TTA[G]CCACCAAT TGCAGTGGACAC AGCCA	A	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1007	cg44001801	1238	AATTCAGAGAAC AAAAGACAGCAC C[C/ <i>gap</i>]AGAAAG TTTCTTCCCTGTT GAATCA	C	<i>gap</i>			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1008	cg44001801	270	TATTTTAAAGCTA TAACAGATTTTG C/GJACATAAAGC CAAAACAGATTG TTTT	C	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10

1009	cg44001801	571	CAGCTCACTCCA TCTCAGTCAGTG G[C/T]TTTGTCT TGTCATGGCTCC ATTTT	C	T				SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1010	cg44001801	714	AAACCTCTTCCC ATTATCCTCATA G[C/A]CCTGGGT GTGGTAACAGCT TCTTGC	C	A				SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1011	cg44001801	747	GTGGTAACAGCT TCITGCTGTTTG G[C/G]TTCTCTTT TATCATCTATGTA AGTC	C	G				SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1012	cg44001801	755	AGCTTCTTGCTG TTTGGCTTCTCT T[T/A]TATCATCT ATGTAAGTCAAT TTCCT	T	A				SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1013	cg43921971	1242	CAGCTGCATTAA AACAAAGGAAGT TTT[C]TCCCTTTTG AACTTGTCACGA ATTCC	T	C				SILENT- NONCODI NG	apoptosis	Human Gene Similar to SWISSPROT- ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	6.10E-68	
1014	cg43042134	636	TAATAAATTAAAT CTAAAGTTTAGA[T/C]GATGTTTGG GTTCTTCTTCAT GAAA	T	C				SILENT- NONCODI NG	apoptosis inhib	Human Gene SPTREMBL-ID:Q13489 INHIBITOR OF APOPTOSIS PROTEIN 1 - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	11

1015	cg43983747	26	TTTTTTTTTTT TTTTTTTTTTT[C /TTCATTAAACTT CTGGGCTTTATT TA	C	T				SILENT- NONCODI NG	apoptosis inhib	Human Gene Homologous to SWISSPROT-ID:Q92843 APOPTOSIS REGULATOR BCL-W (KIAA0271) - HOMO SAPIENS (HUMAN), 193 aa.	2.1E-101	
1016	cg43983747	28	TTTTTTTTTTT TTTTTTTTTTT[C /TATTAAACTTCT GGGCTTTATTTA TT	C	T				SILENT- NONCODI NG	apoptosis inhib	Human Gene Homologous to SWISSPROT-ID:Q92843 APOPTOSIS REGULATOR BCL-W (KIAA0271) - HOMO SAPIENS (HUMAN), 193 aa.	2.1E-101	
1017	cg43324271	2553	CCTGTTAAAAAC AAAGTGCAGTCA G/A/TTCTAAGC CCTGTTCAAGAGA CTTCG	A	T				SILENT- NONCODI NG	apoptosis recep	Human Gene SWISSPROT-ID:Q13546 SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN) - HOMO SAPIENS (HUMAN), 671 aa.	0	6
1018	cg43917593	308	CAGATAAGCAAG TGAGATCCTCTG G/C/TCCCTTAATC ATCAATATACTC AAATG	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:Q99460 26S PROTEASOME REGULATORY SUBUNIT S1 (P112) - HOMO SAPIENS (HUMAN), 953 aa.	0	2
1019	cg43987714	2968	AGTGACCACCAG GGGCTCTGAACT G/C/TAGCTGATG TTATCAGCAGGC CATGC	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa. pcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3

1020	cg43987714	2992	GCAGCTGATGTT ATCAGCAGGCCA T[G/gap]CATCCT GCTGCCAAGGG TGGACACG	G	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa. pcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3
1021	cg43924820	1166	CAAATACCTGGA TTTTTTTTTTTTT gap/TGTACACTG GTTTCATAGATCG GCACT	gap	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:Q14974 IMPORTIN BETA-1 SUBUNIT (KARYOPHERIN BETA-1 SUBUNIT) (NUCLEAR FACTOR P97) (IMPORTIN 90) - HOMO SAPIENS (HUMAN), 876 aa. pcis:SWISSPROT-ID:Q14974 IMPORTIN BETA-1 SUBUNIT (KARYOPHERIN BETA-1 SUBUNIT) (NUCLEAR FACTOR P97) (IMPORTIN 90) - HOMO SAPIENS (HUMAN), 876 aa. pcis:SPTREMBL-ID:Q14974 NUCLEAR FACTOR P97 - HOMO SAPIENS (HUMAN), 876 aa.	0	17
1022	cg43944573	820	AGGAGCCACCTT TGCTGGGCTCG GC[C/gap]TCTAC CAAGCAGAAATG CGATTACA	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:Q99721 TBP-ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 947 aa (fragment).	0	20
1023	cg43277630	3793	ATCATGTTTCTG AGACCACAGTTT A[A/C]AACAGGTG TGCCTGTTGCTT TCCTC	A	C				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)

1024	cg43277630	3794	TCATGTTTCTGA GACCACAGTTTA A[A/C]ACAGGTGT GCCTGTTGCTTT CTTCC	A	C				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1025	cg43277630	4360	TCGTGGGGTTCA GTAGAGAAATTC A[G/T]TGACTAGC GCCTGGCCCTGT GTGGC	G	T				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1026	cg43277630	4504	CCACAGCACCCC GAAGGGAGCAT CT[A/G]TTTACCT GGCAGTGGCTCT CAGAGC	A	G				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1027	cg43920091	21	TTTTTTTTTTTT AGGGGGC[G/A]G GACATGCTTTAT TTTCAGCCACAG	G	A				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:Q13608 PEROXISOME ASSEMBLY FACTOR-2 (PAF-2) (PEROXISOMAL-TYPE ATPASE 1) (PEROXIN-6) - HOMO SAPIENS (HUMAN), 980 aa.	0	6 (6p21.1)
1028	cg43247872	1766	GTTGATAACCAT ATGCACCTTAACA T[T/gap]ATATTCT ATAAACATTAAAG TAGTGC	T	gap				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1029	cg43247872	1802	ACATTAAAGTAGT GCCAGTTATGAG A[gap/C]TTCCCA GTTCTTACTAAAT IGTATT	gap	C				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1030	cg43247872	1878	TATCACATGTAA CTAATAATTGAA [C/G]TATACTTGA AGGACCGTGTG ATGT	C	G				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21

1031	cg43247872	1943	GGTTGGAAGATA GCAGTATTATTA G[C/gap]ATAAGC TGCATACGTAAT ATTCAGT	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1032	cg43247872	2121	TATTCAAATGTTT CAGCACCATATA A/GTAGAAATAC CCAATTATATTCT AGT	A	G				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1033	cg43958825	101	CGTGAGACTGG GGCTGGCCTGT GTG[C/gap]CCTA GGCGTAGTATTG TAGGTTGGC	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1034	cg43958825	103	TGAGACTGGGG CTGGCCTGTGTG CC[C/gap]TAGGC GTAGTATTGTAG GTTGGCTT	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1035	cg43958825	38	TTTTTTTTTTTT TTTTTTTTTTTTT GJTTTGACCCTA AACCATCTTTTAT T	T	G				SILENT- NONCODING	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1036	cg43975309	160	TAGTGTATAGAA CATTTCACAATTA [C/T]TACTCATCTT TTACATAACATCT TGA	C	T				SILENT- NONCODING	ATPase_ associate d	Human Gene SPTREMBL-ID:Q93529 F18C12.2 - CAENORHABDITIS ELEGANS, 2245 aa.	5.8E-184	3
1037	cg43975309	553	AACAAATGTGCT TACATACACCAA G[A/gap]AAAAAA AAATTCCTTGCT ACCCACT	A	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene SPTREMBL-ID:Q93529 F18C12.2 - CAENORHABDITIS ELEGANS, 2245 aa.	5.8E-184	3

1038	cg43300636	224	GGTCAGGAAGG AGGTCTGGCAG GAC[C/gap]TGCA GTGGGCCCTAGT CATCTGTGG	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H+)-TRANSPORTING SYNTHASE) (H+)-TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.7E-175	
1039	cg43945992	1220	CCGATCTCCACT GTTGGGTGGGT GG[G/gap]CCCTG CCGGGACCCCTG CTCACAGGC	G	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P13686 TARTRATE-RESISTANT ACID PHOSPHATASE TYPE 5 PRECURSOR (EC 3.1.3.2) (TR-AP) (TARTRATE- RESISTANT ACID ATPASE) (TRATPASE) - HOMO SAPIENS (HUMAN), 323 aa.	1.1E-173 (19p13.3)	
1040	cg43918426	356	GCAGTCGAGCG CCACGGCTGCTC AT[C/T]GGATGAT CCAGGATGGGT CCTTGGC	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1041	cg43918426	427	CGAGGATGGCC AGGCCGTGTGT GCT[C/T]TTCCCA GTGCCGAGGTA CCTAJCGC	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1042	cg43918426	445	GTGTGCTCTTCC CAGTGCCGAGG TA[C/T]CTATCGC TCACGGCCAGG AGCTTGT	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1043	cg43991972	193	TTTTTTTTTTTT TTTTTTTTTTTTG TTGCCCTTAGAGA GGGCAGTTTTAT TGT	G	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:Q25531 40- KDA V-ATPASE SUBUNIT - MANDUCA SEXTA (TOBACCÓ HAWKMOOTH) (TOBACCÓ HORNWORM), 348 aa.	7.2E-154	

1044	cg43947105	1689	TCTCGTCTTCG TCATGGTGTGCG C[G/gap]CGGACG GCGAGAGGAGC TGGGGCCG	G	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.6E-152	
1045	cg43947105	1763	GCGGAGGCGCG TCCCGGCTCCG GCG[G/gap]CGCA GCCCGGAGACG GCAGTGAAGG	G	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1046	cg43947105	492	CTGTTGACATCA AAATATGACAGT T[G/gap]TTATATC CATAAAATATTTA CATAG	G	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1047	cg43947105	575	TAAACCACATAA AAAGAGGACAAG A[C/A]CCCCATCC TACATGTTTGGA ATCAG	C	A			SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1048	cg43947105	587	AAAGAGGACAAG ACCCCGATCCTA C[A/G]TGTGTTGGA ATCAGGTGTTCA CCGGT	A	G			SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	

1049	cg43947105	609	TACATGTTTGGG ATCAGGTGTTCA C[C/G]GGTCCCT ATCTGGCGACTG TACACT	C	G				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1050	cg43927442	303	TTGTTTTTTTTT TTTTTTTTTTTTTT ATCCACATTCAG TTCCTTTATTAA T	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. lpcis:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.40E-146	17
1051	cg43927442	304	TGTTTTTTTTTT TTTTTTTTTTTTTT AJCCACATTCAGT TCTTTATTAAAT T	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. lpcis:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.40E-146	17
1052	cg43972614	146	GTTGTTTTTTTT TTTTTTTTTTTTTT AJATCGAGAATTC ACTGTTTATTGT G	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G2791859 RIBOSOMAL PROTEIN S4 Y ISOFORM - HOMO SAPIENS (HUMAN), 263 aa.	1.00E-140	Y (Yp11.3)
1053	cg43972614	148	TGTTTTTTTTTT TTTTTTTTTTTTTT AJCGAGAATTC CTGTTTATTGT GCA	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G2791859 RIBOSOMAL PROTEIN S4 Y ISOFORM - HOMO SAPIENS (HUMAN), 263 aa.	1.00E-140	Y (Yp11.3)
1054	cg43918496	1850	GCCTGCTGTTT TATTGCAAGAAT ATT/CJAAGTAGCA TTGCAGTAGTCT ACTTT	T	C				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SWISSPROT-ID:P54813 YME1 PROTEIN HOMOLOG (EC 3.4.24.-) - CAENORHABDITIS ELEGANS, 676 aa.	2.80E-136	10

1055	cg43284434	2578	ATCAGAGAGGAA TAAAAAGACATT TTT/gapJATATTTT ATTCTGCTCCAT TCCCTT	T	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1056	cg43284434	2751	GTGGACCTAAAT TCCTTATCATATC [C/gap]TTTATTAA TTCAGCCAGTGT ATCCA	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1057	cg43284434	2877	CTGAATAGAATT GTATAGCGATGA C[C/T]TCTTAATT ATAATTTGATTG ACTG	C	T				SILENT- NONCODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1058	cg43284434	3312	ATACTAGTTAATT TCTTCCATTCCC C/TJACTACACAG AGAGGTGAGCTT TCAA	C	T				SILENT- NONCODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1059	cg43974574	1219	AAACCACTTAAA TGTGAAGGAACA A[C/gap]AGCAAC AAGACCAGTATG ATATAC	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G2687400 VESICLE SOLUBLE NSF ATTACHMENT PROTEIN RECEPTOR - HOMO SAPIENS (HUMAN), 232 aa.	1.40E-116	14
1060	cg43967912	2065	GGAGACTCCGG GAGCCGAAAGT GAA[G/gap]CGGG TCCCGCACCAAG GAGACGTTG	G	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+)-ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.60E-108	8
1061	cg43954224	3379	GATTTTGTGCAT GTAGTTCAGTCT A[C/G]TGTGGTA GCATGACAGAA GTGGG	C	G				SILENT- NONCODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	3.70E-103	1

1062	cg43250373	1641	TATGCTGGCTGG AGTGAGGAAAA A[A/gap]TCGTCC AGGGAGCATT CCTCCAT	A	gap				SILENT- NONCODING NG	ATPase_ associate d	Human Gene Similar to TREMBLNEW- ID:G2921585 ECTO-ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)
1063	cg43250373	2397	CAGTTACAAC AGGGTCACAAAA A[A/gap]TGCATC TTCCAATGCATA TTTTTAT	A	gap				SILENT- NONCODING NG	ATPase_ associate d	Human Gene Similar to TREMBLNEW- ID:G2921585 ECTO-ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)
1064	cg43986887	104	AAGTAAAGTGAA TGAAACCATTG T[G/A]ATTAAAGAT ACATAGACAGAA CTTCA	G	A				SILENT- NONCODING NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1065	cg43986887	136	ATACATAGACAG AACTTCAATGTA G[A/gap]AAAAAA AAAGACCTTGCT GGGAAAC	A	gap				SILENT- NONCODING NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1066	cg43986887	145	AGAACTTCAATG TAGAAAAAA A[gap/A]GACCTT GCTGGGAAACA GATGATGA	gap	A				SILENT- NONCODING NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1067	cg43969125	681	AATGGACAATAA AGGACTGAGGG AG[A/gap]GGGCT AGAAAATGATTG ATTTTCT	A	gap				SILENT- NONCODING NG	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P18708 VESICULAR-FUSION PROTEIN NSF (N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN) - CRICETULUS GRISEUS (CHINESE HAMSTER), 744 aa.	1.40E-79	17
1068	cg43972161	186	TTTTTTTTTTT TTTTTTTTTTT A[A/gap]TTTAA TCCTTAATTCCG T	T	A				SILENT- NONCODING NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	

1069	cg43972161	306	AGCCCCCTGGGT CGGGCGGGGT CCC[C/gap]TGGG CCGCCCGGGG GTCCACATGC	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1070	cg43972161	314	GGTCGGGGCGG GGTCCCCTGGG CCG[C/gap]CCGG GGGTCCACAT GCAGCCCCTG	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1071	cg43972161	316	TCGGGGCGGGG TCCCCTGGGC GCC[C/gap]GGGG GGTCCACATGCA GCCCCTGGG	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1072	cg43972161	342	GGGGGTCCAC ATGAGCCCCCTG GGT[gap]GGGG CCGGCGCGGG TGAGGTCCG	T	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1073	cg43972161	405	TTGCTGAGGTCC GGCCGGTTGGG GC[C/gap]GCCCC TAGGCGCGCTG GCTGGGCAG	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1074	cg43943233	1023	GCAAGCAAAAC AAAGCTATAACT TTG[A]GCAGTGG TATTCACCCACC ACTTAT	G	A				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:O15511 ARP2/3 COMPLEX 16 KD SUBUNIT (P16-ARC) - HOMO SAPIENS (HUMAN), 151 aa.	3.90E-75	

1075	cg43943233	320	TATCAAAAACAG CAAAGAGTTTAT A[AG]AATTCTG CACCAGTTTGCA CATAA	A	G				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:O15511 ARP2/3 COMPLEX 16 KD SUBUNIT (P16-ARC) - HOMO SAPIENS (HUMAN), 151 aa.	3.90E-75	
1076	cg43917062	179	GGAGACAAATAC ACAAATAACTAG A[ATT]TACAAGGC AGTAAACAAGAG TGGGC	A	T				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSNEW- ID:O42945 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPBC16H5.10C - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 735 aa.	6.10E-65	17
1077	cg43917062	76	ACTGAGTGACTA CTATGTGCAAAG C[A/gap]CTATGC TAGGTGCATGAA AGATACA	A	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSNEW- ID:O42945 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPBC16H5.10C - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 735 aa.	6.10E-65	17
1078	cg44022155	1279	GAGAGCTGGCC GAGCAGCCCTG GCC[A/G]CCGCT GCCCGCCGGCC CCCTGAGGT	A	G				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
1079	cg44015998	172	AGCCAGCGGAT GGCTGTGGGG TCC[C/gap]AGCT CAGTCTTCCAAG GGCGAGACT	C	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P39986 PROBABLE CALCIUM- TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.50E-53	
1080	cg44015998	268	GCCCTGTTGGG GTTCCCGCCAG CG[G/gap]CAGCC AGGGTGGGCAG TGGGTACCA	G	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P39986 PROBABLE CALCIUM- TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.50E-53	

1081	cg43917679	327	CAAGAAGGAAAC AGGATTTATTAG A[C/T]CATTTCCA GGACAGGGACC CAGGGG	C	T				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1082	cg43917679	549	CAGAGCTTGGG CTGGGGTTGCA GGG[G/gap]CATC AGCCAATCTGCT CTCAAGGAG	G	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1083	cg43917679	837	GTAGGAAGAGCA GTGTCCACTGTG T[G/gap]CCCCAG GGCAGTGGAGT GTCTCTGT	G	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1084	cg43966234	2339	AAAAATCACCAA TGGAATTTTCA TT[gap]GATATAA ATACTTGTACAT ATGATT	T	gap				SILENT- NONCODING	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00	13 (13q32)
1085	cg43966234	2357	TTTTCATTGATAT AAATACTTGTAC[A/gap]TATGATTT GTACTTCTGCTG TGAGA	A	gap				SILENT- NONCODING	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00	13 (13q32)
1086	cg43966234	2363	TTGATATAAATAC TTGTACATATGA[T/G]TTGTACTTCT GCTGTGAGATTC CCT	T	G				SILENT- NONCODING	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00	13 (13q32)

1087	cg43009431	3003	CTCCCCAAACGGC CGGTAATGCCG GG[C/gap]GTCCC CGAGACGCGGC TGCCTGTCC	gap			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05747 BIOTIN--PROTEIN LIGASE (EC 6.3.4.-) (BIOTIN APO-PROTEIN LIGASE) (BIOTIN--[METHYLMALONYL-COA- CARBOXYLTRANSFERASE] LIGASE (EC 6.3.4.9) / BIOTIN--[PROPIONYL- COA-CARBOXYLASE (ATP- HYDROLYSING)] LIGASE (EC 6.3.4.10) (HOLOCARBOXYLASE SYNTHETASE) (HCS) / BIOTIN-- [METHYLCROTONOYL COA-CARBOXYLASE] LIGASE (EC 6.3.4.11) / BIOTIN-- [ACETYL-COA- CARBOXYLASE] LIGASE (EC 6.3.4.15)) HOMO SAPIENS (HUMAN), 726 aa.	0.00E+00	21 (21q22.1)
1088	cg43920913	1770	CCATTCTGCCT A TTTGCAATCATG AATACCTGGGA ATCCAAATAGTT GGATA	T			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1089	cg43920913	1777	TGCCTTTTGCAA G TCATGAAACCTG G[G/C]AATCCAA TAGTTGGATAAC TTAGA	C			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1090	cg43920913	1788	TCATGAAACCTG gap GGAATCCAAATA G[gap/G]TTGGAT AACTTAGAATAA CTAAGTT	G			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)

1091	cg43920913	1796	CCTGGGAATCCA AATAGTTGGATA A[gap/G]CTTAGA ATAACTAAGTTTA TTAAAT	gap	G				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1092	cg43920913	1801	GGAATCCAAATA GTTGGATAACTT A[G/T]AATAACTA AGTTTATTAAATT CTAG	G	T				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1093	cg43920913	1809	AATAGTTGGATA ACTTAGAATAAC T[A/G]AGTTTATT AAATTCTAGAAA GATAA	A	G				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.2E-288	3 (3q21)
1094	cg43931765	665	GCCAGGTGACAT GCCCAGGCACC TT[gap/C]CCTGT ACAGGCACTGTG GGCTCCTG	gap	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
1095	cg43931765	692	CTGTACAGGCAC TGTTGGGCTCCTG G[C/gap]CCAGGC TCACTAGAAAGT CTTCTCT	C	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
1096	cg43918042	1005	TTAGAAGGAGCA GTAGCAGCAGCA G[C/gap]AGGAGA AGATGCTGAGGA TGCGGAC	C	gap				SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTOCOLADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
1097	cg43265972	2272	TGATGAGTTCAT TAGCTAAGTTAA A[A/gap]TTAATTT GAACCTTGATCT AAACCA	A	gap				SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5

1098	cg43265972	2279	TTCATTAGCTAA GTTAAAATTAAATT [T/gap]GAACTTT GATCTAAACCAA AACAAA	T	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1099	cg43265972	2333	GGAAATAAAGC TGTAAGGAACT TT[gap]ATCAAG CATTCCAAAACC AACTAGA	T	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1100	cg43265972	2374	ACCAACTAGAAA TTACTTGAAGTTT [T/gap]CGAGTGA GCATTGCCTGTG CCAGTA	T	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1101	cg43265972	2494	TATTCAGCCAAT TTCATGGATGTA A[A/gap]CGATGG ATATAAATAATTG ATAGCA	A	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1102	cg43968898	212	ACGGGGGAGGG GGTCGCCCTTAGC GC[G/gap]TGGAC ACAGCACAAAAC ACAACACG	G	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1103	cg43976828	1294	ACTGTCTTATTT TATTTTCATGTT gap/[T]CCTTCTTT TCCCAGCATTGC AGTTT	gap	T			SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G1881841 R NR-CAM 22=NEUROFASCIN HOMOLOG/IG-FNIII CELL ADHESION MOLECULE {ALTERNATIVELY SPLICED} - RATTUS SP. 1166 aa.	0.00E+00	7
1104	cg43976828	1638	TGTAATGCCCTGG AAGATTAAGAAG C[C/gap]TACGGA GTAACAGGAGCC AAGAGTA	C	gap			SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G1881841 R NR-CAM 22=NEUROFASCIN HOMOLOG/IG-FNIII CELL ADHESION MOLECULE {ALTERNATIVELY SPLICED} - RATTUS SP. 1166 aa.	0.00E+00	7

1105	cg43952088	4171	ACAACCCACCAA AGTTTCCGCAGA G[C/G]GTATACCA GATGCTGTGTC AGAAG	C	G			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1106	cg43952088	4172	CAACCCACCAA GTTTCCGCAGAG C[G/C]TATACCA ATGCTGTGTCA GAAGC	G	C			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1107	cg43952088	4376	GAAAAAGCCTGT AGATTTTGAAAC C[A/G]AAAGAGC CTATAGCTTGAA GGTAGA	A	G			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1108	cg43952088	4475	CAAGGACACTGT GACCGTCAAGAT C[G/T]CAGTAGAA GATGCTGATGAG CCCCC	G	T			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1109	cg43127783	4451	GGCTTCAGGGC GCACAGCATGAG AG[G/C]CTCTGT GCCCCCATCACC CTCGTTT	G	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00 (16p11.2)	16
1110	cg43127783	4541	CATCGTGGGGCT CTCAGTCCGAT TT[C]CCCAGGCT GAATTGGGAGTG AGATG	T	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00 (16p11.2)	16

1111	cg43127783	4602	GGTTCTGCACAG CTGGCCTCCCG CG[ap/G]TTGGG CAACATTGCTGG CTGGAAGG	gap	G				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1112	cg43127783	4607	TGCACAGCTGGC CTCCCGCGTTGG G[ap/T]CAACAT TGCTGGCTGGAA GGGAGGA	gap	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1113	cg43127783	4620	TCCCGCGTTGG GCAACATTGCTG GC[ap/C]TGGAA GGGAGGAGCGC CCTCTAGGG	gap	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1114	cg43127783	4679	GGCCCCGGTGC GGCTGCAGCTCA CC[C/gap]AGCCC CAGGGCAGAA GAGACCCAA	C gap	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)

1115	cg43127783	4756	ATATAGTACCTG AAAAAATGCCAA G[C/gap]ACAAGA TTATTTTTTTAA AAGCGT	C	gap			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1116	cg43127783	4759	TAGTACCTGAAA AAATGCCAAGCA C[AT]AGATTATT TTTTTAAAAAGC GTACT	A	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1117	cg43127783	4760	AGTACCTGAAA AATGCCAAGCAC A[AT]GATTATTT TTTTTAAAAAGCG TACTT	A	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1118	cg44026923	187	GCTCTGTGCATG CGGGTGGGCTG GG[gap/C]CCCCA GGGGTGCAAGG ATGGAGTAG	gap	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)
1119	cg44026923	191	CTGTGCATGCGG GTGGGCTGGGC CC[C/gap]AGGGG TGCAAGGATGGA GTAGCTGA	C	gap			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)

1120	cg44026923	258	GAGTCGGGAGG ACGCCTAGTGG GAC(A/G)TGGCG GGGTGGGGCA GGGTGCGGT	A	G				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
1121	cg42558238	2838	CACCGCCACATG GCTTCCTCCTGC G(C/T)GCATGTG CGCACACACACA CACACA	C	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
1122	cg42558238	2999	CCACTCTCCTTG CTACCCAGAAAT C(C/gap)ATCTAA ATACCTGCCCTG ACATGCA	C	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)

1123	cg42558238	3220	GGGAAAGCCCA GAAAGGACAGA AA[C/T]GAAGTAG AAAGGGCCCA GTCCTGG	C	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
1124	cg43994411	1460	TC TTCAGAAAGT AGGCTTTCAAAT T[A/G]CTCTTCTC CATATTTTGTAG ATAT	A	G				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.lpcis:SWISSPROT- ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0	2 (2q31)
1125	cg43994411	1714	CAACATATTTTCA GAAATGACTGTTI A/G]CTAGGTGGT AAACTGTTAGG GTAA	A	G				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.lpcis:SWISSPROT- ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0	2 (2q31)
1126	cg43994411	393	ATACAAATATTTG TTTATATTAGGC T/C]TACTAAATTA ATGACAACTTTG AAA	T	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.lpcis:SWISSPROT- ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0	2 (2q31)

1127	cg43980086	250	CCAAGTCCAGG ACTGGCTGATAG C[C/gap]TCTCCC AGTGATAGCAG GTCCTAA	C	gap			SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P38570 INTEGRIN ALPHA-E PRECURSOR (MUCOSAL LYMPHOCYTE-1 ANTIGEN) (HML-1 ANTIGEN) (CD103 ANTIGEN) (INTEGRIN ALPHA-IEL) - HOMO SAPIENS (HUMAN), 1178 aa.lpcis:SWISSPROT-ID:P38570 INTEGRIN ALPHA-E PRECURSOR (MUCOSAL LYMPHOCYTE-1 ANTIGEN) (HML-1 ANTIGEN) (CD103 ANTIGEN) (INTEGRIN ALPHA-IEL) - HOMO SAPIENS (HUMAN), 1178 aa.	0	
1128	cg43948700	159	AAGCTCTGAGCC CGCCCTCTTGG G[C/gap]CACAGT GGTAGGGATGG GGGAAGGG	C	gap			SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G2739450 INTEGRIN BINDING PROTEIN KINASE - MUS MUSCULUS (MOUSE), 452 aa.	4.9E-251	11
1129	cg43948700	204	GAAGGGGATGG ACCCATGGCTG GG[G/gap]TAGTA CCATGACTGGAG GCGGGGGA	G	gap			SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G2739450 INTEGRIN BINDING PROTEIN KINASE - MUS MUSCULUS (MOUSE), 452 aa.	4.90E-251	11
1130	cg43949264	14175	ATCGTGAGGTTT TCATCGGCTGTG C[gap/C]ATTTC CAACGTCCTTTG GGATTTA	gap	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1131	cg43949264	14400	TTGTTTCAACTG AATTTTGGTGT G[G/T]TAGTGCCA TTATCTAGCACC CTGAT	G	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4

1132	cg43949264	14436	ATCTAGCACCCT GATTTTTTTTTT T/gap]ACTATAAC CAGGGTTTCATT CTGTC	T	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1133	cg43949264	14436	TCTAGCACCCTG ATTTTTTTTTT gap/]ACTATAAC CAGGGTTTCATT CTGTC	gap	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1134	cg43956560	1579	TTCTGAGGAGAA ACAAATAAGACC A[T/C]AAAGGGAA AGGATTCATGTG GAATA	T	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)
1135	cg42701303	989	GTGGCTCCACTT GCCCCGTCTGCTT G[G/gap]CCCCAG GCTGCTCTTTGTC CTGTTTG	G	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:Q14242 P SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND) (CD162 ANTIGEN) - HOMO SAPIENS (HUMAN), 412 aa.	2.50E-215	12 (12q24)
1136	cg42701303	1083	CTCCGAGGAAG CCCAGAGCTGTG GA/TTTGGGGT CTGGGCACTCAG GGGTGGC	A	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:Q14242 P SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND) (CD162 ANTIGEN) - HOMO SAPIENS (HUMAN), 412 aa.	2.50E-215	12 (12q24)

1137	cg43977724	1602	TCATTCCCAACA ACATCCTCTGCC A[C/T]ACACAACA AAACGTAAGTTT CATT	C	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:Q14982 OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR (OBCAM) (OPIOID-BINDING CELL ADHESION MOLECULE) (OPCML) - HOMO SAPIENS (HUMAN), 345 aa.	1.80E-182	11
1138	cg43956668	1161	AGTAAGACGTGA AAGGAATACACT T[G/C]TGTTTAAG CACCATGGCCTT GATGA	G	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.lpcis:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa	1.20E-167	3 (3q13.1)
1139	cg43943478	366	GAGGAGAGGCC CTGACAACGAGG GC[C/gap]GCCCC TGCCCGGGGTG AGGCTGCAC	C	gap			SILENT- NONCODI NG	cadherin	Human Gene Similar to SPTREMBL- ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1140	cg43943478	398	CCCGGGGTGAG GCTGCACAGCG CCA[gap/G]CTCC AGGCTGGGCCA GCTTGGCCCG	gap	G			SILENT- NONCODI NG	cadherin	Human Gene Similar to SPTREMBL- ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1141	cg43943478	408	AGGCTGCACAG CGCCACTCCAG GCT[G/gap]GGCC AGCTTGGCCCG CACTGGCAAC	G	gap			SILENT- NONCODI NG	cadherin	Human Gene Similar to SPTREMBL- ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	

1142	cg43943478	410	GCTGCACAGCG CCACTCCAGGCT GG[G/gap]CCAGC TTGGCCCGCACT GGCAAGAC	G	gap			SILENT- NONCODI NG	cadherin	Human Gene Similar to SPTREMBL- ID:Q9971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1143	cg42924171	1026	CCCAACTTCCCC TGGAGCTCAGAG GTT/GTCTCCCA CTGTACCAGCCT CTGATA	T	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1144	cg42924171	1028	CAACTTCCCCTG GAGCTCAGAGT GTT/GTCCCCACT GTACCAGCCTCT GATAAG	T	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1145	cg42924171	1160	TCTCTTTCTCGG TGATAAAACACA CIC/G]CGCTCCG GTGAGCCCCAGC GTCCCCCT	C	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1146	cg42924171	1169	CGGTGATAAAAC ACACCCGCTCCG GTT/gap]GAGCCC AGCGTCCCCCTCC TTGGCTT	T	gap			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1147	cg42924171	1177	AACACACCCGCT CCGGTGAGCCC AG[gap/G]CGTCC CCTCCTTGGCTT CCAGGAGC	gap	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17

1148	cg42924171	1179	ACACACCCGCTC CGGTGAGCCCA GC[G/C]TCCCCT CCTGGCTTCCA GGAGCCC	G	C				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1149	cg42924171	1184	CCGCTCCGGTG AGCCCAGCGTC CCC[gap /C]TCCT TGGCTTCCAGGA GCCCTGGGA	gap	C				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1150	cg42924171	1204	GTCCCCCTCCTTG GCTTCCAGGAGC C[C/ gap]TGGGAA GCATTTTAACT GGGTAGA	C	gap				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1151	cg42924171	1208	CCTCCTTGCTT CCAGGAGCCCT GG[G/ gap]AAGCA TTTTTAACTGGG TAGAATCT	G	gap				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1152	cg42924171	746	ATGCTGAGCCCGC AGCACTAACCCCT C[C/ gap]TGCGGC CCTAGCGACCCCT CAGGCTT	C	gap				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1153	cg42924171	868	GCTCCCATCTGC CCCCCTGCAACA G[T/C]CGCAGGC TGCTTCCTCTCT CTGAGT	T	C				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17

1154	cg42924171	869	CTCCCATCTGCC CCCCTGCAACAG TTC/TGCAGGCT GCTTCCTCTCTC TGAGTT	C	T				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1155	cg42924171	907	CTCTCTCTGAGT TCCTCTGGGCTG C/C[gap]GCAGGC TCCCCTGGGAAT AGAGCAA	C	gap				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1156	cg42924171	958	GACGTGAGTCCT AACCTGGCCACA G/C/T]TGGGGA GGCAGAGCCAG CAGGTGG	C	T				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1157	cg42924171	967	CCTAACCTGGCC ACAGCTGGGG AG[G/gap]CAGAG CCAGCAGGTGG ACAGGTGTT	G	gap				SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1158	cg43246381	243	ACCTGGATTGT TTTCAGCTTTCT C/G/A]ATTTTCAC ATGCACGTTAGG CTATC	G	A				SILENT- NONCODI NG	calcium_ channel	Human Gene Similar to TREMBLNEW- ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	1.00E-73	12
1159	cg43933897	195	TCAGATGCCAGC TCTCCTCAGCGG A/C[gap]GCTCCT GATCCCTCAATT TGCCATC	C	gap				SILENT- NONCODI NG	calcium_ channel	Human Gene Similar to TREMBLNEW- ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	9.70E-66	

1160	cg43919581	2171	AGGAATGCCTCC TCCCTGGGCAGA A[A/gap]GTGGCC ATGCCACCCTGT TTTCAGC	A	gap			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T- PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0.00E+00	8 (8p12)
1161	cg43919581	2357	TATAGTCACAAG AGCCCAGCAGG GC[C/gap]TCAAA GTTGGGGCAGG CTGGCTGGC	C	gap			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T- PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0.00E+00	8 (8p12)
1162	cg43946028	394	GAATCTCGTGCC TCAGCCTCCCAA G[T/C]AGCTGGG ATTACAGGCATG CACCCAC	T	C			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1163	cg43946028	403	GCCTCAGCCTCC CAAGTAGCTGGG A[T/C]TACAGGCA TGCACCACCGTG CTCGG	T	C			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1164	cg43946028	468	TTTATAGTAGAGA TGGGGTTTCACC A[T/C]GTTAGCCA GGCTGCTCTTTA ACTCC	T	C			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1165	cg43264626	197	ATAGACATTTCT ACCTTGAGGATA T[AT]GAAGGGAA CTTAGGAAGTGA GAAGT	A	T			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.10E-183	1
1166	cg43264626	41	TTTGAATGTGTA CTAGATGCTATT T[AT]TTAAACTG TAGACAGGAGAT AAATA	A	T			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1

1167	cg43264626	437	TGAAAAAGGTCA TGGGTGGAGAG AA[G/C]CAAAGTA GGAAGGATCATT TGAAGC	G	C				SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1
1168	cg42926989	826	TCTTCGGTTCCT ACGACCCCGAA G[G/gap]CAGATT TGTGTGGGGA CCGGCGGG	G	gap				SILENT- NONCODI NG	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136 (14q11.2)	14
1169	cg42926989	908	AGGCCCCCTGCT GTGTAACAATGT G[G/gap]CCCACG GCATCGTCTCCT ATGGAAA	G	gap				SILENT- NONCODI NG	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136 (14q11.2)	14
1170	cg42094318	1232	CCAACCCCTGAG CACCCCTATCAA C[C/T]CCCTATTG TAGTAAACTTGG AACCT	C	T				SILENT- NONCODI NG	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	5.5E-110 (19q13)	19
1171	cg43982945	461	ACACATGTCAGG CTGGGGCAGCA GC[G/gap]ACTCT GATCAGCACCCAG GTCCCGAG	C	gap				SILENT- NONCODI NG	cathepsin	Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2E-80	11
1172	cg43982945	97	GGTTACAAAGTT CCTGGACATGGA G[A/G]GGGACAC TATCCCTAAATC CAAGGG	A	G				SILENT- NONCODI NG	cathepsin	Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2E-80	11
1173	cg43925458	591	TCTGGACATAAA TCTGCCATTATT [A/G]AACCATTCA CTACAACAAATA AATA	A	G				SILENT- NONCODI NG	cathepsin inhib	Human Gene SWISSPROT-ID:P20810 CALPAIN INHIBITOR (CALPASTATIN) (SPERM BS-17 COMPONENT) - HOMO SAPIENS (HUMAN), 708 aa.	0 5 (5q15)	

1174	cg43980411	1763	AGTAGGTATCCC TCCATGCCCTTC T[G/A]TAATAAAT ATCTGGAAAAAA CATT	G	A				SILENT- NONCODI NG	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
1175	cg43971453	1029	CTGTAGCTGCCT CCTGCCCTTCCGA A[G/gap]GCAGAA GGAATGAAAGAT GCACATT	G	gap				SILENT- NONCODI NG	chloride_ channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
1176	cg43971453	536	GGGTGTTAATGC CCACGTAGTGGA G[G/gap]CCTCTG GCAGATCCTGCA TTCCAAG	G	gap				SILENT- NONCODI NG	chloride_ channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
1177	cg43971453	885	CCCCAACCCATC CTGCCAGGGCA GG[G/gap]CCTAT CTTCCCTGCCCTCT GGAAGACT	G	gap				SILENT- NONCODI NG	chloride_ channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0.00E+00	3
1178	cg43970982	5505	GACCAATGCCTT AATTAAAGAATTT [A/T]AAAAAGTTG TAATAGAGAATA TTTT	A	T				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0.00E+00	2
1179	cg43970982	5564	CTCTAATGTTGT GTGTTTTTTTTT [T/G]TGTGTGCTG GAGGGAGGGGA TTTAA	T	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0.00E+00	2
1180	cg42201364	2443	TTAAAAACAAC AACAAAAACAA A[gap/G]CAACAA AAAAAAAATTAA AAAAAA	gap	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6

1181	cg42201364	2818	GC TTT CATCAAT GAACCTTTTCAA A[<u>gap</u>]/AJCTTTTCT ATGATTGCAGAG AAGCTT	gap	A				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1182	cg42201384	3169	GTTTACCTACT CCTTATTACGA C[A/G]CAATAAAA TAACATCAATAG AATT	A	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1183	cg42201364	3191	GACACAATAAAA TAACATCAATAG A[A/T]TTTAGGC TGAATTAAATTTGA AAGC	A	T				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1184	cg41035069	3660	GCTTTTTTTTTT TTTTTTTTTTTTT[<u>T</u>] gap]GGGAGTAAG CCAGGCATTAAA AGCA	T	gap				SILENT- NONCODI NG	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0.00E+00	6 (6q12)
1185	cg43917054	12431	ACCGTCTTGATC GGAAAGCTCTTC C[T/G]AATCGCTA ATCAGTCATTTT TTTCAT	T	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1186	cg43917054	12851	GAGGATGCAACA AATGTGGCCAAG C[C/gap]TATCAA AGGAAATGAGAA TGACAGC	C	gap				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1187	cg43917054	12916	CAGAAGTAGAGG GGGTGGTGCG TA[A/gap]GGATG TGTGAGTTTTGC TTTTGACT	A	gap				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)

1188	cg43917054	13001	TCTCAGAAAGTCC CTGTTTATTCCA A[A/T]TGCCATCC AGATGTGTGCAA TGTGG	A	T				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1189	cg43917054	13009	GTCCCTGTTTAT TCCAAATGCCAT C[C/gap]AGATGT GTGCAATGTGGC AAACTGA	C	gap				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1190	cg42740351	1046	TGAAGCTAAAA AGACAGCAGAAC T[G/C]GTATTTT CATCCTAAAGAA CAAAG	G	C				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1191	cg42740351	1047	GAAGCTAAAA GACAGCAGAACT G[G/C]TATTTTC ATCCTAAAGAAC AAAGT	G	C				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1192	cg42740351	1131	CTTTAACCAAC AATATTGCTCCA T[G/C]ATGACTTA GTACAAAGTTTC AATT	G	C				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1193	cg43988268	20	TTTTAAATATATA CAAAGG[AC]ATT TTATTATTAACCA AAGAAAGGG	A	C				SILENT- NONCODI NG	collagen	Human Gene Homologous to SPTREMBL-ID:Q61429 TYPE III COLLAGEN - MUS MUSCULUS (MOUSE), 1464 aa.	8.20E-128	1 (1p21)
1194	cg439881318	328	AACAGCAATTAA AAACAACAACAA C[A/gap]ACAAAA AAAAACAATTCAC AACCTGT	A	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.30E-73	1 (1p34)

1195	cg43991318	339	AAAACAACAACA ACAACAACAAAA A[A/gap]CATTCA CAACCTGTCACA GAGTCCT	A	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.30E-73	1 (1p34)
1196	cg43938820	487	TCTGCGGGAGG GAGGAGCAGAC GGG[G/gap]TTAG CACCGTTAATCT CGAGGGTCT	G	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment).	5.00E-59	21 (21q22.3)
1197	cg43938820	862	GGCGTCTTGCT CAGGCTGGTGG GA[T/C]GCAGCA CAGAGGTGCCTA GGGAAGG	T	C				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment).	5.00E-59	21 (21q22.3)
1198	cg39659519	2155	GTGTGTATGTGT GCGTGTGTGTAT G[C/T]GTGCATGT GTGTGTGTGTGT GTGTG	C	T				SILENT- NONCODI NG	collagen	Human Gene Similar to SWISSPROT- ID:Q99715 COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa. pcls: SPTREMBL- ID:Q99715 COLLAGEN TYPE XII ALPHA 1 PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa.	4.10E-52	1 (1p35)
1199	cg43278293	369	TTTCCTGCCTCT GCCTTGACCCGA A[G/gap]GTCTTA CAGGAAGACAAT AAATAAA	G	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14058 PRO ALPHA 1(II) COLLAGEN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	6.50E-50	12 (12q13.1 1)
1200	cg43278293	370	TTCCCTGCCTCTG CCTTGACCCGAA G[G/gap]TCTTAC AGGAAGACAATA AATAAAT	G	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14058 PRO ALPHA 1(II) COLLAGEN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	6.50E-50	12 (12q13.1 1)

1201	cg43063256	2090	AGAGCCCTGAG CCCTCAAGAACT CA[C/T]GCCAGCT CAGCCCTACACC AGTTTC	C	T				SILENT- NONCODING	complement	Human Gene SWISSNEW-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa. pcis:SWISSPROT- ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	1 (1p32)
1202	cg43281450	229	AATCCTCAGAAG AAAGAAAGGG CC[C/gap]TTTGG GTTGTTTCAGGT AAAGTACA	C	gap				SILENT- NONCODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1203	cg43281450	368	GTCAGTTGTTTT TTGTTTTTTTTT T/gap]CCACACTG CTCTCTGGATTG GAACC	T	gap				SILENT- NONCODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1204	cg43281450	368	TCAGTTGTTTTT GTTTTTTTTTTT[g ap/T]CCACACTG CTCTCTGGATTG GAACC	gap	T				SILENT- NONCODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1205	cg43049885	3106	CTCAAAGTTACT GACAAAATTAT TT[C]TCTGTTAG TTTGAGATCATT ATTCT	T	C				SILENT- NONCODING	complement	Human Gene TREMBLNEW-ID:G386348 COMPLEMENT C6 - HOMO SAPIENS, 941 aa.	0.00E+00	5 (5p13)
1206	cg43049885	3303	GTAGCCTGTGAC ATTAAGCATTCT C[A/G]CAATTAGA AATAAGAATAAA ACCCA	A	G				SILENT- NONCODING	complement	Human Gene TREMBLNEW-ID:G386348 COMPLEMENT C6 - HOMO SAPIENS, 941 aa.	0.00E+00	5 (5p13)
1207	cg43933757	3223	GTTCAAGCGATT CTTGTCCTCAG C[C/T]TCCCAAGC AGCTGGGATTAC AGGTG	C	T				SILENT- NONCODING	complement	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)

1208	cg43958722	254	GAAACCAGCCTG GGCAACATAGGA A[A/G]ATCCTGTC TCTACAAAAAAT AAATT	A	G				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P08174 COMPLEMENT DECAY- ACCELERATING FACTOR PRECURSOR (CD55) - HOMO SAPIENS (HUMAN), 381 aa.	3.40E-192	1 (1q32)
1209	cg43958722	287	CTCTACAAAAA TAAATTTCAAAA [C/gap]TTAGCCG GGTGTCGTGGC ACACACC	C	gap				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P08174 COMPLEMENT DECAY- ACCELERATING FACTOR PRECURSOR (CD55) - HOMO SAPIENS (HUMAN), 381 aa.	3.40E-192	1 (1q32)
1210	cg43956185	308	TTTTGGAGTTTT TAGTTTTCCAAG[T/A]TTTAATATGG TGCTTTTAAGAA GAG	T	A				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1211	cg43956185	423	AAAGGAGTAAAA CAATACTTAAAA A[T/A]TAAATTAA GAACTGATTAA TACTA	T	A				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1212	cg43956185	430	TAAACAATACTT AAAAATTAAATT[A/G]AGAACTGAT TTAATACTAAAGT TCT	A	G				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1213	cg43956185	471	CTAAAGTTCTGA ATAAAGGTGTGC A[T/C]TTTATGAT TGATTCTATCTTT TTGC	T	C				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
1214	cg43945714	1056	TACCCCCAACAC CACCCCTTGCCC A[G/A]CCAATGCA CACAGTAGGGCT TGGTG	G	A				SILENT- NONCODI NG	complem ent	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)

1215	cg43945714	1083	AACACCACCCCT TGCCAGCCAAT G[C/G]ACACAGT AGGGCTTGGTGA ATGCTG	C	G				SILENT- NONCODI NG	complem ent	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1216	cg43945714	1124	GAGTAAATAAAC TCTTCAAGGCCA A[G/A]GAACAGT GGTCTAATTCAA CTCTGT	G	A				SILENT- NONCODI NG	complem ent	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1217	cg43945714	1125	AGTAAATAAACT CTTCAAGGCCAA G[G/A]AACAGTG GTCTAATTCAAC TCTGTG	G	A				SILENT- NONCODI NG	complem ent	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1218	cg43945714	1126	GTAATAAACTC TTCAAGGCCAAG G[G/A]ACAGTGG TCTAATTCAACT CTGTGT	A	G				SILENT- NONCODI NG	complem ent	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1219	cg43945714	1160	CTAATTCAACTC TGTGTCCCAGCA C[C/gap]TGGCAC ACCAAGAGTGCC ATGCTCA	C	gap				SILENT- NONCODI NG	complem ent	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)

1220	cg43947909	969	CAGAAAAAATG ATAATAAATGAG A[A/G]CACAAAAC ATATAATTTAAAT TTGG	A	G				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1221	cg43947909	991	AGAACACAAAAC ATATAATTTAAAT [T/C]TGGTATTTT TTCCCCCATGAT ATTA	T	C				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1222	cg43947909	326	ATTCAACAGGAG CTGATCAACCAA G[A/G]GCAGTCC ATCATCAGCGAG TATGAG	A	G				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17

1223	cg43947909	575	ATAAATGAGCAC AGTGCACATTGT C[C/T]CCACACAC CTGAATTTTCAG TCACT	C	T				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1224	cg43947909	839	ACATCTGTTCTT GGTCTTTTGTGA C[G/A]CAGGTTG AAGGGGGAGGA ATAGAAA	G	A				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1225	cg43984382	141	CAGCCAGTCCTG GGGCTCTCAGA GC[C/gap]AGCCC CCTCCCTTCAGC AGCTGAAG	C	gap				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02745 COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 245 aa.	8.8E-101	1
1226	cg43942011	2028	TTTTCTATGAAG AGCCCCAGATG GA[gap/A]GTTTT GGGGGGTGCA GGCCTGCT	gap	A				SILENT- NONCODING	complement	Human Gene Similar to TREMBLNEW- ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE), 651 aa (fragment).	1.10E-69	1 (1q32)
1227	cg44028879	1058	TCTTCAGTCAGA GCTGCCCTGTA G[C/G]CTCTCTGT CTGTGCCCTCCC CTCCC	C	G				SILENT- NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)

1228	cg44028879	1129	CTTCCCTCTTGG GAATGTCAAAGT G[C/G]AAGATGC AGAAACCTGGGC GAACAA	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1229	cg44028879	119	AAATAGATATTTA AATGACTTTATA T/AJAAAATAATTC ACCACTTCCAAG TAT	T	A				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1230	cg44028879	1152	TGCAAGATGCAG AAACCTGGGCGA A[C/G]AACACAG CCTAAAGACCGG CTCTGG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1231	cg44028879	1168	CTGGGCGAACAA CACAGCCTAAAG A[C/G]CGGCTCT GGCTGGCGGCC CAGGAGG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1232	cg44028879	134	TGACTTTATATA ATAATTACCA C/GJTCCAAGTA TAAACACAAAAT CTCA	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1233	cg44028879	137	CTTATATAAAAT AATTCACCACTT C/GJCAAGTATAA AAACAAAATCTC ACAG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1234	cg44028879	183	CACAGTGCGTGA GCCAATGTCCTC TTC/GJTGACTTC TCAGAGAACAGA AGGGG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)

1235	cg44028879	188	TGCGTGAGCCAA TGTCCTCTCTTG A/C/G/TTCCTCAGA GAACAGAAAGGG GTTCTCT	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1236	cg44028879	232	GGTTCTCTGAGCA GGTAGCCTGGG GG[G/gap]ACACC AGAGGTGGCTCT GGGGCTCC	G	gap				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1237	cg44028879	480	AGGCTAAGCCCC ATATGCAAGTTC A/C/G/TGCCCTTC CCTAAGCTGTCTG GCATC	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1238	cg44028879	679	GCTCGTTGCCTA GGCCTCAGAGC CA/C/G/CACCCAC AGGCTGGCCAC AAAGTGGA	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1239	cg42542496	1400	ACACTGCCGACA TCAGCATTGTCT C/G/A/JGTACAGC TCCCTTCCCTGC AGGGC	G	A				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
1240	cg42542496	1635	AGAAATTGCAA CTCACTGATTCT C/T/A/JACATGCTC TTTTTCTGTGATA ACTC	T	A				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)

1241	cg42542496	1668	CTTTTCTGTGATG AACTCTGCAAAG[G/A]CCTGGGCTG GCCTGGCAGTTG AACA	A				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
1242	cg42542496	1728	ACTAACCTTGAG A TCAGAAAACAGA G/A]G/AAGGGTA ATTTCCTTTGCTT CAAAAT	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
1243	cg41533258	1246	GTTTGACTCCCG T AACATCACCAGAC G[T/C]GTCTCCTG TTTTTCTGGGTG GCCTC	C				SILENT- NONCODI NG	csf	Human Gene Homologous to SWISSPROT-ID:P09919 GRANULOCYTE COLONY- STIMULATING FACTOR PRECURSOR (G-CSF) (PLURIPOLIETIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.50E-107	17 (17q11.2)
1244	cg2752665	774	GGAGTGGCCTG C GACCTGCCCTG GGC[C/gap]ACAC TGACCCTGATAC AGGCATGGC	gap				SILENT- NONCODI NG	csf	Human Gene Similar to SWISSPROT- ID:P04141 GRANULOCYTE- MACROPHAGE COLONY- STIMULATING FACTOR PRECURSOR (GM-CSF) (COLONY-STIMULATING FACTOR) (CSF) - HOMO SAPIENS (HUMAN), 144 aa.	5.00E-75	5 (5q31.1)
1245	cg43931046	2754	AACCTCTTCAAA A GAAATAGGAGCA A[A/gap]CCCCCA AGAGGCTTAATT TACCAAT	gap				SILENT- NONCODI NG	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7
1246	cg43931046	3843	AATTGTATATTCA T GTTTAACAGAAA[T/A]AAAAAGAAATAT TTGTCTTAAGAT GCA	A				SILENT- NONCODI NG	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7

1247	cg43920512	101	TGGCCTGGGCT GCGACCGGGA GCA[AC]GACTAT TCTTTGGCCGGG TCGGTGC	A	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1248	cg43920512	103	GCCTGGGCTGC GACCGGGGAGC AAG[AC]CTATTTC TTTGGCCGGGTC GGTGCGA	A	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1249	cg43920512	1574	GTGTACAGTTTT TAACCTAGGTTTT [gap]/TJAATTTTAC AATCATTCTCTGA ATACA	gap	T				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1250	cg43920512	2224	GAATAAAAAATA CCAGGGTTCTT TTT/GJAATGGAAT AAATATCCCTTTT AATA	T	G				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1251	cg43920512	95	GTAGGCTGGCCTG GGGCTGCGACC GG[G/C]GAGCAA GACTATTCTTTG GCCGGGT	G	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1252	cg43920512	98	GGCTGGCCTGG GCTGGGACCGG GGA[G/C]CAAGA CTATTCTTTGGC CGGGTGG	G	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1253	cg43927697	2010	AGCGGGGAGAA GCAGAACACCG GAG[G/gap]CCCG ACCAGCCAAGGA CCTACACCC	G	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)

1254	cg43927697	609	CAGTAATATGTA CAGATGGCACAT G[G/gap]TGCCAA TTTTATTTGTAA TATAGT	G	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1255	cg43927697	620	CAGATGGCACAT GGTGCCCAATTT A[gap/G]TTTGTA ATATAGTACTCC AACTCA	gap	G				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1256	cg43927697	628	ACATGGTGCCAA TTTTATTTGTAA [gap/G]TATAGTA CTCCAACTCAAG TTTACA	gap	G				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1257	cg43957094	1145	CCAAACATTTAT AATCAAGAGATT T[gap/A]TAATCAA TTATGTACTAGA ATCATA	gap	A				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1258	cg43957094	1145	CCAAACATTTAT AATCAAGAGATT T[gap/A]TAATCAA TTATGTACTAGA ATCATA	gap	A				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1259	cg43957094	1184	ACTAGAAATCATA TTAAAGAAAAAC TT[gap]ATTTTGC AAAAATAAAATC ACTTTC	T	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1260	cg43957094	1189	AATCATATTAAA GAAAAACTTATTT TT[gap]GCAAAA TAAATCACTTTC CAATA	T	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6

1261	cg43957094	800	TAAATACACTTT TAAATCAATATAI gap/CJGGTACTTG ATTAATTTCCCT GAAAT	gap	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1262	cg43242733	1125	ACTGGATTATTA CAGCACCAAAAA A[ap/A]CTTCTCT GAAGCCTTTCTC CACAAAC	gap	A				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
1263	cg43242733	1205	TGGATTAAAGCT ATGAAGCCTCAA A[A]gap]CATCAC GAGATAAGCATG ATGGICT	A	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
1264	cg43951588	138	AAGAGTTCTAAA CCAATAAGAAAA A[G/A]GGCACAAT GAAGCACACATC CCGAG	G	A				SILENT- NONCODI NG	cyclin	Human Gene Similar to SWISSPROT- ID:P37883 G2/MITOTIC-SPECIFIC CYCLIN B2 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 397 aa.	2.10E-92	15
1265	cg43969364	569	TTAACCAGGCGT GGGGCCTCATG CT[A]TJGCAAGTC CAGCCACTCCG GAGGCTG	A	T				SILENT- NONCODI NG	cyclin	Human Gene Similar to TREMBLNEW- ID:G2668505 PUTATIVE CYCLIN G1 INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 154 aa.	9.70E-67	7
1266	cg43996855	1221	TTTCTTCCATATA AACACAGCTTTTCI C/gap]TTTTGCCG CAAGCATCTGAT GACGA	C	gap				SILENT- NONCODI NG	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)
1267	cg43996855	2882	ATGCATACTTTA AAATTCATGATA A[A/C]TCATGGAA CCCCACTATACT CACTA	A	C				SILENT- NONCODI NG	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)

1268	cg43143315	2383	GGTTACAAACCG TTTCAGGCCCTG C[C/gap]TACCAC ATTCACCTGTTTG AATCTTT	C	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.pcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513.aa	1.90E-279	20
1269	cg43143315	2717	CTAGTGATTCAC TGGGGCATTATT TTT[gap]GTTAGA GGACCTTAAAT TGTTTAT	T	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.pcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513.aa	1.90E-279	20

1270	cg43143315	2951	GATTTAGGATCT A GTGGTGCAGGG CA[A/gap]TGTTC AAAGTTTAGTCA CAGCTTA	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lcds:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20
1271	cg43143315	3396	TGTGAAATTATTT A TTAGAAATTATAA A/gap]TTCACGTC TTGTCAGATTTC ATCTG	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lcds:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20

1272	cg43143315	3411	AGAAATTATAAATT CACGTCCTTGTCAT G/TATTTCATCTG TATACCTTCAAAT TC	G	T				SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450-CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450-CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	1.90E-279	20
1273	cg34413296	1732	CGCTGTGAACAT GTCCAGGCGCG GC[T/gap]GCTTC TCCATCAATTGA AGAAAGACA	T	gap				SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (CYP1A2) (P450-P3) (P(3)450) (P450 4) - HOMO SAPIENS (HUMAN), 515 aa.lpcis:SWISSPROT-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (P450-P3) (P450-4) - HOMO SAPIENS (HUMAN), 515 aa.	4.60E-278	15 (15q22)
1274	cg43309495	230	TTCCTCTCCCTCC TCATCTGAGACA T[G/gap]GCAGCA GCCAGGAACCA CTGTGCCA	G	gap				SILENT- NONCODI NG	cytochro me	Human Gene SPTREMBL-ID:Q64639 CYTOCHROME P-450C27/25 (EC 1.14.14.1) - RATTUS NORVEGICUS (RAT), 540 aa.	1.90E-202 2 (2q33)	
1275	cg43923430	130	AGAACTGTATAG GAAGCATGGCG CT[gap/G]GGCAT CTGCTTCTGGTG AGGGCCTC	gap	G				SILENT- NONCODI NG	cytochro me	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10

1276	cg43923430	132	GAACGTGTATAGG AAGCATGGCGCT G[G/gap]CATCTG CTTCTGGTGAGG GCCTCAC	G	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1277	cg43923430	2721	CTGATGCAATCA CACTGTGCTCTA G[G/gap]CGCTGC CCTAGGAGCCA GGAGCGGC	G	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1278	cg43923430	2744	AGGCGCTGCC TAGGAGCCAGG AGC[G/gap]GCAG ATACTGCCTCC CTTCAAGGC	G	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1279	cg43923430	390	CCCACCTCTAAC ACTGAATGTCAC A[C/gap]TTTGAA CATGAGATTGG AGGGGAC	C	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1280	cg43923204	1029	AAAATGCAGGCC CTGGCTCAGTCA C[C/A]AGGAAGG GGTGCTCCGA GGCCTTT	C	A				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1281	cg43923204	114	TGTGAAGGCTGT AACAAGTTGTAG A[G/A]GCTTTTC CAGACATTCCTA TGCAA	G	A				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

1282	cg43923204	1258	TGGGGTTGGAG GAGAGATGTATA AA[gap/A]GACCC TCAAAGGGAAAA ATAATTCC	gap	A			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1283	cg43923204	277	CTGTTTAAATGTT GTTTAACTCTCC C/TJACCCCGACC AATGAATCCCTA CGGA	C	T			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1284	cg43923204	289	GTTTAACTCTCC CACCCCGACCAA T[gap/C]GAATCC CTACGGACCCAGC AGTGCCC	gap	C			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1285	cg43923204	296	CTCTCCACCC GACCAATGAATC C[C/gap]TACGGA CCAGCAGTGCC CTGGGAGA	C	gap			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1286	cg43923204	307	CGACCAATGAAT CCCTACGGACCA G[C/T]AGTGCCCT GGGAGACTGAG TAATGA	C	T			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1287	cg43923204	330	GCAGTGCCCTG GGAGACTGAGTA AT[gap/C]GAAAA CATCCTGTCAAG CTTCAAGA	gap	C			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

1288	cg43923204	378	AGACCTTTGGGC AGATGGACTCT G/C/TAGACCCG TGGGAGCACAAA GGACTA	C	T				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1289	cg43923204	421	AAGGACTAAAA GCTGCAGGTAAC C/G/A/TATTGGT AACGAGACCCAC ACCTG	G	A				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1290	cg43923204	423	GGACTAAAAAGC TGCAGGTAACCG T/A/G/TTTGGTAA CCGAGACCCACAC CTGGC	A	G				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1291	cg43275625	92	TTTCCTTTTATTG AGAACATCTCAA A/G/TCCCTTTGTC TGATTTTGACAG CGTC	A	G				SILENT- NONCODING	deaminase	Human Gene SPTREMBL-ID:O00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa.	0	21
1292	cg43318865	1205	GAGACCCCTGG AGGGCTGGAG TTT(T/gap)ATCCA GCGCCTCGTCGT ATGTTTGG	T	gap				SILENT- NONCODING	deaminase	Human Gene SWISSPROT-ID:P20132 L- SERINE DEHYDRATASE (EC 4.2.1.13) (L-SERINE DEAMINASE) - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-173	12
1293	cg43318865	1246	TATGTTTGGCTG AGCACCTGTGGC C(gap/C)TGGGTG CAGGTAACTTC TTGTTAT	gap	C				SILENT- NONCODING	deaminase	Human Gene SWISSPROT-ID:P20132 L- SERINE DEHYDRATASE (EC 4.2.1.13) (L-SERINE DEAMINASE) - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-173	12

1294	cg41626024	838	TGGGACTTAGAA CACCGCCGCC CC[C/gap]TGCCC CACCTTTCCTTT CCTTCCTG	C	gap				SILENT- NONCODING	deaminase	Human Gene Similar to SWISSPROT- ID:P32320 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) - HOMO SAPIENS (HUMAN), 146 aa.[pcis:TREMBLNEW- ID:E1228801 CYTIDINE DEAMINASE (EC 3.5.4.5) - HOMO SAPIENS (HUMAN), 146 aa.	8.8E-78	1 (1p36.2)
1295	cg43967318	133	GGCACAGTGCT GGGAACACTAG GCC[C/gap]CTTC GGGACAAACCA GGGCCTTAAG	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1296	cg43967318	134	GCACAGTGCTG GGAACACTAGGC CC[C/gap]TTCGG GACAAACCAGG GCCTTAAGG	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1297	cg43967318	210	GGAAGGCACATA ACTGGGACAGG CC[C/gap]TGGCG GGGAGTATTCAG AAGCCAAG	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1298	cg43967318	215	GCACATAACTGG GACAGGCCCTG GC[G/C]GGGAGT ATTCAGAAAGCCA AGTGGGT	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1299	cg44033747	3686	ATCTGTAATCAC ATTCTGAGTGT TT[C]TCCTCTTT TTCTGTGTGAGG TTTTT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)

1300	cg44033747	3707	TGTTTTCTCTCTT TTCTGTGTGAGG [T/gap]TTTTTTTT TTTTTAATCTGCA TTTA	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0 9 (9p22)
1301	cg44033747	3720	TTCTGTGTGAGG TTTTTTTTTTTTT T/gap]AATCTGCA TTTATTAGTATTC TAAT	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0 9 (9p22)
1302	cg43314766	267	GCTAAATGCAAC TGTTCCCTTTCTA [T/gap]AAAAATTAT TATCCTGCAGAA GTAGC	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALDH1) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.2E-273 9 (9q21)
1303	cg43918671	1029	ACAAATAAGTAGC TTTTGTCTTACA [T/C]ATTAGTGCA CTGAAACAAAAT ACTA	T	C			SILENT- NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272 7 (7q31)
1304	cg43918671	1218	GCTCCCAGGAAA TTTCAGAAAAAA A[T/gap]ATATATA ATCTTCTAATTCA AAAGT	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272 7 (7q31)
1305	cg43918671	749	GGTTAAATAAAA CAAGTGAGAGAC C[AG]TTTACTTA CATCAGTTCGGT TTATA	A	G			SILENT- NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272 7 (7q31)
1306	cg43996714	391	TCATTCATGCTT CTTTATCCTCTT [T/G]CTTAGAAG TTCACAGTGTTA TATA	T	G			SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266 11

1307	cg43996714	549	TATTATCCAGAA TAAACTTCTGTA C[C/A]TATTAAAT TCTTCAAGTATAT CTAG	C	A				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266	11
1308	cg43330439	86	GCTGACCCCTGTG TGAGGGCAAAG GG[T/C]TTTTTTT TGCAGGAACAGT GGTTTA	T	C				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1309	cg43330439	88	TGACCCCTGTGTG AGGGCAAAGGG TT[T/C]TTTTTTG CAGGAACAGTG GTTTATT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1310	cg43330439	92	CCTGTGTGAGG GCAAAGGGTTTT TT[T/G]TTCAGG AACAGTGGTTTA TTGACC	T	G				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1311	cg43330439	93	CTGTGTGAGGG CAAAGGGTTTTT TT[T/C]TGCAGGA ACAGTGGTTTAT TGACCA	T	C				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1312	cg43264442	3020	TACTTGTGCTCT GCTGAGAATGTA C[A/G]GTTTGCAT TAAACATCCCAG GTCTC	A	G				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT [EC 1.1.1.22} - BOS TAURUS, 468 aa.	8.6E-240	4
1313	cg43259523	1624	TCTGTCTTACTC TGTCACCCAGGG T[A/G]GAGTGCA GTGGCGCGATCT CAGCTC	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1314	cg43259523	1625	CTGCTTACTCT GTCACCCAGGCT A[G/A]AGTGCAGT GGCGGATCTCA GCTCA	G	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1315	cg43259523	1626	TGCTTACTCTG TCACCCAGGCTA G[A/G]GTGCAGT GGCGGATCTCA GCTCAC	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1316	cg43259523	1642	CCAGGCTAGAGT GCAGTGGCGG AT[C/T]TCAGCTC ACTGCAGCCTTG ACCTCC	C	T				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1317	cg43259523	1643	CAGGCTAGAGTG CAGTGGCGGGA TC[T/C]CAGCTCA CTGCAGCCTTGA CCTCCT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1318	cg43259523	1859	GCTGGGATTACA GGGATGAGCCA CC[A/G]TGCCTG GCTGGGTATTTA TATTATC	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1319	cg43259523	2043	GTTACATAGTAG GCAATTTTATC C[A/gap]GTACTTT ATAGATTCAACT CTAAGT	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1320	cg43259523	2365	AAATATTCAATAC AGTGTGGATAT T/gap]CTGTCATG CACTATTTTCA GTTGA	T	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1321	cg43259523	2383	TGGATATTCTGT CATGCACTATTT TTT/gap]CAGTTG ACAAATTTCTGTAT TTTAAT	T	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1322	cg43259523	2437	TACTGTTTCTTCA GTCATGGTTATTI gap/AJGCACTTTA TCCTGAATAATA ATTCA	gap	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1323	cg43259523	2458	TTATTGCACTTTA TCCTGAATAATA A/GJTTCAGAAAT TGGGTTTTGGTT CAGT	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1324	cg43259523	2564	GAATGAGGGAG AGAAAGGGGCT GTA/G/CJAGTTTG AAAAGCATATT CAATATT	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1325	cg43259523	2650	CTATTGTTTTC AATATAGGTTAT A[Agap]ACAGGC AAATGCAATAA AATATAT	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1326	cg43259523	2651	TATTGTTTGCATA TATAGTTATAA A/gap]CAGGCAAA ATGCAATAAAAT ATATA	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1327	cg43259523	2656	TTTGCATATA GGTTATAACAG G[C/gap]AAAATG CAATAAAATATAT ATCTGG	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1328	cg43057018	1713	ATTGATGAACC AAGGAAAGCCAT G[C/A]GTTTAAAC AAATATTTACATT TAAT	C	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.pcds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
1329	cg43057018	1805	CTGTTATATAT GAATATCCCTA T/C]GTTAAATAAT AATAATAACTAG TGT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.pcds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
1330	cg44016790	1302	CCATCTTGAGCC ATGTCCCCCAGC C[A/gap]TGGCAT GGTGCACTGTA AACGCCA	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment).	1.4E-207	16

1331	cg44016790	1310	AGCCATGTCCCC CAGCCATGGCAT G[G/C]GTGCACT GTAAACGCCAAT CGGGGG	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment).	1.4E-207	16
1332	cg44016790	1311	GCCATGTCCCC AGCCATGGCATG G[G/C]TGCACTG TAAACGCCAATC GGGGGG	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment).	1.4E-207	16
1333	cg3000385	494	AACAGAGTGAAC TGAGCATCAGTC A[G/C]AAAAAGTC TATGTTTGCAGA AATAC	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.4E-202	4 (4q23)
1334	cg3000385	530	TGTTTGCAGAA TACAGATCCAAG A[G/C]AAAGACA GGATGGGCACT GCTGGAA	C	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.4E-202	4 (4q23)
1335	cg43923979	126	TATCTTGTTGG ATACATCTTTCAT [C/G]AGGACTCT GCCACATCCATA CTTTG	C	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1336	cg43923979	179	CTTGTGGTGAGA GAGGATAAAATG TTT/GATATAATT TGTTATTCAAAG AACAT	T	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)

1337	cg43923979	323	AATACCTGCTGT TGCTTTAGAAAT CIG/AJTITTCGGT TATGAATAGTCA GGTCT	G	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1338	cg43923979	330	GCTGTTGCTTTA GAAATCGTTTTC CIG/TJTATGAAT AGTCAGGTCTTG CAGTA	G	T				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1339	cg43923979	69	ATCAAAACAAC TAACAGTAAATG T[A/G]TATTATAT GCTTTAATTTTAT ACAT	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1340	cg43998926	248	TGACCCAGACAG GGATATCATTGC T[A/gap]AAAAAAA AAAATCCCCCTT GTGACC	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15
1341	cg43998926	260	GGATATCATTGC TAAAAA A[A/gap]TCCCCCT TGTGACCTGGGT ACATTTT	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15
1342	cg43998926	260	GATATCATTGCT AAAAA A[gap/A]TCCCCCT TGTGACCTGGGT ACATTTT	gap	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15

1343	cg43998926	339	AAGGGCCAAAG GAGGCCATGAGT TG[T/gap]CTTTG GTTGTGGGGACA GAGGGTAA	T	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
1344	cg43998926	445	GAGAAGGGAGA GGAAGACAGGA AGG[G/A]AAAGG AGATGCCTGAGG GTCAAAG	G	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
1345	cg43948373	1817	AACATCCCTTAA TTTGAGGTGTT C[A/T]GCAGCTGT TTTTGGAGAAGA CAAAG	A	T				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1346	cg43948373	1828	ATTGAGGTGTT CCAGCAGCTGTT TT[C/T]GGAGAAG ACAAAGAAAATT AAAGT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1347	cg43948373	1845	AGCTGTTTTTGG AGAAGACAAAGA A[A/G]ATTAAAGT TTTCCCTGAATA AATGC	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1348	cg43948373	1873	TAAAGTTTCCC TGAATAAATGCA TT[C/A]TTATGAC TGTGACAGTGAC TAATC	T	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5

1349	cg43255016	114	AATATCATCATT GGCTCTGAAATG C[G/A]TCTAAAGA TGTCATTCTTAA GTCAA	G	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1350	cg43255016	159	AGTCAAAAATA CGTAGTAAGAAT G[T/A]ACAAGAAA GAAAAAATATA AAAC	T	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1351	cg43255016	168	ATACGTAGTAAG AATGTACAAGAA A[G/A]AAAAAAT ATAAAAAACAAGT CTGCT	G	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1352	cg43941594	1818	CCGAGGACCGC CCTTGGAGTGGC AC[C/T]TGTGAG AGGATGGCCTG CATAGAT	C	T			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1353	cg43941594	2210	TGTCCTGTTACC TCTGAGCCTTGA C[G/A]AAGGCATA TTCTGACAACATA ACGAA	G	A			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1354	cg43941594	238	TGTGGATGCCAT GGGGCCATGCT GT[A/gap]GTCAA AAGTTAAATGAA AAACCACA	A	gap			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3

1355	cg43941594	322	TCATTTCAGATATT TGTTCCATATT T/CJAGGAGGGTG GATCCTAGCAAG GCAA	T	C				SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8). (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1356	cg43941594	754	GCTACTTACTAG ACACCACAAATTA G[C/gap]TTACAG CCCTTTATATATC TTTTAA	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8). (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1357	cg43991070	297	GGGGTCAGCAAT TCCATTCTCTCT C[T/gap]CCGGCT CAGTTCAGAAGC TGTCATG	T	gap				SILENT- NONCODING	dehydrogenase	Human Gene Similar to TREMBLNEW- ID:E321870 VERY-LONG-CHAIN ACYL- COA DEHYDROGENASE - MUS MUSCULUS (MOUSE), 656 aa.	4.70E-95	3
1358	cg44000219	353	AGCGCAGGCTCT GAGAGCCGGGA CG[C/A]GTACAG CTATGTGGTGGT GGCGCGG	C	A				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL- ID:Q84644 CHOLINE DEHYDROGENASE (EC 1.1.99.1) - RATTUS NORVEGICUS (RAT), 441 aa (fragment).	3.30E-93	

1359	cg43104003	266	AAATGTTACCTTTTC TAGTTCACACTCTC C/TJTAATCCCTTA GTCCCCATAAAA TAA	T				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa. pcls:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6
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1360	cg43104003	452	AAGAAATCTTTG GCCTATTTACCC ATT/CJGTCTCCAG CATTGCATAACA GACAT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.jpcls:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934-aa.	7.10E-92	6
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1361	cg43104003	547	AGTAGTCTGTTT CAGGAGTCTGCA TTC/AJGGGTCCT GTGAGAGCCTTG TCCACT	C	A				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.lpcis:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6
1362	cg43990226	103	ACACATGAGCTG TGGCTGCATTTC A[C/T]ACAGAAGC TGACACATCTCG CAGGA	C	T				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10
1363	cg43990226	388	AAGATGGGAGCA GCTGGGGGATG CT[C/gap]CAGCA CAGTAGCCTGCC TATAGGAC	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10

1364	cg43980226	408	ATGCTCCAGCAC AGTAGCCTGCCT A[T/C]AGGACTCG TCTGGCTCCCTC AGTCC	T	C				SILENT- NONCODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10
1365	cg43300900	479	CTTGGTCTGCGC TCCAGCGTGGG CC[T/C]GGCTGT GCAGGCACGAG GTGTCCAT	T	C				SILENT- NONCODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P29918 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3) (NADH DEHYDROGENASE 1, CHAIN 6) (NDH-1, CHAIN 6) - PARACOCUS DENITRIFICANS, 173 aa.	4.90E-61	
1366	cg44029571	1685	CCCAATGGAGAC TTTCTGATGCAT C[G/A]TTTCTTT GCTGTGCCAAAG CAGGT	G	A				SILENT- NONCODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	3.50E-53	7 (7p14)
1367	cg44029571	767	AGCCACCGGCA ACAAGAAGACCC AC[C/gap]TGACG GAGCTGCAGCG CCTCCTGGA	C	gap				SILENT- NONCODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	3.50E-53	7 (7p14)
1368	cg43918191	1244	CTGCCATGACTC ACAGGCAAAGGA G[G/gap]CAGGTC TGCCACCTGCGC TGCCGCT	G	gap				SILENT- NONCODING	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q23612 SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE. NCBI GI: 1086671 - CAENORHABDITIS ELEGANS, 325 aa.	3.70E-51	14
1369	cg43918191	229	GGCTGCTGTTTC ACTGAGACAGGA C[G/A]AACCACCA AGTCCAAATGAG AAGAC	G	A				SILENT- NONCODING	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q23612 SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE. NCBI GI: 1086671 - CAENORHABDITIS ELEGANS, 325 aa.	3.70E-51	14

1370	cg43979957	133	ACTTTATTAAAGT TACTTTTCCAGAT G/AJAATTCAGTA AATATGGTAATA TAGG	G	A				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL- ID:Q29259 NADH DEHYDROGENASE (UBIQUINONE) - SUS SCROFA (PIG), 128 aa (fragment).	4.00E-50	9
1371	cg43937259	397	CCCCCTGGAAAG TGATCCCGGCAT C/C/GJGAGAGCC AAGATGCCGGC CCACTTG	C	G				SILENT- NONCODING	desaturase	Human Gene SWISSPROT-ID:O00767 ACYL-COA DESATURASE (EC 1.14.99.5) (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)- DESATURASE) - HOMO SAPIENS (HUMAN), 359 aa. pcls:SPTREMBL- ID:O00767 ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1) (FATTY ACID DESATURASE 1) - HOMO SAPIENS (HUMAN), 359 aa.	8.10E-194	
1372	cg44000579	1236	CTTACAGCCATT TCCTGAATGGCT G/gap/CJTGGCGT TTCCCTCTGTCA TCTCCTT	gap	C				SILENT- NONCODING	desaturase	Human Gene Homologous to SPTREMBL-ID:O00119 FUNGAL STEROL-C5-DESATURASE HOMOLOG HOMO SAPIENS (HUMAN), 236 aa.	6.20E-128	20
1373	cg44000579	47	CGCCGACCTTTT TTTTTTTTTTTTT T/AJTTTTAATTAT GATCAACTTTTAT TG	T	A				SILENT- NONCODING	desaturase	Human Gene Homologous to SPTREMBL-ID:O00119 FUNGAL STEROL-C5-DESATURASE HOMOLOG HOMO SAPIENS (HUMAN), 236 aa.	6.20E-128	20
1374	cg43291836	264	TCTAAAGTGCCA GTATTATTACAC [T/gap]TTTTTTTT TTTTTTAGCCAAA AGTC	T	gap				SILENT- NONCODING	dna_mn_bind	Human Gene TREMBLNEW- ID:G2828110 ZINC FINGER DNA BINDING PROTEIN 89 KDA - HOMO SAPIENS (HUMAN), 794 aa.	0.00E+00	3
1375	cg40993080	282	AAGTTTATTG TATCTTTGGAAA G/gap/GJAAATTA TAAAGATTGTC TGGGAAA	gap	G				SILENT- NONCODING	dna_mn_bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0.00E+00	6

1376	cg43926092	37	TTTTTTTTTTTT TTTTTTTTTTTTTT AJTTTTTCTTCTT ATATTCTACTTTA T	T	A				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P33194 POSSIBLE DNA-REPAIR PROTEIN XP- E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB) - CERCOPIHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 1140 aa.	0.00E+00	11 (11q12)
1377	cg43962927	198	GATGCTGAGGCT GTGGGGCAGCT TT[gap/T]CCCGG GACAACCACGTG GGAGAGCC	gap	T				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1378	cg43962927	208	GCTGTGGGGCA GCTTTCCCGGA CA[A/G]CCACGT GGGAGAGCCGG CTCACCTG	A	G				SILENT- NONCODING	dna_rna_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1379	cg43962927	224	CCCGGGACAAC CACGTGGGAGA GCC[G/A]GCTCA CCTGGTCCCCAC GGTGAGGC	G	A				SILENT- NONCODING	dna_rna_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1380	cg43962927	264	CACGGTGAGGC GCAACAAGGAG GGG[C/T]TGGA CAGGCCAGGCA CCTTTATAA	C	T				SILENT- NONCODING	dna_rna_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1381	cg43962927	612	ACCTTCCCCAGG ATCCAGAGGCTG G[A/G]GTGTGGT TTTGGGCGGG AGTGAGG	A	G				SILENT- NONCODING	dna_rna_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)

1382	cg43962927	613	CCTTCCCCAGGA TCCAGAGGCTG GA[G/A]TGTGTT TTGGCGGGGA GTGAGGG	G	A				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1383	cg43962927	634	TGGAGTGTGTT TTGGCGGGGA GT[G/A]AGGGGA AGGACGTGCAT TTCCCAA	G	A				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1384	cg43968816	1025	TTCTGAGATGCG CACGAGGGAGG AA[A/gap]TTGCTT AGTCCACCATCA AGAGCCT	A	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1385	cg43968816	357	TAGCTTTAGTCA AAAAAACAAAA T[A/G]CATGAATG CAGGAATGTGTA CAGGT	A	G				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1386	cg43968816	431	CGAAGCGCAGC ATTAATTGAAGT GA[A/G]AAGTAA GAAACGCTTTGT AGCCGC	A	G				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1387	cg43968816	476	AGCCGCTCGGAT TTCCTTAGGGGA C[A/G]GCAAGTC AATGCTTATCAG CGGTCC	A	G				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)

1388	cg43968816	482	TCGGATTTCCTT AGGGGACAGCA AGT[A]CAATGCT TATCAGCGGTCC TCAGAA	T	A				SILENT- NONCODING	dna_rna_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1389	cg43968816	555	GACCCATCTGAC TCAGTCTATTAA A[C/G]CCTGAAG GAAGGATACTCT TCAGAT	C	G				SILENT- NONCODING	dna_rna_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1390	cg44129390	4713	CACCAATACACA TAAATGGGGAG G[ap/A]AAGCT ATGAAACTGTAT AGGGCTG	gap	A				SILENT- NONCODING	dna_rna_ bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa. [pcds:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)
1391	cg44129390	4716	CAATACACATAA ATGGGGGAGGA AA[ap/A]GCTAT GAAACTGTATAG GGCTGTAT	gap	A				SILENT- NONCODING	dna_rna_ bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa. [pcds:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)

1392	cg44129390	5268	TCTGAATACATG TTAAAAA [A/gap]TCAAAAG GAACGCAGAAAGT GCTAGC	A	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.lpcis:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)
1393	cg44005808	3654	CGTGTAACCAA AGCCCTAAATT C[C/gap]ACTGCG TTGTCCACAAGA CAGAAGC	C	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.lpcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1394	cg44005808	3835	ATCTAGCAATCA CAACACTGGCTG AIG/AJCGGATGC ATCTGGGGATGA GGTTGC	G	A			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.lpcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	

1395	cg44005808	3841	CAATCACAACAC TGGCTGAGCGG AT[G/gap]CATCT GGGATGAGGT TGCTTACTA	G	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa. pcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1396	cg44005808	3962	TATTGTCATTAA GGTATCAGGTC [G/gap]CCACCTG GCATTCTCTG ACCACA	G	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa. pcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1397	cg43258220	4244	AAAATCAGATCC GAGGCTTGTTT TT[gap]CCTTGTC TAGATATGTTTA AAAGA	T	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene SPTREMBL-ID:O00425 PUTATIVE RNA BINDING PROTEIN KOC (KOC) - HOMO SAPIENS (HUMAN), 579 aa.	1.30E-300	7
1398	cg43094267	1953	ACAGAAGAACT ACGCAAAAAAG TIGTTGAAGTCA TGCAAACTCCTA CTTA	G	T			SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSNEW-ID:Q13422 DNA-BINDING PROTEIN IKAROS (LYMPHOID TRANSCRIPTION FACTOR LYF-1) - HOMO SAPIENS (HUMAN), 519 aa.	5.40E-285	7

1399	cg43950470	3069	ATTTTAACCTTAGA GCTTTTTTTTTTIG ap/TJAATTTTGTGTC TGCCCCCAAGTTT TGTG	gap	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:P70568 RNA BINDING PROTEIN - RATTUS NORVEGICUS (RAT), 550 aa (fragment).	2.00E-271	X (Xq27.3)
1400	cg43931615	417	AGACACCTGAGC TCACTGGTGAAC TTC/TJTGCTTCAA GTCCTCCTGCAA AGCAC	C	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.30E-227	20
1401	cg43931615	832	TTTCTCGCTCAT ACTAGCCTTTCA TIG/gap]CCTCGG CACCACCATCAA TCCCACA	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.30E-227	20
1402	cg43962830	137	TCTTCTGATCAC AGATGGAGTGGA A[A/T]GAGTTGAA AATGCCTTCTAG AATCC	A	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene TREMBLNEW- ID:G2801552 RNA BINDING PROTEIN ELAVL4 - MUS MUSCULUS (MOUSE), 346 aa.	2.90E-184	1 (1p34)
1403	cg43956159	1034	CATCTCATCTCA TGGTATACTCCT T[A/T]CACACAAA ACATTCAAACTA CTTTT	A	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1404	cg43956159	1175	AACCATTAGCAT TCTCAGTGTGCA TIG/gap]CTCACG GCAAAGGCTTAG GCGCCGC	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1405	cg43956159	1195	GCATGCTCACGG CAAAGGCTTAGG C[gap/C]GCGGCT CGGAAGGGCGG GTACCAGT	gap	C				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10

1406	cg43956159	1250	GTCCAGGGTCAC CCACATACCATG C[gap]/CJACCACG GGTGCTATGCCG CTTCTTA	gap	C			SILENT- NONCODING NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1407	cg43971682	415	TTTTTGCTTTAT TGACTTTATTTT gap/TJAGTTTTTG TACATAAAGAAA AATCA	gap	T			SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P52912 NUCLEOLYSIN TIA-1 (RNA BINDING PROTEIN TIA-1) - MUS MUSCULUS (MOUSE), 386 aa.	6.10E-157	
1408	cg43917883	2776	TGTTTGAACAG GAGAAATTTTTT [T/gap]CCTTTTA TTTCTTTAATTTT TCTT	T	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1409	cg43917883	2884	CAAAGTGACCA ATTTTTTTTTTT T/gap]ACTGTGCT TCAATAAATAG AAAAA	T	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1410	cg43917883	3009	CATGAGAGTGTC TAGGCCCTTGAA T[G/gap]GCATAT GCCATTCTGGG AAATGCA	G	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1411	cg43917883	555	GCGGCCTCCAC GACTTCCGTTCT CC[C/gap]GCCGC CCGGCATGGC CTCAATCAG	C	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1412	cg43967456	1506	CATTGTTTCAAT CCTGGCTATCTA G[gap/AJAAAAA AAAGTCAGTGGT ATGCCTT	gap	A			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	

1413	cg43967456	1515	ATTCCTGGCTAT CTAGAAAAAAA A[gap/A]GTCAGT GGTATGCCCTTTA TACTTTT	gap	A				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1414	cg43967456	1523	GCTATCTAGAAA AAAAAAGTCAGT GIG/AJTATGCCCTT TATACCTTTTACCT GTTA	G	A				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1415	cg43967456	1593	TTGTTAATGTAT GTAGACTTAAAA G[T/gap]TTTTTTT TTTTGTAAAACTT GAGGT	T	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1416	cg43967456	1604	GTAGACTTAAAA GTTTTTTTTTTTTT gap/TJGTAAACT TGAGGTTTTTGT ATTTT	gap	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1417	cg43967456	1751	TAGTACTGTGAA ATCTATGTAGTT A[gap/A]ATCTCAA TAAAGAAATCAT TTTGGG	gap	A				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1418	cg44031794	336	CCGATCTCAGCC TTGCTGATCATC TTC/TGTACAGCA GCAGAAAATGAC CATGT	C	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.40E-137	5
1419	cg43930612	629	GAGGTAGAGCG GGCGCGCGGCA GCG[G/gap]CGG GGATTACTTTGC TGCTAGTTTC	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.30E-134	4 (4q21.1)

1420	cg43930612	668	GCTGCTAGTTTC GGTTCGCGGCA GC[G/gap]GCGG GTGTAGTCTCGG CGGCAGCGG	G	gap				SILENT- NONCODING	dna_ma_ blind	Human Gene Homologous to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.30E-134	4 (4q21.1)
1421	cg43933275	1461	AGCACCACCTGC CTCTGGGAATAG G[G/gap]CTCACC CGCGCCGAGAG GTCTGGAG	G	gap				SILENT- NONCODING	dna_ma_ blind	Human Gene Homologous to SPTREMBL-ID:Q64012 MERC=RNA- BINDING PROTEIN {ALTERNATIVELY SPLICED, EXON 1AY} - MUS MUSCULUS (MOUSE), 296 aa.	1.20E-131	20
1422	cg43933275	256	GGGAGGGGAG GTAGTATGGGA AA[C/gap]CCCTG TGCTCTACCCCTC TGGCCTGG	C	gap				SILENT- NONCODING	dna_ma_ blind	Human Gene Homologous to SPTREMBL-ID:Q64012 MERC=RNA- BINDING PROTEIN {ALTERNATIVELY SPLICED, EXON 1AY} - MUS MUSCULUS (MOUSE), 296 aa.	1.20E-131	20
1423	cg43281802	290	GAGATTTCTTTT CCAGGCCCAGG C[C/gap]TGTGAA AAACGATGGCTA AGIGTTA	C	gap				SILENT- NONCODING	dna_ma_ blind	Human Gene Homologous to SWISSPROT-ID:P29558 SINGLE- STRANDED DNA-BINDING PROTEIN MSSP-1 - HOMO SAPIENS (HUMAN), 372 aa.	1.30E-122	12
1424	cg43935457	728	CAGAACTGGTTT CTTTTTTTTTTTT T[gap]CAAGTTTT AGAGAACTAAAT TIGCA	T	gap				SILENT- NONCODING	dna_ma_ blind	Human Gene Homologous to SPTREMBL-ID:Q62262 SPERMATID PERINUCLEAR RNA BINDING PROTEIN - MUS MUSCULUS (MOUSE), 648 aa.	6.00E-118	
1425	cg43973273	1019	CCATGGAAATGA TAAGGAATCAAA T[G/T]TTCTGCAT CAGTAATTTTAAT AAAG	G	T				SILENT- NONCODING	dna_ma_ blind	Human Gene Homologous to SPTREMBL-ID:Q13097 DNA/RNA- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 363 aa (fragment).	2.00E-112	

1426	cg43955901	20	TTTTTTTTTTTT TTTTAT[G/T]TTT GTAAATTTTACTT AGGCCATCA	G	T				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.40E-97	2
1427	cg43955901	24	TTTTTTTTTTTT TTTTATGTTT[G/T] JTAAATTTTACTT AGGCCATCATTT T	G	T				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.40E-97	2
1428	cg44922718	1197	CATACTTATCAA GCAGTTGCAGAT A[A/gap]TGAAAC ATTATCAGCTAT CAATAAT	A	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1429	cg44922718	1251	TGCGACCTTCA CTTTTGTTTATAA [A/gap]ATTTCCAA TACACTGTACCA CAGTT	A	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	

1430	cg44922718	1252	TGGCACCTTTCAC TTTTGTTTATAAA [A/gap]TTTCCAAT ACACTGTACCAC AGTTA	A	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1431	cg44922718	1261	CACTTTGTGTTAT AAAATTTCCAAT [A/gap]CACTGTAC CACAGTTATGTG TCTAA	A	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1432	cg44922718	1263	CTTTGTTTATAA AATTTCCAATACI [A/gap]CTGTACCA CAGTTATGTGTC TAAAC	A	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1433	cg44922718	1318	AGGATGTTAATG GAGTAATGACTG TT[GCCAGGCGATG GGATCAGT	T	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1434	cg44922718	1356	CGATGGGATCAG TAGTGAATTCAG TTG[ACAAATGTACAA ACCTCT	G	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1435	cg44922718	1372	GAATTCAGTGCT TAAACACAAATG TIA/GICAAACCTC TGAAGAGGTGG GACTCC	A	G			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1436	cg44922718	1376	TCAGTGCCTTAA AACAAATGTACA AIA/gap]CCTCTG AAGAGGTGGGA CTCCAATGT	A	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	

1437	cg44922718	1447	CAAATGATGAAG AATGGGCCATGG C[C/gap]AGCATG CAGCATTATTTC CATTGTC	C	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1438	cg43931745	278	GCCTGGGCAGT AGGAGAACTAC CC[C/G]CTATCTC TCCAGGTACATC CCAGCT	C	G			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q02395 M96=METAL RESPONSE ELEMENT DNA-BINDING PROTEIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 373 aa.	2.00E-80	6
1439	cg43931745	369	GTGTGAATGGG GAGCTGGCAG AGG[C/gap]AGGC TGTTCAGAAAGAT GCCCCCTCC	C	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q02395 M96=METAL RESPONSE ELEMENT DNA-BINDING PROTEIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 373 aa.	2.00E-80	6
1440	cg43920750	1030	CTGCCGCGACC CGGACTGCGCG CCA[G/gap]CACC CCCCTGCCGACA GCTCCGTCA	G	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.70E-77	4
1441	cg43918693	1192	GGGACGAGTT GATAAGCTGGGC GG[G/T]GGGGGG GGGTCCCACTGT CACTTGA	G	T			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6
1442	cg43918693	2361	GATTTTTTCTAT ACAGGAGGTTT [A/gap]AAAAAAA TACTTGAACAGT TTGCC	A	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6
1443	cg43918693	2443	TTCTCATATTTT TTAGGTGTAAA T/AJAAAGATTCA GTAATTTTAACTC AGA	T	A			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6

1444	cg43920744	180	GACAAACACAACT TAAAAATGAACCT TACJCCTTCCATT CCCTAAAGTTGC ATGTT	A	C			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1445	cg43920744	196	AATGAACCTACT TCCATTCCCTAA A[G/A]TTGCATGT TGAATGAACAGA ATCCC	G	A			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1446	cg43920744	365	GCAGGCACCAAA TTAAAAA [gap/A]GGGAGGG CTCATGAGCATA AGAAAC	gap	A			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1447	cg43920744	365	GCAGGCACCAAA TTAAAAA [gap/A]GGGAGGG CTCATGAGCATA AGAAAC	gap	A			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1448	cg43920744	58	TTTTTGTTTAA AGGCTTTATTCA T/gap]TTTTTGAT CAGGGAAAAGG ACAATC	T	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1449	cg43920744	63	TTTAAAGGCT TTATTCATTTT gap/T]GATCAGG GAAAGGACAAT CTCAAT	gap	T			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1450	cg43144895	903	TGAGCCCACTGT GGTGCTCCTGCA G[G/gap]CTGAGC CACAACTGCTGG ACAGACA	G	gap			SILENT- NONCODING NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.40E-59	11

1451	cg43327954	984	AACTGAAGCAGG CCTTGAAGCCTT GT[C]CCCCCTTGA GGACAAGAAACC CGAGG	T	C				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.50E-57	1
1452	cg43327954	985	ACTGAAGCAGGC CTTGAAGCCTTG T[C]TCCCTTGAG GACAAGAAACCC GAGGA	C	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.50E-57	1
1453	cg43936210	235	TAAATCAGTGG TGGAAGAGCCG AA[G/gap]GTTCCG TATGAGCGAGGA TGATTCCTC	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1454	cg43936210	236	AAATCAGTGGT GGAAGAGCCGA AG[G/gap]TTCGT ATGAGCGAGGAT GATTCCTCA	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1455	cg43936210	308	CAACTTGTGTCAG CAGCAGAACC GA[G/gap]GGAGC CGCAATGTACGC CACACCCAC	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1456	cg43936210	587	ACTTCATCGAAA GCACTTGTGGAT G[G/gap]TGTCTA AGCCACCAATAG TTTGCCCT	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1457	cg43946971	245	AGCAGTTTGCCA TGAGAGAGCTTGG G[G/C]CTGCACA CGGTGACCCCTTA GTGATG	G	C				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52 (6p21.3)	6

1458	cg43917203	916	TCATCTTAGAAA GGTCTGGTCGCA TTC/gap]CTACGG GCCCGCTTCTTG CTGCTCT	C	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SWISSPROT- ID:O14646 CHROMODOMAIN- HELICASE-DNA-BINDING PROTEIN 1 (CHD-1) - HOMO SAPIENS (HUMAN), 1709 aa.	5.90E-50	14
1459	cg43980504	81	CACAGAACTATT GTAAACAATAT TTT/CITCAGTCGG TGATCATTGTAA TATAC	T	C				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:P41134 DNA-BINDING PROTEIN INHIBITOR ID-1 (ID) - HOMO SAPIENS (HUMAN), 154 aa.[pcis:SWISSPROT- ID:P41134 DNA-BINDING PROTEIN INHIBITOR ID-1 (ID) - HOMO SAPIENS (HUMAN), 154 aa.	6.60E-74 (20q11)	20
1460	cg43299462	639	AACTGCAGAAAG GGCAATTTAAAG TTC/TTTTTTCATA AATAACGAATAT CACA	C	T				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.[pcis:SWISSPROT- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.20E-67 3 (2p25)	3 (2p25)
1461	cg43299462	726	TAGTTTTCTTC CATTTTTTTTT[g ap/TJCTTTTAA AAGGTCCATTCA ACTT	gap	T				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.[pcis:SWISSPROT- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.20E-67 3 (2p25)	3 (2p25)
1462	cg43971258	1074	AGAGAAAGAAA CCAAAAGAAGTC C[C/gap]GCTACA GTGACCTGCAAC GCGCGCA	C	gap				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.[pcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60 (1p36.13)	1 (1p36.13)

1463	cg43971258	146	TAAAGAACAATA CTTTTTTTTTTTT ATTJCACAAAGTGT TTAAAAATCGTTT ATT	A	T				SILENT- NONCODING	dna_ma_ bind_inhib	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.lpcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1464	cg43971258	245	CAGAAAGTCACC TTCCTGTAAAAA A[gap/A]GGTACA AAACCTATATAC TCTATTA	gap	A				SILENT- NONCODING	dna_ma_ bind_inhib	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.lpcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1465	cg43971258	343	AAGACCAGCTCT GCCGCCGCCTT GG[C/gap]ATAGT TTGGAGAGCAGC CACTCCTT	C	gap				SILENT- NONCODING	dna_ma_ bind_inhib	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.lpcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)

1466	cg43971258	389	TCC TTCCACACC A TCCACGCTCTGA A/A/GJAGACCTTA GAACTTGGGGT GGGGT	G				SILENT- NONCODI NG	dna_rna_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.pcls:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1467	cg43949306	169	CTTCTCTATTAC T AATCTGAAGAAT T/CJTCTCCTTTG GAAAACTTCAAT CCTG	C				SILENT- NONCODI NG	dynein	Human Gene SWISSPROT-ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	0.00E+00	14
1468	cg43947402	258	CTTTTGAAGGAA G AAGGCAGAGGC AT[G/T]TTTACAT TATCCCAGAAAA CAGAAT	T				SILENT- NONCODI NG	dynein	Human Gene SWISSPROT-ID:Q90828 DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A) - GALLUS GALLUS (CHICKEN), 515 aa.	3.70E-214	3
1469	cg43972836	644	GGAGCTGCTGA G GTTCTGGACACA GC[G/A]TTTCTTT CCCAGAATGAGA CTGGCT	A				SILENT- NONCODI NG	dynein	Human Gene Homologous to SPTREMBL-ID:Q12019 SIMILARITY NEAR N-TERMINUS TO S. CEREVISIAE DYNEIN HEAVY CHAIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 4910 aa.	1.20E-132	6
1470	cg43932150	78	ACCGCCTTCTCA G TCGCTCCTGGAA G[G/gap]TCCCGA GCGCGACACCAT GTCGGAG	gap				SILENT- NONCODI NG	dynein	Human Gene Similar to SWISSPROT- ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	1.10E-89	

1471	cg43923118	1830	GCTGCTCCATGG TGAAAACCGACA G[G/gap]CCGCCG AGGCACGCTCC GGGCTCCG	G	gap			SILENT- NONCODI NG	elastasei nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1472	cg43923118	1840	GGTGAAACCGA CAGGCCGCCGA GG[C/gap]ACGCT CCGGGCTCCGA GCTGGGGGC	C	gap			SILENT- NONCODI NG	elastasei nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1473	cg43923118	1863	GGCAGCTCCG GGCTCCGAGCT GGG[G/T]GCGAG GTCAGGAAGGA GGA	G	T			SILENT- NONCODI NG	elastasei nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1474	cg42184167	207	CAGGTGCAGCAA GGACCGGCTCC CT[C/gap]TCACT GGGAAACGAAA CAGGCCATC	C	gap			SILENT- NONCODI NG	elastasei nhib	Human Gene Similar to SWISSPROT- ID:P19957 ELAFIN PRECURSOR (ELASTASE-SPECIFIC INHIBITOR) (ESI) (SKIN-DERIVED ANTILEUKOPROTEINASE) (SKALP) - HOMO SAPIENS (HUMAN), 117 aa.	1.60E-60	20
1475	cg43958656	2602	TTTTTGGTGAA GTACTGAACTTG C[gap/C]TTTTTTT CCGGTTTCTACA TGCAGA	gap	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
1476	cg43958656	521	CGTTTCCAGCCC CCAATCTCAGAG C[G/C]GAGCCGA CAGAGAGCAGG GAACCGG	G	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6

1477	cg43958656	546	GGAGCCGACAG AGAGCAGGGAA CCG[G/gap]CATG GCCAAAGCCGC GGCGATCGGC	G	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
1478	cg44017749	14845	CGTTTTAATAATT TTTGCTGAATTCT C/gap]TTTACAAC TAAATAACACAG ATATT	C	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLEPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0.00E+00	12
1479	cg43982507	3293	ACAAATAATACC CCCGTCGGAATG GTT/gap]AACCGA GCCAGCAGCTG AAGTCTCT	T	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)
1480	cg43982507	533	CCTCCAGCCCC CACCTTCTTCCT C[C/gap]TTTCGG AAGGGCTGGTAA CTTGTCG	C	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)
1481	cg43982507	594	CGGCGGCGGCG GCGGCGGCGGC GGC[gap/G]ACCA TCCAGGCGGGC ACCATGGGCA	gap	G			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)
1482	cg43982507	594	CGGCGGCGGCG GCGGCGGCGGC GGC[gap/G]ACCA TCCAGGCGGGC ACCATGGGCA	gap	G			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)

1483	cg43965833	3513	GTTTGGTTGCTG GGGGGCTTTT TTA/GJGGTTTGG GGCATTGTGTTT TTGTA	A	G				SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1484	cg43965833	3763	GTTTATATGTGT ATGTGTGTGACA G/A/GJAAATCTG TAGAGAAAGAGGC ACATC	A	G				SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1485	cg43965833	3890	AAAGCCTTTGG AAATCTGGATCA G/A/GJAAATAGAT ACCATGGTTTGT GCAAT	A	G				SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1486	cg43965833	4483	TGGCTTAAGTC AGAACAACTGGC C/A/CJAAATTGAA GTCATATTTGAG GGGG	A	C				SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1487	cg43965833	4484	TGGCTTAAGTC GAACAACTGGCC A/A/CJAAATTGAAG TCATATTTGAGG GGGA	A	C				SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1488	cg43965833	4502	CTGGCCAAAT GAAGTCATATTT G/A/TJGGGGGA AATGGCATACGC AATATT	A	T				SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1489	cg43965833	4514	GAAGTCATATTT GAGGGGGGAA TG[G/gap]CATAC GCAATATTATATT ATATTGG	G	gap				SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	

1490	cg44007516	377	TAATAAAATAAC A TGGAGCAGAGAA [A/gap]GCTTTAG GAGTTATACCAT TAGTTC	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:Q03933 HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR 2) (HSTF 2) HOMO SAPIENS (HUMAN), 536 aa.	6.20E-283	
1491	cg43945212	2872	TGTCCTGTGTCT A ATGTACCTCTAG C[A/gap]TGTTCTT TTTTGTACTTTTC TGGTT	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P43135 APOLOPROTEIN A1 REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.80E-232	7
1492	cg43945212	926	GTCCCCCTCCCC G TCCCCCTCCGGC G[G/C]AAAGCCC CCCGAAACCAAC AAAGCT	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P43135 APOLOPROTEIN A1 REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.80E-232	7
1493	cg43945167	405	TGCTACCAACCAC G CAAGCCCTGTGT C[G/A]CGACGGC AGCGGCTGCAG TCACCAG	A			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)
1494	cg43945167	475	GACACCCGTGC C CAGCCCCAGCC ACC[C/gap]TGAC GGCGGGCTGTC CACGGAATG	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)

1495	cg43945167	561	CTTCCCTGCCGG GCTGGGCTCCC CA[A/G]TGCCTTC AGAGTTGCTTGT GCCGAG	A	G				SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)
1496	cg38775224	1064	TGGTAACCACAG AATTAATAACTGT [A/gap]CTACCCT GACAAGCTATAT ACATGT	A	gap				SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:Q13790 APOLOPROTEIN F PRECURSOR (APO-F) - HOMO SAPIENS (HUMAN), 308 aa.	1.30E-161	12
1497	cg43262939	524	CCTTCAATAGCA TGTC AAGTGGAG T[G/A]AAAAAAGA ATTGGCCATGA ATTG	G	A				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSPROT-ID:P08519 APOLOPROTEIN(A) PRECURSOR (EC 3.4.21.-) (APO(A)) (LP(A)) - HOMO SAPIENS (HUMAN), 4548 aa.	4.60E-108	
1498	cg43918531	1635	GAATGATTTGA AGATTGATGACA TT[C]CGTAAGCC TGGAGAATCTGA AGAA	T	C				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa.lpcds:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
1499	cg43918531	1729	TAAGTAAATGGA TGTCCTCGTGATG C[G/A]TCTACAGT TATTATTGTTAC ATCC	G	A				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa.lpcds:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5

1500	cg43918531	1843	CAAAGCTGTGTA ATCGTGGGGTA CTT/CJATCTCAAC TGCTTTTGTATTC ATTG	T	C				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. pcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
1501	cg43944783	39	TTTTTTTTTTT TTTTTTTTTTT TTTAAACCACGCC CAACTGGCTTGT TTT	A	T				SILENT- NONCODI NG	eph	Human Gene Similar to SWISSPROT- ID:P15705 HEAT SHOCK PROTEIN ST11 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 589 aa.	2.80E-74	11
1502	cg43984905	2387	CTAGGCTGGAG GAAGCCAGTGG GGT[C/gap]CCCC CTGAGTGGGCT GGGCCCTCTG	C	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1503	cg43984905	2392	TGGAGGAAGCC AGTGGGGTCCC CCC[gap/C]TGAG TGGGCTGGGCC CTCTGTCCAC	gap	C				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1504	cg43984905	2440	CACATGTGGGGA CAGGGCTGGTG TG[G/gap]CTGCT CCCAGCCTCTTG CTCAGAGC	G	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

1505	cg43984905	2575	GTCCTTCATTCC GTTAGGAATAAC AIC/AJTGACGCC CTCTCCAACCTC CGGCCA	C	A			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1506	cg43984905	2599	ACTGCAGCCCTC TCCAACCTCCGG C[C/gap]AGCGAG TGGTCAAGGATT TTTATAA	C	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1507	cg43274299	2011	CTGCTCAGACCT GTGACCCCGGC GG[G/gap]ACCCC CATGTCCTCCGC TCCGCCCG	G	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1508	cg43274299	2149	GTCCCCCGGGG CTCCCGGTCCTC TG[gap/G]CATGT CTCAGGCTGAGC TCCCTCCC	gap	G			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1509	cg43274299	2156	GGGGCTCCCGG TCCTCTGCATGT CT[gap/T]CAGGC TGAGCTCCCTCC CCCGCGGT	gap	T			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1510	cg43274299	2170	CTCTGCATGTCT CAGGCTGAGCTC C[C/gap]TCCCCC GCGGTGCCTTC GCCCTCTG	C	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7

1511	cg43274299	2176	ATGTCTCAGGCT GAGCTCCCTCCC C[C/gap]GCGGTG CCTTCGCCCTCT GGCTGCA	C	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1512	cg43274299	2180	CTCAGGCTGAGC TCCCTCCCCCGC G[G/gap]JTGCTT CGCCCTCTGGCT GCAAATA	G	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1513	cg43972012	102	CAGGGTTCCTGG CTGGGCAGCAC AG[G/gap]CCTGG GGCGACACTCCT GTCCTGTC	G	gap			SILENT- NONCODI NG	esterase	Human Gene SPTREMBL-ID:Q16837 ACID SPHINGOMYELINASE (EC 3.1.4.12) (SPHINGOMYELIN PHOSPHODIESTERASE) (NEUTRAL SPHINGOMYELINASE) - HOMO SAPIENS (HUMAN), 629 aa.	0.00E+00	11 (11p15.4)
1514	cg44011461	172	ATTATCAAGGT TTTCATTGCTTTT [gap/T]ATTCAATG AGGTTTGAACA TGAGA	gap	T			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1515	cg44011461	188	CATTGCTTTTATT CAATGAGGTTTG G/CJAACATGAGA GGCCAAAATGA GGAG	G	C			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)

1516	cg44011461	241	CATTTTGGGAA /A TCCTCTATAAAG A[A/gap]TATAAGT TAAGAAAAGTTGT CCAAGA	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1517	cg44011461	251	AATCCTCTATAA /A AGAATATAAGTT A[A/gap]GAAAGT TGTCCAAGATGA AAATAAT	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1518	cg44011461	255	CTCTATAAAGAA /A TATAAGTTAAGA A[A/gap]GTTGTC CAAGATGAAAAT AATAGGA	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1519	cg44011461	524	TGCATTTCCTCCT /C GGTACAGCTGGA G[C/gap]TGGTTC TCATTAAACACTG AACTCTT	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1520	cg43984524	860	TATCACCCCTGAA /A CGCGCCTGATCT C[A/G]TCTGATCT CGGAAGCTAAGC AGGGT	G				SILENT- NONCODI NG	esterase	Human Gene Similar to SPTREMBL- ID:P70665 SIALIC ACID-SPECIFIC 9-O- ACETYLESTERASE - MUS MUSCULUS (MOUSE), 541 aa.	3.20E-99	

1521	cg43319420	1886	CTGCAGTTCTGG ACGGGCTGGCC GA[G/gap]TGGC GGATCCTTGTG CAGGGAAG	G	gap				SILENT- NONCODI NG	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.[pcis:SWISSPROT- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
1522	cg43319420	1816	CGGGATCCTTGT GCAGGGAAGAG CT[G/gap]CCCTG GGCACCTGGCA CCACAAGAC	G	gap				SILENT- NONCODI NG	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.[pcis:SWISSPROT- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
1523	cg43934722	737	GGGATTTTGTGG ACGTCTCCGTGC A[G/T]GAACTGCT GGACTGTGGCC GCTGTG	G	T				SILENT- NONCODI NG	fgf	Human Gene TREMBLNEW- ID:G2738520 FGF-1 INTRACELLULAR BINDING PROTEIN - HOMO SAPIENS (HUMAN), 372 aa.[pcis:TREMBLNEW- ID:G2738522 FGF-1 INTRACELLULAR BINDING PROTEIN - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRINEL), 372 aa.	9.80E-184	
1524	cg43281831	2016	TCCTTTAACCAC TGCCCTCTCCTT CT[gap]TCTCCT TCAAGGTTCTTT CCCCCT	T	gap				SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	9.20E-83	4

1525	cg43281831	2017	CCTTTAACCACT GCCCTCTCCTTC TTT/gapTCTCCTT CAAGGTTCTTTC CCCCTC	T	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	9.20E-83	4
1526	cg43919380	1038	CGAGGGGTCCT CACCTGGTTGAC CC[C/gap]AAAA TGTTCCCTTGAC CATTGGCT	C	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1527	cg43919380	1257	TGCGCTCTTGCA GGCTGAGTCCCT C[A/C]ATGCAAAA GTGGGGCTAAAT GAAGT	A	C			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1528	cg43919380	2230	TGTAAGGAG CATGATTTAAG A[G/T]GCTTTGGC CCAATGCCTATA AAATG	G	T			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1529	cg43919380	2240	AGCATGATTTTA AGAGGCTTTGGC C[C/gap]AATGCC TATAAAATGCCC ATTTCGA	C	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)

1530	cg43919380	3274	TTAAGGTGCCTA CTGTGTGCTAGG C[A/gap]CTGTAC TGGATACTGGGG ACCTTGT	A	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1531	cg43919380	3702	AAGTCTCATAGC CAGCTCCTGTCA C[G/A]TGACTCTC ATATGGATTTCAT TTTCG	G	A			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1532	cg43919380	395	GGGCTACTCTGA GAAGAAGACACC A[G/A]GGGGATT CCTCTTCCCCCTG GGACAG	G	A			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1533	cg43919380	404	TGAGAAGAAGAC ACCAGGGGATT C[C/T]TCTTCCCG TGGGACAGCACT GAGCG	C	T			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)

1534	cg43919380	406	AGAAGAAGACAC CAGGGGATTG CT[C/T]TTCCCT GGACAGCACT GAGCGAG	C	T				SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF-BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1535	cg43918792	691	ACCGCAACAGC AAAGACTATCCC A[A/C]CTTTCTAT TAACAGTGCCAA GATTA	A	C				SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	1.70E-56	13
1536	cg43918792	697	AACAGCAAGAC TATCCCAACTTT CT[G/A]TTAACAG TGCCAAAGATTAT AACTG	T	G				SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	1.70E-56	13
1537	cg43937658	1026	CAAAGGCAGTAA CCCCAGCGACC AG[C/gap]TGCTG CTGCTGCACGGT GAGGAGGA	C	gap				SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1538	cg43937658	353	AGCCTCAGCAG GGCCGGTCCAG ACA[T/C]GGCTGA GTCCTGTGCTGC CCTGGAG	T	C				SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1539	cg43937658	561	CCACAGAAATAC CCATGGCTGTGG G[G/gap]CTGTGA CCAGCAGTGGCT GATTAGG	G	gap				SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1540	cg43937658	898	TTTTTTTGGTGG TTTTCTTAAAAA [gap/A]GCCTTTG AGTTGCAGGTCA GGTGAG	gap	A				SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16

1541	cg43837658	950	TGGTTCTGGAAG TACCGGAAGTTC T[G/T]TTGGTATG AGAGAGACTTGT CTACA	G	T				SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1542	cg43284508	306	CTCTATCCATA CCTTTGCAAGG A[G/A]GGGAGGG GTCTACAAGCCA GAACTT	G	A				SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1543	cg43284508	443	ACATCAGAAGCA CTGACTGGTAGA G[C/T]CCTTGGAA ATCATACAGTCC ACCCA	C	T				SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1544	cg43284508	475	AAATCATACAGT CCACCCATCCCC C[G/A]CCAGACA CATGGACACACC GAGGCT	G	A				SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1545	cg43284508	881	CCACGCCCATAT GAGGGGTGGAG AG[G/gap]AGAAG CCAGCAGCACTG GGTGAGC	G	gap				SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1546	cg43284508	883	ACGCCCATATGA GGGGTGGAGAG GA[G/gap]AAGCC AGCAGCACTGG GGTGAGCCCT	G	gap				SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1547	cg43320667	576	ATTAAAAAGGTC ACCAGCCCGCC AG[G/gap]TGCCA GAAGCCACCGG GTATCCTTG	G	gap				SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00 3 (3p25)	

1548	cg43320667	674	TCTCTGCGTGGT GATGGTGTCTGG A[C/gap]TCGCCA CTCGAGGTAGGT TGAGATG	C	gap				SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
1549	cg43975899	1613	TTTACTCACATT CTGTTGTTTCAGT gap/T]CCTCTGCA CTGGGAATTTAT TTATG	gap	T				SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P14867 GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1.30E-248	5 (5q34)
1550	cg43975899	1664	TCTCAACGCAGT AATCCCATCTG C[ap/C]TTTATTG CCTCTGTCCTAA AGAAT	gap	C				SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P14867 GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1.30E-248	5 (5q34)
1551	cg43299024	3522	TTTCTCCCTAGA TCGCACTGTGGG C[C/T]GGGGCCC TGGAGGGCTGC TCTGTGT	C	T				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1552	cg43299024	3529	CTAGATCGCACT GTGGGCCGGGG CC[C/gap]TGGAG GGCTGCTCTGTG TTAATAAG	C	gap				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1553	cg43299024	3718	GCTGCTCTGCC CAACGCGACCG CT[G/T]CCCGGC TGCCCGAGAGGG CTGGATGC	G	T				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1554	cg43299024	3744	CCCGGCTGCC AGAGGGCTGGA TGC[C/gap]TGCC GGTCCCCGAGC AAGCCTGGGA	C	gap				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)

1555	cg43992911	397	CTTCTTCCAAGA TTTCACGCTCTTG G[C/T]GGCCGTT CCAAGGAGCGC GAGGTGC	C	T				SILENT- NONCODING NG	glycoprot ein	Human Gene SWISSPROT-ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	7
1556	cg43943531	2247	TAAATGTCACGT CCAGCTCTGATA T[G/gap]CTTCGC ACTGAGCACATC ACATTAA	G	gap				SILENT- NONCODING NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1557	cg43943531	2343	TGTAAGAACAA ACTGGATGGCAT C[A/C]GAATTGTC TGGAAGTTTTGT CTTGG	A	C				SILENT- NONCODING NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1558	cg43943531	2372	TTGCTGGAAGT TTTGCTTGGGC AIG/TJATGGGCT GGCCCAATGAA ATGAT	G	T				SILENT- NONCODING NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1559	cg43943531	2373	TGCTGGAAGT TTGCTTGGCA GT/GJATGGGCT GGCCCAATGAA ATGATT	T	G				SILENT- NONCODING NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1560	cg44021330	3335	AACACACATGAT GACTGAGGCATT C[G/A]GGAACCC CTTCATCCAAA GAATAA	G	A				SILENT- NONCODING NG	glycoprot ein	Human Gene SWISSPROT-ID:Q12860 CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) - HOMO SAPIENS (HUMAN), 1018 aa.	0.00E+00	12 (12q11)
1561	cg43997653	2551	GAGCTATTTTA CCTCCGGCCTCC C[C/T]TGCTGTC CCCCCACCTGAC GTCTT	C	T				SILENT- NONCODING NG	glycoprot ein	Human Gene SWISSPROT-ID:P50895 LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM) CELL SURFACE GLYCOPROTEIN (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN) - HOMO SAPIENS (HUMAN), 628 aa.	0.00E+00	

1562	cg44003301	1920	TGAGATAAAAGA TGTAAGTTGTGAC C[AG]TTGTAAACA ATAGCACAAATA AAGCA	A	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16671 PLATELET GLYCOPROTEIN IV (GP1B) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) - HOMO SAPIENS (HUMAN), 471 aa.	2.00E-254	7 (7q11.2)
1563	cg43957605	150	TTATAGAAAGTT GCAGTTAAAC G[C/T]TTCTCCA AAATAAAAGAC AAATG	C	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P55) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)
1564	cg43957605	510	CAAATGCTGGAG AGGGGCATACA GT[G/gap]GGTTC CCCCATTCTACA AGCTTAGT	G	gap				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P55) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)
1565	cg43926590	415	TTCAGACAATTC AGCCTTTATTTTA [G/A]AAATAATT CTGTAGCTTCCA CTTT	G	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P26572 ALPHA-1,3-MANNOSYL- GLYCOPROTEIN BETA-1,2-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL- OLIGOSACCHARIDE-GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-T I) - HOMO SAPIENS (HUMAN), 445 aa. pcis:SWISSPROT-ID:P26572 ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL- OLIGOSACCHARIDE-GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-T I) - HOMO SAPIENS (HUMAN), 445 aa.	4.20E-245	5 (5q35)

1566	cg44003218	158	GATTCITTTCTGT GACTCATCAGTT C[A/C]TTTCCTGT AAATTTCATGTC TTGCT	A	C				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16671 PLATELET GLYCOPROTEIN IV (GPV) (GPIIB) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) - HOMO SAPIENS (HUMAN), 471 aa.	2.40E-242	7 (7q11.2)
1567	cg42360692	1557	AGAAAGAGGATA CACAAAACGTAC C[C/gap]TTATCT GTTTCCCTTCC TTGTCAG	C	gap				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERAS E (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1568	cg42360692	1584	TATCTGTTTCCC CTTCCTTGTCAG C[G/A]TCGGAA GATGGTATGAAG TCCTCT	G	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERAS E (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1569	cg42360692	1826	GCCGATGCATAA AGTCAGCCTGTT C[A/C]AAGTGCTC AGGGACTTAGCA AAATG	A	C				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERAS E (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)

1570	cg42360692	1914	TAAATGTGACCA TTTTCTGGTAT G[ap/C]AATAAA CTTACAGCAACA AATAATC	gap	C				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1571	cg42360692	1914	TAAATGTGACCA TTTTCTGGTAT G[ap/C]AATAAA CTTACAGCAACA AATAATC	gap	C				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1572	cg43924995	1830	GGCCAAATTTTG ATCCTAACCTTG A[A/C]GTATGCCT TGAACCTATTAA CATGG	A	C				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.20E-222	X (Xq24)
1573	cg43987514	76	TTTTTTTTTTT TTGGCAGGTAAA [A/G]GAAAAGACT TTATTAATAATCA GTG	A	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-215	

1574	cg43301245	232	TTCCTAAGTGAA GGTTTCAAGCTG G[G/gap]CTTTGC AGGGGGTATAAT TAGTATG	G	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383.aa	3.00E-210	1
1575	cg43301245	334	ATGGTGTCTTT GATAAGGAGGG CTTGAJGGGGC AGGGAGTTGAAG AAATTCC	G	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383.aa	3.00E-210	1
1576	cg43301245	399	GATCTGTAAACA TTTCCATTATCA [gap/T]ACAAGTG TGTAATAATCCC GAGTCT	gap	T			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383.aa	3.00E-210	1
1577	cg43958670	1152	CATACGGAGTTC TCCTTGGGAAA CIGAJACAAGACT ACAGTGTTCACT TCGCA	G	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207 1 (1q32)	1

1578	cg43958670	15	TTTTTTTTTT TTT/AJTTTTTTCC AAATGTACAATTT TAT	T	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1579	cg43958670	16	TTTTTTTTTT TTT/AJTTTTTTCC AAATGTACAATTT TATT	T	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1580	cg43958670	174	GAATTCATATAC GCTTCTGTCAAT TTC/JAACAACT TCCAGAGAAAC TGGTC	A	C				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1581	cg43958670	1953	AATCTATTGAGC CTCTCTGCTCTG C/A/TGGAGTGG TTGATTTAGTCT GGTAAG	A	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1582	cg43958670	3091	CTCGCGGCGGC CGGAGGCTCC ATG[C/G]GCGG GCGGGAAGACG CTGTTATT	C	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1583	cg43958670	3092	TCGCGGCGGCC GGGAGGCTCCA TGC[G/C]GCGG CGGGAAGACG TGTTATTC	G	C				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)

1584	cg43958670	3099	GGCCGGGAGGC TCCATGCGCGG CGC[G/gap]GGAA GACGCTGTTATT TCTCCGGAG	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1585	cg43958670	3101	CCGGGAGGCTC CATGCGCGCGG CGG[G/gap]AAGA CGCTGTTATTTC TCCGGAGGA	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1586	cg44034752	1702	TAGGTTGACAAC TTGTCATGATTTT [G/A]ACGGTAAG CCACCATGATTG TGTTC	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1587	cg44034752	1763	TTGACCTTACAA AAACCATGGAA C[ap/C]TGTGAC TTTGAAAGGTGC TCTTGCT	gap	C				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1588	cg44034752	1801	GGTGCTCTTGCT AAGCTTATATGT G[ap/G]CCTGTT AATGAAAGTGCC TGAAAGA	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1589	cg44034752	1815	GCTTATATGTGC CTGTTAATGAAA G[ap/G]TGCCTG AAAGACCTTCCT TAATAAA	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1590	cg34243197	2123	GCTTCTCTGGGC CTCTCAGTTGAA C[ap/C]AAAGCA GCAAAACAAAGG CAGTTT	gap	C				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSNEW-ID:Q61207 SULFATED GLYCOPROTEIN 1 PRECURSOR (SGP-1) (PROSAPOSIN) - MUS MUSCULUS (MOUSE), 557 aa.	5.00E-202	10 (10q22.1)

1591	cg43059879	106	GAACAAGAAACA AGTGTGACATTT T[A/G]TGTGGAAT CTGAAACCCACC TTAGC	A	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.[pcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.[pcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa	6.60E-199	17 (17q23)
1592	cg43932434	606	CTTTAAAGAAACA AAACACAAAAA CTT[A/T]TAAGAGT AGAAAAATTTTAT GCTAA	T	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)

1593	cg43932434	607	TTTAAAGAACAA AACACAAAAAAC TTTATAAGAGTA GAAAATTTTATG CTAAA	T	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
1594	cg43932434	608	TTTAAAGAACAA ACACAAAAAAGT TTTATAAGAGTAG AAAATTTTATGCT AAAA	T	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
1595	cg43988092	636	AATGCTTTTGTAG AGCCTTTCTGTA GTCATGATACAAA TATATATATATAT ATT	C	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.00E-192	8
1596	cg43988092	775	GTAAGACTATT ATCCACCTGAAT TTCATTCAATTTC TTTAAAGTTAGT GCATT	C	T			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.00E-192	8

1597	cg43115790	122	GGTGGTCTGAC TACAAGGGCTAG G[C/gap]CCTAGG ACATCTGGTTT CTTCTT	C	gap				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:Q03395 ROD OUTER SEGMENT MEMBRANE PROTEIN 1 (ROSP1) - HOMO SAPIENS (HUMAN), 351 aa.	1.40E-191	11 (11q13)
1598	cg43918166	985	AAAATTCCTTTT TTTTTTTTTTTTT gap]TTTTTTTGCA TGTTGTTTAAACA ATC	T	gap				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1599	cg43918166	986	AAATTCCTTTT TTTTTTTTTTTTT gap]TTTTTTGCAT GTGTTTAAACAA TCC	T	gap				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1600	cg43918166	987	AATTCCTTTT TTTTTTTTTTTTT gap]TTTTTTGCAT GTGTTTAAACAA TCCC	T	gap				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1601	cg43918166	992	TTTTTTTTTTTTT TTTTTTTTTTTTT[g ap/T]GCATGTGTT TTAACAATCCCC CACC	gap	T				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5

1602	cg43918166	992	TTTTTTTTTTTT TTTTTTTTTTTT[9 ap/TJGCATGTGTT TTAACAATCCCC CACC	gap	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1603	cg43918166	199	AAAATAGAAACC TACTAGATCAAC AIC/AJAGTGTGT TCTGTGCTCTAA AATAC	C	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1604	cg43918166	274	AACAACCAAGG AACCTGCTTAA C/A/GTACTGTGT ATTATTGTAGCT AGAGT	A	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1605	cg43918166	310	TATTGTAGCTAG AGTCATTCCTTC T/TATJAGCCAAAG GAGGTTTATAA AAAAG	A	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1606	cg43918166	334	AAGCCAAAGGAG GTTTTATAAAAA [gap/AJGAATCAA TATTGGGCAAT CCCTTT	gap	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5

1607	cg43918166	3444	ATTCCTCACTTG ATGGTTTGAAAG T[C/T]GCCTTCAAT ATTACATGAATT TCCT	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1608	cg43918166	968	AAAATGGTTATA TATACAAAATTTC [T/gap]TTTTTTTT TTTTTTTTTTTT TTTG	T	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1609	cg44022653	246	TATAACCCCTTTC ATACTAGTTGAA C[gap/T]TTTTTTT TTATAATGTACAT GTACT	gap	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1610	cg44022653	247	TATAACCCCTTTC ATACTAGTTGAA C[T/gap]TTTTTTT TATAATGTACAT GTACTA	T	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1611	cg44022653	255	TTTCATACTAGTT GAACCTTTTTTTT T[gap]ATAATGTA CATGTACTACTT TATAA	T	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1612	cg44022653	258	ATACTAGTTGAA CTTTTTTTTTTATA gap/TJATGTACAT GTACTACTTTATA ATTA	gap	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1613	cg44022653	280	TATAATGTACAT GTACTACTTTATA [A/G]TTAAACAAA AAACTTTAAAT GATT	A	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

1614	cg44022653	323	AATGATTTTTTAA AAAAGAAAAGAA[gap/GJTAAATCAC AGTGGAAACATGA AATGG	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1615	cg44022653	357	GTGGAACATGAA ATGGAATGTCAA C[ap/GJTGTGGG GACGGGTCATCC AGAGGAG	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1616	cg44022653	367	GAAATGGAATGT CAACTTTGGGA C[G/A]GGTCATC CAGAGGAGTCCA AGAGCC	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1617	cg44022653	401	AGAGGAGTCCAA GAGCCCCAACAT G[G/T]TCGCGTG TCTCTGGTCCTC AGGTCA	G	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1618	cg44022653	414	AGCCCCAACATG GTCGCGTGTCTC T[G/T]GTCCTCAG GTCATCACCCAG CCTCA	G	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1619	cg44022653	421	ACATGGTCGCGT GTCTCTGTCCT C[AT]GGTCATCA CCCAGCCTCACC CACAG	A	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1620	cg44022653	496	CCGTGCAAGCTT CCACTTGGTGCC T[G/A]CGTGGGA ACGCACACACCTG CCGTGG	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

1621	cg44022653	498	GTGCAAGCTTCC ACTTGGTGCCTG CIG/AJTGGGAAC GCACCCACCTGCC GTGGAA	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1622	cg44022653	654	CCCTCCACGCA GTGTGAGCCCTG G[G/gap]CTGCGC CACACCCGCAG GTGGCCCG	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1623	cg43318219	1858	TTTTCAAGAAA CTGGAATCTGG [A/T]TTTTCAGCG AACATGCCTGAT TTTA	A	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSNEW-ID:P15813 T- CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa. pcds:SWISSPROT-ID:P15813 T- CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa.	3.10E-185	1 (1q21)
1624	cg40915005	1796	GGTCCTAGCAAC CTCCACATGTTT A[A/C]CTATTAAT GGATCATCAGGC CTGTT	A	C				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSNEW-ID:P06126 T- CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa. pcds:SWISSPROT-ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T- CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183	1 (1q21)

1625	cg43958915	205	GTAGATTTAACC ACAGAACTGTCT C[G/A]ATTTTAT AAAAATTGATCC CAAGA	G	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.lpcis:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11
1626	cg43958915	331	CCCAAAGGGGA GAGGTGTGGGG CGG[C/T]GGGGC GGGAGGGCGCC TTGTGCTGT	C	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.lpcis:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11

1627	cg43958915	346	TGTGGGGCGGC GGGGCGGGGAG GCG[C/gap]CTTG TGCTGTGGCACT GGACACGGT	C	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.[pcis:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11
1628	cg43958915	387	TGGACACGGTG CTCATCTGCAGG AT[G/A]GCCACG AAGACAAACGGC ACAGACG	G	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.[pcis:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11

1629	cg43977071	1845	TGCAGGTTAGGT TCCAGACCACTT A[G/T]GAGTCTGC GAAACGCCCCAC GCTCCA	G	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P28328 PEROXISOME ASSEMBLY FACTOR-1 (PAF-1) (PEROXIN-2) (35 KD PEROXISOMAL MEMBRANE PROTEIN) - HOMO SAPIENS (HUMAN), 305 aa.[pcis:SWISSPROT-ID:P28328 PEROXISOME ASSEMBLY FACTOR-1 (PAF-1) (PEROXIN-2) (35 KD PEROXISOMAL MEMBRANE PROTEIN) - HOMO SAPIENS (HUMAN), 305 aa.	1.20E-169	8 (8q21.1)
1630	cg43124001	1942	CAGGGGATTTTA TCCCCCACCACAA A[A/G]CACAGTGA AAGGCCTGCTTT TGTTGT	A	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:O42281 PERIPHERIN (RETINAL DEGENERATION SLOW PROTEIN) (PHOTORECEPTOR OUTER SEGMENT MEMBRANE GLYCOPROTEIN 1) (CRDS1) - GALLUS GALLUS (CHICKEN), 354 aa.[pcis:SWISSPROT- ID:O42281 PERIPHERIN (RETINAL DEGENERATION SLOW PROTEIN) (PHOTORECEPTOR OUTER SEGMENT MEMBRANE GLYCOPROTEIN 1) (CRDS1) - GALLUS GALLUS (CHICKEN), 354 aa.	5.50E-156	6 (6p21.1)
1631	cg43248459	577	CACAGAGAGGAT GAGAAACAAAA A[A/gap]GAGAAA AGGAAAAGTAGG TTGAAGA	A	gap				SILENT- NONCODING	glycoprotein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	7.10E-155	20
1632	cg43248459	85	AACAGAGAGCAC ACGCATACAGCA C[G/A]GAGCACT GAGGTGGGGA GCATGGG	G	A				SILENT- NONCODING	glycoprotein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	7.10E-155	20

1633	cg43953517	2391	AATAAAATTTAT TGAGTGAACAA ATTAAAAATACAA TGACTAGTCATG CAT	A	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.90E-150	4
1634	cg43953517	2396	AAATTTATTGAGT GAAACAAAAAA A/GJTACAATGAC TAGTCATGCATC ATCA	A	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.90E-150	4
1635	cg43922980	3766	TTATTIATTACAA AATTATATTCAC C/GJTAAATGCCA ACCATCTACAAA AACA	C	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P97449 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CD13) (P161 MEMBRANE PROTEIN) - MUS MUSCULUS (MOUSE), 965 aa.	2.00E-135	5
1636	cg43922980	3957	AGGCCGCTGGTT TGTCAGCCATCT GT/CJTGCTTCTT ATTGATAGATGG CATTG	T	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P97449 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CD13) (P161 MEMBRANE PROTEIN) - MUS MUSCULUS (MOUSE), 965 aa.	2.00E-135	5
1637	cg43951991	152	TTACGCACCGCA TGAGAACCGTTA G[gap/GJTTATAA AATCTATCATCA ACCAAGTA	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1638	cg43951991	27	TTTTTTTTTTT TTTTTTTTTTC[C /TJTTTATCAATG TTTTATTTTAA A	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1639	cg43951991	836	ATATTTTAAACAA GGAAAAAA gap/AJGCAACATT CACAGCACATCA AGCCC	gap	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	

1640	cg43951991	881	AAGCCCAAAATA GTTACACCTTC TATCACTGAAG CATTGTTTAAAT GTAC	A	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1641	cg43948148	88	GTTTCTTTAAAA TAAACCCACACI gap/AJAAAAAAGC CAGAACACCCCTA CCCAA	gap	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01650 INTEGRAL MEMBRANE PROTEIN E16 - HOMO SAPIENS (HUMAN), 241 aa.	2.00E-128	16
1642	cg44004667	2076	AAAGAAAATCTC TGTAACCCCT ATTCGTGGAGG CGGAATTGCTCT CCCAGC	T	C				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T- LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.[pcls:SWISSPROT- ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU- 2) - HOMO SAPIENS (HUMAN), 235 aa.	7.60E-127	
1643	cg44004667	2296	GAGCCCTCACA CAGCCCTGGCCT CTTCGCTCAACT AGCAGATACAGG GATGA	T	C				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T- LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.[pcls:SWISSPROT- ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU- 2) - HOMO SAPIENS (HUMAN), 235 aa.	7.60E-127	

1644	cg43301424	1194	TGCCCCACCTCC TAACCTAATCCC C[C/A]CGCCCCG CTGCCTTTCCCA GGCTCC	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.[pcis:SWISSPROT- ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE- BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.	2.30E-125	19 (19q13.2)
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1645	cg43301424	1228	TGCCCTTTCCAG GCTCCCCTCACC C[C/gap]AGCGGG TAATGAGCCCTT AATCGCT	gap				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa. pcis:SWISSPROT- ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE- BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.	2.30E-125	19 (19q13.2)
1646	cg42852276	1537	AAAGGCATTATT CTCCAGCCTTAA G[gap/T]ATCTTA GGACGTTTCCTT TGCTATG	gap	T			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P26718 NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 216 aa. pcis:SWISSPROT-ID:P26718 NKG2- D TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 216 aa.	5.70E-122	12
1647	cg43068999	874	TGGATACTAGAT CTTACATCTGCA G[C/gap]TCTTTCT TCTTTGAATTTC TATCT	gap	gap			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P02743 SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1- GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 223 aa.	1.60E-119	1 (1q21)

1648	cg43986150	1655	ATAAACAGTTT ATTATCTCAATCA [A/C]AACATTCTCT ATATATCAAAACA CTCC	A	C				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P19397 LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53) - HOMO SAPIENS (HUMAN), 219 aa.	2.60E-117	1 (1p21)
1649	cg43986150	206	CTCGGCCACCTC AAGGATAATCAC T[G/A]AATTCTGC CGAAAGGACTGA GGAAC	G	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P19397 LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53) - HOMO SAPIENS (HUMAN), 219 aa.	2.60E-117	1 (1p21)
1650	cg44018623	203	TATTTTATAATAG TATTACAGGAAG[C/A]AAAATATCAT TTAATACAACCTT GAG	C	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SPTRMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.90E-114	6
1651	cg43051796	1421	TGGCCAGAGAGT CCTTGTAATTGT C[C/T]CCAATTCA ATCAGTATTTTG GGGCT	C	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.[pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3
1652	cg43051796	259	ACAACAAATAAC AATACTTAGGAT A[C/A]ATCAATCA TTCTTTTTCCTCT TAA	C	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.[pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3

1653	cg43051798	286	TCAATCATTCTTT TTCCTCTTAAAI ATTCAGAAATTG GTCTTAGTTTCT CATT	A	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa. pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3
1654	cg43287997	1244	CCCTCCTTTTCT TGCAATGTAAGTT G[gap/G]TCCCCC ATCCCAAAGTAT TCCATCT	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa. pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1655	cg43287997	1430	ACCCCCCTAATCC CCTACTCCCTCC A[gap/A]CCCCC CTCCACTGTAGG CCACTGG	gap	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa. pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1656	cg43287997	1440	CCCCTACTCCCT CCACCCCCCTC C[GGCCACTGGAT GGTCATTT	gap	C				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1657	cg43287997	1466	CTGTAGGCCACT GGATGGTCATTT G[CGTAAATGTGCT CTGCTCC	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1658	cg43287997	1477	CTGGATGGTCAT TTGCATCTCCGT A[TGCTCCTCAGCT GAGAG	A	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1659	cg43287997	1487	TTTGCATCTCCG TAAATGTGCTCT G[gap/G]CTCCTC AGCTGAGAGAGA AAAAAAT	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1660	cg43287997	903	GCCTGAATCAGAC GACGCATCTGAC C[C/gap]TCTGGA GAACACTGCCTC CCGCTGG	C gap	gap				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1661	cg43287997	908	GAATCAGAGACG CATCTGACCCTC T[gap/T]GGAGAA CACTGCCCTCCCG CTGGCCCC	gap	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1662	cg43924574	155	GGCTTGGAAGA GAGATCCAAAGG CC[A/G]GCCCTGG CAAGGGGAATCC CACATGA	A	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. aa.pcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	1.00E-106	1
1663	cg41598396	225	CAAAGCTGGGAC TGGAGGGGCTTT A[G/gap]CGACTC AATCCAGGTGC AGCATTT	G	gap				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. aa.pcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	4.50E-106	1
1664	cg43917157	1386	GGTGAAACTGTC ACAATCCGTGTC C[C/A]TTTTATAT ATAACTATACTG AGGTA	C	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1665	cg43917157	1545	CACGCAATCTGC TTGGGACAAAA G[C/T]CTACAGG GGTTGCCAAGCA CGAAAG	C	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6

1666	cg43917157	1650	GGAAGTCCATAA AAGAATGAGGCA G[C/T]TTTCACTG GGGAGAACTGG TCTTCA	C	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1667	cg43917157	21	TTTTTTTTTTTT TTTTTTTTT/GTTA ATTTCTGCCCTT TATTGTTAT	T	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1668	cg43917157	222	TTTTTTACATGAA AGCATAAATACG G/A]CAGGTACAA ATTTTCCTTGAG TTCC	G	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1669	cg43917157	3218	GGGAAGCAGAG CCTAAGCTGACC CC[G/A]GCCACT GGGCTGGTGG ACACATC	G	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1670	cg43917157	3305	AGAGACAGGGA CATGAAGTTGTG GC[G/A]TCTCTG GCACGCAAGTGT CCTGGGA	G	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1671	cg43917157	3322	GTTGTGGCGTCT CTGGACGCAA GT[G/gap]TCCTG GGACAGAGCAAT GGAAACCT	G	gap				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6

1672	cg43917157	4330	TGCCTGCCACTA CACCTAATTTTT [T/gap]GTATTTTT AGTAGAGATGGG GTTTC	T	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1673	cg43917157	776	TGGCTATTTCTT GTGTAAGGGATG A[C/T]GACTCCCC CTCCCATGGGTC CCATT	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1674	cg43255952	160	AACGGGGCTGAG AAGCCCCGTCA GGG[gap/G]CCCCA GGTCCCCACAGA GAGGCCTGGG	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcis:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)
1675	cg43255952	226	GAGGGCAGAC TGGGCAGTGGG GAG[C/gap]CCCC ATCGTGCCCCCAG AGGTGGCCA	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcis:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)

1676	cg43255952	373	AAAAGCACCAG GTCAGGCAGGG CC[C/gap]GAGGG CCCAGATCCCA GGAGGGCC	C	gap			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa. pcis:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)
1677	cg43094350	507	ACCAAAATACC CCTCTCTCCCA C[A/T]CCTCTTCT CCGACCCTCCG GGAGGC	A	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P21754 ZONA PELLUCIDA SPERM- BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	5.4E-95	7
1678	cg43094350	715	CAGGATGGTGTG TAGCCCAGTGAC T[C/G]TGAGGATC GCCCTCCTGAC AGAAG	C	G			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P21754 ZONA PELLUCIDA SPERM- BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	5.4E-95	7
1679	cg36834323	24	CAGGGAAGCTC CAGCTGTCCCTC [G/C]CGCAGTTG GCCCTGTGGTGT TCCGA	G	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.4E-91	
1680	cg43054905	341	ATCCAATGATCA GCGTGAGATGAT C[A/T]TTGATTAA ACTTGCTTGAGA TGGCT	A	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMAGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.1 1)

1681	cg43054905	382	TGAGATGGCTAG TCAAACGTCGAA A[G/C]TTGCTTGA GATGGCTAGTCA AACGT	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.1 1)
1682	cg43054905	454	TAACTAGACTTTT ACAATTTTTTTT[g ap/T]AAAGGGTAA AAAGACATGAAC CCTA	gap	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.1 1)
1683	cg43949899	236	TCCCATTTTATT TTTTTTTTTTTT[G /T]AGTATTCAATG AATGGAATTTAA TG	G	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P20172 CLATHRIN COAT ASSEMBLY PROTEIN AP50 (CLATHRIN COAT ASSOCIATED PROTEIN AP50) (PLASMA MEMBRANE ADAPTOR AP-2 50 KD PROTEIN) (HA2 50 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 MEDIUM CHAIN) (KIAA0109) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 435 aa.	1.1E-84	19
1684	cg44021513	202	GTCCGCTGGGC AGTTATAGGTCC CA[AT]GTGTTGG GTCTTCCTGCCA GGCCTT	A	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
1685	cg44021513	209	GGCAGTTATAG GTCCCAAGTGT G[G/C]GTCCTTCT GCGAGGCCTTCA CAAAG	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)

1686	cg44021513	319	ACTTTATTACACA CTGTGTAACCAC A[gap/C]TGTTTT TATGCCACTTTG TGCACA	gap	C				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SWISSPROT- ID:P20863 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
1687	cg44019290	969	GTGCCCTCACAT G CTGGGGTCTTCA G[G/gap]CACACAG CCATGCCTGCCG AGGAGTG	G	gap				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1688	cg44019290	1029	CAGACCATGTCC G GTGCTAGGCCCA G[G/gap]CACAGC CCAACCACTCCT CATCCAA	G	gap				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1689	cg44019290	1380	CTTCTCCTCAAG C GTTTGAGGGATT G[C/G]GGGGAGG GGGTCAGCTGA CTCAGAG	C	G				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1690	cg44019290	411	TCCTGGGTCTCA C CTCCATGGCTTG C[C/gap]TCAGGC CCCGCAGAAAGTC CCTGAGA	C	gap				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1691	cg44019290	773	TACCTCCTTCTC G CAACCCTCCACT A[G/gap]CGCTGC TTTCCTGGTCAA ACCTGCA	G	gap				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11

1692	cg42876034	122	CTGGGGCAGCA CCACCTGAAGGC AG[T/C]GACTGC CTTTTAAAGA CAGGGTT	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q07066 22 KD PEROXISOMAL MEMBRANE PROTEIN - RATTUS NORVEGICUS (RAT), 193 aa.	2.6E-78	
1693	cg41672027	1002	GCATCAATTTAATT GCGACATACCCAG [G/T]GGAAATTGT ATGTATGTTAGT GACA	G	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q03401 SPERM-COATING GLYCOPROTEIN 1 PRECURSOR (SCP 1) (ACIDIC EPIDIDYMAL GLYCOPROTEIN 1) (CYSTEINE-RICH SECRETORY PROTEIN-1) (CRISP-1) - MUS MUSCULUS (MOUSE), 244 aa.	3E-77	6 (6p21)
1694	cg43919735	302	AATTCTCACTCT ATCCAAAGCCCC G[G/gap]ATGAGG TCACTGCTTTTAT GAGCCT	G	gap				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P08962 CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491) (LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP 3) (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H) (GRANULOPHYSIN) - HOMO SAPIENS (HUMAN), 237 aa. pcis:SWISSPROT- ID:P08962 CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491) (LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP 3) (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H) - HOMO SAPIENS (HUMAN), 237 aa.	2.2E-76	11 (11q12)

1695	cg43981337	1111	GATTGAATCAGC CCACTGCGAGCA C[G/A]GATCTTGA TTGAATCAGCCT ATTGG	A				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) -HOMO SAPIENS (HUMAN), 244 aa. pcis:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.9E-75	X
1696	cg43981337	1146	TGAATCAGCCTA TTGGTGTAGTTT T[A/G]GGTCTACA TACATCTTGATT GAATC	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) -HOMO SAPIENS (HUMAN), 244 aa. pcis:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X

1697	cg43981337	1256	GCAACTTTCTAA TTCACAGGGG GA[C/gap]CCTAA ATGTCCTTAAAG GTAGAGAG	gap				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa. pcids:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X
1698	cg43981337	1258	AACTTTCTAATTC ACAGGGGGAC C[C/gap]TAAATG TCCTTAAAGGTA GAGAGGA	gap				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa. pcids:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X

1699	cg43981337	567	CTCAATTTGGAG GCAAAGAAATGT A[A/G]GTTGTGTG CTGAAACCTGAT GTATC	A	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) -HOMO SAPIENS (HUMAN), 244 aa. pcis:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X
1700	cg43983795	1810	CGCCGCTCTCCA GATCGCTTGGGT C[G/gap]CGCCAG TCGCCACCACAT CCTCGGC	G	gap				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X
1701	cg43983795	1810	GCCGCTCTCCAG ATCGCTTGGGTC G[gap/G]CGCCAG TCGCCACCACAT CCTCGGC	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X
1702	cg43983795	45	TTTTTTTTTTT TTTTTTTTTTT[A /T]GTGGGTAAA CCATTTTATTAA CT	A	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X

1703	cg41602760	1820	GCCCACTGAGAA GAGCTTCCAGGA C[G/gap]CACCCA GGACGCTGAGC CCAGGAGC	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	3.40E-73	15 (15q26.1)
1704	cg41568631	143	GATGTGGGCGG TTGGGGTGGCAA CC[C/gap]CTTGC AGCCCCCTACCA CGCCATCT	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1705	cg41568631	144	ATGTGGGCGGTT GGGGTGGCAAC CC[C/gap]TTGCA GCCCCCTACCAC GCCATCTC	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1706	cg41568631	70	TCCATCTCAGCC CCAGGACTCAGT A[C/T]TGC GGTTG CCAACACTGCTG CCAGG	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1707	cg41568631	71	CCATCTCAGCCC CAGGACTCAGTA C[T/C]GCGGTTG CCAACACTGCTG CCAGGC	T	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1708	cg43918233	1667	TTATGCTGGTGG CTTCCATCCGTT C[C/gap]TCCTCT GAGGGTGAGTG GAGAGGTA	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2

1709	cg43918233	1675	GTGGCTTCCATC CGTTCCTCCTCT G[AG]GGGTGA GTGGAGAGGTAT ATGGAAA	A	gap				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2
1710	cg43918233	1688	GTTCCTCCTCTG AGGGTGAGTGG AG[AG]GGTATAT GGAACACGGCT GTGACC	A	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2
1711	cg43918233	1708	TGGAGAGGTATA TGGAAACACGGC T[G/A]TGACCAAA GGGAGATCCCA GCCTGG	G	A				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1712	cg43918233	1738	CAAAGGAGATC CCAGCCTGGGC AG[G/C]CTGCGC TGCTGACCAACC TCCCTGG	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1713	cg43918233	1988	TCTTCAAAGACT TCAGCAGCAAC C[AT]AAACAGCA GGTTAAAAAAA AGATG	A	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1714	cg43918233	319	GAAGACACCCCC AACAAAGTCGGT G[C/G]GGAGGCA AAGACCCAAAA GACAGC	C	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2

1715	cg43918233	334	AAGTCGGTGC GGAGGCAAGA CCC[AT]JAAAAGA CAGCTCCAACAA GTCGGGT	A	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1716	cg43918233	369	CTCCAACAAGTC GGGTGCGGAGG CA[AC]JAGACCCA AAAAGGCAGCAC TAGCAA	A	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1717	cg43918233	377	AGTCGGGTGCG GAGGCAAGAC CCA[AC]JAAAGG CAGCACTAGCAA GTCGGGT	A	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1718	cg43927045	1406	TAAAAACGCGG CTGTGGAGACAG GTT[A]GAGCTGCT GGGAAGCCATGT TTTTG	T	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1719	cg43927045	1420	GTGGAGACAGG TGAGCTGCTGG GAA[G/gap]CCAT GTTTTTGATTTTC AGACAGGT	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1720	cg43927045	1556	ATCAATACACAA GAGACTCTTTGT G[G/A]CTCAACAC GTGGGTGCGG AGGCAG	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1721	cg43927045	2176	GAAGTGGCGG CACGATGATGGA CT[G/gap]CCGCT GGCCCCGGAGG GTCAGGCAG	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13

1722	cg43927045	2184	GGCCACGATGAT C GGACTGCCGCT GG[C/gap]CCCCG AGGTCAGGCA GTGGGGCAC	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1723	cg43927045	2203	CGCTGGCCCCG G GAGGGTCAGGC AGT[G/gap]GGGC ACCCCCCACTCG TCCTCGCTC	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1724	cg43927045	234	TTTGCAAGTTGC C TGTTTGTTCCTCA G[C/G]TACACCA GTCAGAGCTCCA CAGAGA	G			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1725	cg43927045	448	ACGTTTCCCGAG C TAGGGGCCCAA GC[C/gap]ACTGG AAACCGTGTTC CTGTGCAG	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1726	cg43927045	520	CCTGGGGGAA G TGAGTATAAAA GG[G]AAATGTT TTTGAAGACAGG CACGAT	T			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13

1727	cg44014928	1879	GAGTGGAGCTTT AAGTAAATATGC C[A/gap]AAAAAA ATATTCCTAGCA CAAAAGC	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.lpcis:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5
1728	cg44014928	1886	GCTTTAAGTAAA TATGCCAAAAAA A[A/gap]TATTCCT AGCACAAAAGCC TGCACC	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.lpcis:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5

1729	cg44014928	2113	GAAAAGCAAAGC AAGAGAATTCTG CT/CJAAGAAGTT TTATTCTGAATCT GAGG	T	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.lpcis:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5
1730	cg44024345	797	AGCTTTACTGCC TTCCTCCTTATC CT/CJACAGTACA ATCAGCAGTCTA GTTCT	T	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.lpcis:SWISSPROT- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.	7.70E-63	6
1731	cg44024345	848	TTTCATTGGAAT GAATACAGCATT T/AJAGCTTGTTT CACTGCAAAATA AGCC	T	A			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.lpcis:SWISSPROT- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.	7.7E-63	6
1732	cg43965368	773	CACTAACTAAAG AGATAAATCTT C[gap/C]ACTTTA CTTCCTAGTATT GCATCCC	gap	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)

1733	cg43965366	828	AGGGTTAAAGTA AGGGATATTGGC TTC/TCTGCTGAT CAGGCCACAGT GTGACA	C	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)
1734	cg43279524	926	CTCCCCGCCCC CGTGTTGAGACA GGT/GTCTCAAG GCTCAGGGGAA GATGCAT	T	G			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P17426 ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) MUS MUSCULUS (MOUSE), 977 aa. pcis:SWISSPROT-ID:P17426 ALPHA ADAPTIN (A) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) - MUS MUSCULUS (MOUSE), 977 aa.	2.8E-60	14
1735	cg43252235	1172	TTAAAGGATGGG GTCTTGCTATAT T[ap/A]GCCCCAG GCTGGAGTGCA GTGGCTAT	gap	A			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.8E-60	

1736	cg43252235	1172	TTAAAGGATGGG GTCTTGCTATAT T[<i>gap</i> /A]GCCCAG GCTGGAGTGCA GTGGCTAT	<i>gap</i>	A			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1737	cg43252235	68	TTTTTTGAATGTA ATATTTATTGG[T/G]GAATTTACAT GTGAGGTCATTT ACA	T	G			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1738	cg43252235	848	AGACCTGGACCT GGTAGTTAGTC C[C/T]TAGAGATG AAGGTGAGCTCA CTACA	C	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1739	cg44965847	200	CAGTAGGCTCCC CCAGGCTGAGC CC[C/ <i>gap</i>]AGCCC TAACACTGATGC TTGGCAGC	C	<i>gap</i>			SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q27127 P-GLYCOPROTEIN - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 302 aa (fragment).	2.60E-58	

1740	cg43322513	1069	GCTGTCCGATGG CGTGGAAACACAA G[G/C]CCCCCA CACGGAACATGT GCAGCC	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1741	cg43322513	11318	TTCCTGCAAGTA AGCAGGGAACAT G[T/C]CCTCCAGT TTGCTCTTCTTG CGCCC	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1742	cg43322513	11333	AGGGAACATGTC CTCCAGTTTGCT C[T/C]TCTTGCGC CCTCGCCGCTGT TGCTT	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1743	cg43322513	11379	TGCTTCTTCTCT CATCCCCCTTCAGT G[C]CAAGCTCTG CTCCACGGCGC CCTCT	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1744	cg43322513	1268	CATGCACTTGGC ACGGATGGCACA A[G/C]CAAAATGG TAGACATTGGGG CAACG	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1745	cg43322513	1390	GGGCAACCTCCA CATTATCAGTG C[C/T]CCGCCCT GGGTCTCATACA CCTCCG	C	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.3E-54	12

1746	cg43322513	8482	AGCTGCCCTGGA GGCCCCACTGCT CC[T/C]GCAGCT GCTGCAGCTGTT TCCTTCT	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.3E-54	12
1747	cg43982558	1399	CAACTGAATGTG CCCTTAGAGCGC A[T/C]CAGTTTTA AAGTCATTAAGA ACATG	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.1E-53	5 (5q13)
1748	cg43982558	1400	AACTGAATGTGC CCTTAGAGCGCA T[C/T]AGTTTAA AGTCATTAAGAA CATGT	C	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.1E-53	5 (5q13)
1749	cg43982558	1443	GAACATGTGAA GGTGTTTTTTTT [T/gap]CCAATAT GAACTCATGCAA GTTACC	T	gap				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1750	cg43982558	1653	AGCTGTATCATC CCAACAAAGTAT C[C/T]TTTCATGA ACGGGGCATGC AATAGC	C	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)

1751	cg43982558	218	CTTAAGGTGAGG AGAAAGAGCGCT A[G/C]CTTCACTT GATCTCCAGCTT CCAAC	G	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1752	cg43982558	219	TTAAGGTGAGGA GAAAGAGCGCTA G[C/G]TTCACTTG ATCTCCAGCTTC CAACT	C	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1753	cg43937369	378	GGCCAAGAAGG GCTCTAACAGCA GT[A/G]TCCCAG CAGTGTGTTTCC AGATTTA	A	G				SILENT- NONCODI NG	Guanylyl	Human Gene SWISSNEW-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.lpcds:SWISSPROT-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	4
1754	cg43937369	424	ATTATTCTTGGA TGTTGGTTGGAGC [G/T]CCCAACATT TAGCCTGAACTA ATGT	G	T				SILENT- NONCODI NG	Guanylyl	Human Gene SWISSNEW-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.lpcds:SWISSPROT-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	4

1755	cg42716105	484	GAGTCCTTATAC CTCATTTAGGTT T[<u>gap</u>]/AJAAATAG GTGCTCTCCTTG TCTGTG	gap	A				SILENT- NONCODI NG	Guanylyl	Human Gene SWISSPROT-ID:P25092 HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL GUANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR) - HOMO SAPIENS (HUMAN), 1073 aa.	0.00E+00	12
1756	cg43069304	129	TCTAGCATTAGT ACATAGTAGGCG C[<u>gap</u>]/C]TCAGTA AATGCTTGTTGA AGGGAGG	gap	C				SILENT- NONCODI NG	Guanylyl	Human Gene Homologous to SWISSPROT-ID:P43080 GUANYLATE CYCLASE ACTIVATING PROTEIN 1 (GCAP 1) - HOMO SAPIENS (HUMAN), 200 aa.	8.40E-105	6
1757	cg42905276	2266	AAGGAAGCCCC CCACTTTTTTTT T[<u>gap</u>]/T]CTGCCT GAGATTCTTTAA GGAGATA	gap	T				SILENT- NONCODI NG	Guanylyl	Human Gene Similar to SWISSPROT- ID:P16066 ATRIAL NATRIURETIC PEPTIDE RECEPTOR A PRECURSOR (ANP-A) (ANPRA) (GC-A) (GUANYLATE CYCLASE) (EC 4.6.1.2) - HOMO SAPIENS (HUMAN), 1061 aa.	1.20E-51	
1758	cg44913214	2375	GATTCGGACTAG TTTTCTGTCCT G[T/ <u>gap</u>]/CTTTTTT TTTTTATTTAATT TTGCA	T gap	gap				SILENT- NONCODI NG	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
1759	cg44913214	2387	TTTTCTGTCCT GTCTTTTTTTTTTT T[<u>gap</u>]/ATTTAATT TGCAAAATAAAAA TTTA	T gap	gap				SILENT- NONCODI NG	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
1760	cg43956596	4029	AGGATGGCAGC AGGTATTGGGTC CT[G/C]AGCCCTC TGGCGGGAGCC CTGAGGC	G	C				SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. ipcls:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16

1761	cg43956596	4158	CTCTCTGGCAGA GGAGGTGGAGT TC[T/C]TCCATGC AGGAGCACGGC ATGGCGG	T	C				SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.lpcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16
1762	cg43931763	105	TTGAGCTGTGGG GAGGTTCCAGCA G[T/C]AGCTACAG TGACGACTAAGA CTCCA	T	C				SILENT- NONCODI NG	helicase	Human Gene TREMBLNEW- ID:G2308766 ZINC FINGER HELICASE - HOMO SAPIENS (HUMAN), 2492 aa.	0.00E+00	X
1763	cg43937443	306	TCAACAACAAA CTACACGCTCTT T[A/T]TTCGGTGT AATACTTTATTT CTAT	A	T				SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q08211 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) - HOMO SAPIENS (HUMAN), 1270 aa.lpcis:SPTREMBL-ID:Q99556 NUCLEAR DNA HELICASE II - HOMO SAPIENS (HUMAN), 1270 aa (fragment).	1.90E-189	1
1764	cg43937443	399	AAATCTTTACTC CTTAAAGAAAA A[gap/A]TACAAA CTGTGGTATTTT TAAGAGA	gap	A				SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q08211 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) - HOMO SAPIENS (HUMAN), 1270 aa.lpcis:SPTREMBL-ID:Q99556 NUCLEAR DNA HELICASE II - HOMO SAPIENS (HUMAN), 1270 aa (fragment).	1.90E-189	1
1765	cg43924685	497	CTTTTATACCCA CCCCAACAGTCT A[A/G]CTCTAAAG AGGATAAGCCA ATGAC	A	G				SILENT- NONCODI NG	helicase	Human Gene Homologous to SWISSPROT-ID:Q12099 PROBABLE ATP-DEPENDENT RNA HELICASE FAL1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 399 aa.	9.40E-121	3 (18p11.2)

1766	cg43329991	20	TGCGGCCGCCG TGCTGCCG[C/ga p]GCACTCTGGG CTGCTCTGGGC GCTG	C	gap			SILENT- NONCODI NG	helicase	Human Gene Homologous to SWISSPROT-ID:Q14147 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0134 - HOMO SAPIENS (HUMAN), 576 aa.	6.10E-102	19
1767	cg43958815	437	ATTCTGTTGTCA AGGGGCAAGAT GC[C/gap]AGCTT GGAAGTGCCAA GGAGCTAA	C	gap			SILENT- NONCODI NG	helicase	Human Gene Similar to SWISSPROT- ID:Q06218 PROBABLE ATP- DEPENDENT RNA HELICASE DBP9 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 594 aa.	3.90E-100	
1768	cg43969995	1606	TACTAAATAAAA CCCATCAGTTTT TT[G]TTTATGTA GAAAGCAATTT ATTCC	T	G			SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.lpcis:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.90E-214	
1769	cg43969995	1607	ACTAAATAAAC CCATCAGTTTTT TTGTTATGTAGA AAAGCAATTTATT CCA	T	G			SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.lpcis:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.90E-214	

1770	cg43969995	1903	CCAAGTTAAAA AAAAA A[A/gap]CCAACA ACAAAAA ACACCAT	A	gap			SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa. pcis:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.9E-214	
1771	cg43969995	3855	CCATGGCGGC AGCGAGCCGG GGG[A/gap]ATCC TGGGTCGAGC GTTGCGGGAG	A	gap			SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa. pcis:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.9E-214	
1772	cg44026400	225	TTGGGTTT TAGA AGTAGGCGTTCCG C[C/gap]TATTTCT TCTTGGGCGCC GCCTTCT	C	gap			SILENT- NONCODI NG	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
1773	cg43948414	725	CCCCCTCCCGCA GCTACAACTACT T[A/T]TAATAAAG GACTCAAAAAGA GATCG	A	T			SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	

1774	cg43948414	726	CCCTCCCGCA GCTACAACTACT TA[T/A]AATAAAG GACTCAAAAAGA GATCGG	T	A				SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1775	cg43948414	729	CTCCCGCAGCTA CAACTACTTATA A[T/A]AAGGACT CAAAAAGAGATC GGGAG	T	A				SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1776	cg43948414	772	ATCGGAGGTTT TAAGTGCCGCA G[C/gap]CCCCACC AAACCAAGCAAA GACACCT	C	gap				SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1777	cg43250123	8190	AGCGAGCGCG CCCGCCCTCACT GG[C/T]CTTGTA CGGTTTATTCTG ATTGAG	C	T				SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P53973 HISTONE DEACETYLASE HDA1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 706 aa.	2.4E-57	
1778	cg43918434	147	TAATTCAGTTAT GGTAAAAA A[A/gap]CTATGTA CATCTCAATCAG ATCACG	A	gap				SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1779	cg43918434	434	ACAGAAATCATT TTAAAAAGGGA A[G/gap]GAGTTT TGTGTTGGAATC AATTGIG	G	gap				SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1780	cg43918434	435	CAGAAATCATTT TAAAAAGGGAA G[G/gap]AGTTT GTGTTGGAATCA ATTGTC	G	gap				SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21

1781	cg43918434	437	GAAATCATTTTAAAG AAAGGGGAAGG A[G/gap]TTTTGT GTTGGAATCAAT TGTGCTA	G	gap				SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1782	cg43918434	454	GGGAAGGAGTTT A TGTGTTGGAATC A[A/G]TTGTGCTA CCTCTGTAAAAA TGAAG	G	G				SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1783	cg43918434	592	TCTGCGGCAAG C GCACCTGTCTG CC[C/gap]TCCGG ACAGCCTTTGCG CCAGTCTT	C	gap				SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0.00E+00	21
1784	cg42341753	2020	TGGAGCCTACCT C CCCGACATTCAC G[C/gap]TTCGCC CCACGCTGCTCC GACTGGC	C	gap				SILENT- NONCODI NG	homeobo x	Human Gene SWISSPROT-ID:Q14774 HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24) - HOMO SAPIENS (HUMAN), 488 aa.	5.20E-263	1
1785	cg43918574	415	TCACTCAGAGGC T CAAAGTCTGGG GTT/GTAGAAAGA AGGAAGCTTGAC CCAAA	T	G				SILENT- NONCODI NG	homeobo x	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa. pcls:SWISSPROT- ID:Q06710 PAIRED BOX PROTEIN PAX- 8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2
1786	cg43918574	453	AGCTTGACCCAA T ACAAAGTTTCAT TTT/GJACAGTATA TACAGTCAGGCC TTGGG	T	G				SILENT- NONCODI NG	homeobo x	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa. pcls:SWISSPROT- ID:Q06710 PAIRED BOX PROTEIN PAX- 8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2

1787	cg43918574	459	ACCCAAACAAAG TTTCATTACAGT [A/G]TATACAGTC AGGCCTTGGGG GCAGG	A	G				SILENT- NONCODING	homeobo x	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa. [pcis:SWISSPROT- ID:Q06710 PAIRED BOX PROTEIN PAX- 8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2
1788	cg43988803	2504	ACAAAAA ACCCTCCTTTTT [T/gap]CCTTTTCGT CAGACTTGGCAG CAAAG	T	gap				SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242 (13q14.1)	13
1789	cg43988803	3493	ATGTATGTA AAAGAAATTTCA T/gap]CTGCTTCT ACTGAACTATGC GTACT	T	gap				SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242 (13q14.1)	13
1790	cg43988803	3502	TTTAAAGAAAT TCATCTGCTTCT A/gap]CTGAACTA TGCGTACTGCAT AGCAT	A	gap				SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242 (13q14.1)	13
1791	cg43988803	3590	CTCATAATGTT GTAGATACAGAA A/gap]GGGAGA TCTGCATCTAAA GCAATGG	A	gap				SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13
1792	cg43988803	3597	TGTTTGTAGATA CAGAAAAGGGA GA[T/gap]CTGCA TCTAAAGCAATG GTCCCTTIG	T	gap				SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13
1793	cg43988803	780	CACCGCAGCC CCGCCGCCCGG GCC[G/C]CTGTC GCAGCACCCGC CGGTGCCCC	G	C				SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13

1794	cg43988803	781	ACCGCAGCCCC CGCCGCCCGGG CCG[C/G]TGTCG CAGCACCCGCC GGTGCCCCC	C	G				SILENT- NONCODING NG	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242	13 (13q14.1)
1795	cg43986910	2486	GCCCTTGACAAA AAGTTTTTTTTT T/gap]GTTTGT TTGCTTTCTGAA ATTCA	T	gap				SILENT- NONCODING NG	homeobo x	Human Gene TREMBLNEW- ID:G2822167 HOMEBOX PROTEIN HOX-A10 - HOMO SAPIENS (HUMAN), 415 aa.	1.40E-230	7
1796	cg44931625	1329	ACGGTAGCTAAC TTTGGGCAGGT C[G/A]TTAAATTT GGTCAATTCAGA ACATT	G	A				SILENT- NONCODING NG	homeobo x	Human Gene SWISSPROT-ID:P55347 HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1) - HOMO SAPIENS (HUMAN), 435 aa.	7.60E-230	21
1797	cg43027377	222	TGGCTTCTACCC AGAAAAAAAGG G[A/G]AGAGAGT ATAAAGAAGTGT CCAGAT	A	G				SILENT- NONCODING NG	homeobo x	Human Gene SWISSPROT-ID:P40424 PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEBOX PROTEIN PBX1) (HOMEBOX PROTEIN PRL) - HOMO SAPIENS (HUMAN), 430 aa.	5.70E-225	1 (1q23)
1798	cg43983917	1208	GTGCGGATCTG GCGGCCTACACA CG[C/gap]TGCGC TAAGCTGCAACG AAAACGAC	C	gap				SILENT- NONCODING NG	homeobo x	Human Gene SWISSPROT-ID:P50458 HOMEBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.30E-216	
1799	cg43927965	1412	TTCAAGCAGGTA ACAATACTACTG G[A/gap]AAAAAA AAATAGGAAGCT TAAATG	A	gap				SILENT- NONCODING NG	homeobo x	Human Gene SPTREMBL-ID:Q62947 ZINC FINGER HOMEODOMAIN ENHANCER-BINDING PROTEIN-1 - RATTUS NORVEGICUS (RAT), 1104 aa (fragment).	1.50E-207	
1800	cg43980506	1041	GCATGGAAAAAGT TTTTATCTCTTCT [G/C]TTTCCTCTC CTGTAAGTAAAG ATTT	G	C				SILENT- NONCODING NG	homeobo x	Human Gene TREMBLNEW- ID:G2896172 LIM HOMEBOX PROTEIN COFACTOR - HOMO SAPIENS (HUMAN), 373 aa.	1.60E-206	

1801	cg43923014	1801	TGGCAGGGGTG AGGGCTGACGG GGG[A/G]ACAAC TTCAGCAGCTCA TGTCCTCGA	A	G				SILENT- NONCODING	homeobox	Human Gene TREMBLNEW- ID:G2738116 LIM HOMEBOX PROTEIN COFACTOR CLIM-2 - MUS MUSCULUS (MOUSE), 375 aa.	1.10E-203	
1802	cg43923014	457	CTGGGGGGCA AATCTTGGCACC TG[C/gap]CCCCA GAGAGTCCAGTT CCTCCCTG	C	gap				SILENT- NONCODING	homeobox	Human Gene TREMBLNEW- ID:G2738116 LIM HOMEBOX PROTEIN COFACTOR CLIM-2 - MUS MUSCULUS (MOUSE), 375 aa.	1.10E-203	
1803	cg42730878	692	AAGCACCAACA CCACAAAGGAA A[A/gap]CAGCAA CAACAACAATC CGCTGCC	A	gap				SILENT- NONCODING	homeobox	Human Gene SWISSPROT-ID:P28356 HOMEBOX PROTEIN HOX-D9 (HOX- 4C) (HOX-5.2) - HOMO SAPIENS (HUMAN), 342 aa.	2.60E-188	2
1804	cg43971818	518	CTCAGGGGCA GTGGCCTGCTG CAG[C/gap]CTCT TGGCTTTTCCAC ATCTCCAC	C	gap				SILENT- NONCODING	homeobox	Human Gene TREMBLNEW- ID:G2822168 HXAB_HUMAN HOMEBOX PROTEIN HOX-A11 - HOMO SAPIENS (HUMAN), 313 aa. pcis:TREMBLNEW-ID:G2745851 HOMEBOX A11 - HOMO SAPIENS (HUMAN), 313 aa.	1.50E-169	7
1805	cg43926691	262	CAGAGGGTGT GGCCTTTGGAAC CG[C/T]CGTGAA GTCCTTCTGCCTG GAACCCG	C	T				SILENT- NONCODING	homeobox	Human Gene SWISSPROT-ID:P50222 HOMEBOX PROTEIN MOX-2 (GROWTH ARREST-SPECIFIC HOMEBOX) - HOMO SAPIENS (HUMAN), 303 aa.	2.00E-167	7
1806	cg43928699	1040	GGAGACCTTAAT TTTGACTTAACA A[A/gap]TAGTTTA TGTAAGTCTCTT AGGTTC	A	gap				SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1807	cg43928699	1075	TACTGCTCTTAG GTTGTTTGATA A[A/gap]GTGACA TTATAGTGATTAA ATTCTT	A	gap				SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10

1808	cg43928699	1080	TCCTAGGTTGTT TTGATAAAGTGA C[<i>gap</i> /G]ATTATA GTGATTAAATTC TTCCCCC	<i>gap</i>	G			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1809	cg43928699	1492	ACCTGTTTGACC AAGGTGTTAAGG G[G/ <i>gap</i>]ATAGTA CCTCCCAATTCA AGCAGAG	G	<i>gap</i>			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1810	cg43928699	1506	GGTGTAAAGG GATAGTACCTCC CA[A/ <i>gap</i>]TTCAA GCAGAGAAACTG ACCTGACT	A	<i>gap</i>			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1811	cg43928699	1511	TAAGGGGATAGT ACCTCCCAATTC A[A/ <i>gap</i>]GCAGAG AAACTGACCTGA CTAAAGT	A	<i>gap</i>			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1812	cg43928699	1564	ATCGCAGATGAA CTAGAAAGTCACA G[G/ <i>gap</i>]TTAATTA AATGTAAGTAGA TTGTAG	G	<i>gap</i>			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1813	cg43928699	1585	ACAGGTTAATTA AATGTAAGTAGA TTT[<i>gap</i>]GTAGATA CTGTTTATATCA AACAA	T	<i>gap</i>			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1814	cg43971192	191	GTATTGCACAGT CTGAAAAAATAA C[A/ <i>gap</i>]AAAAAA GGGAAGGGGAG GAAAAAA	A	<i>gap</i>			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18

1815	cg43971192	210	AATAACAAAAA AGGGAAGGGA GG[A/gap]AAAAA AAATCACATGA TATTGGGA	A	gap				SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1816	cg43971192	219	AAAGGGAAGG GGAGGAAAAA AA[A/gap]TCACAT GATAATTGGGAAC CATCICA	A	gap				SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1817	cg43971192	50	ATACCTTTATTATG TCATGAAAAA A/gapJGGCATCAA CCAACTAGATTG ATACT	A	gap				SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1818	cg43988027	16	CTTATTTTTTTT TTT/GGCTTTT ATTGATTTTATT CTCCG	T	G				SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	5.50E-140	17
1819	cg42908326	1284	GAGTCTGGAGA GAGACTGGACA GGG[G/T]AGTGC TGGAACCGCGG AGTTGGCT	G	T				SILENT- NONCODING	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1820	cg42908326	1341	AAAGCTACAACG ATGGACTCTTGC A/C/TJAGAAAAA AAATCTTGTTAA CAATG	C	T				SILENT- NONCODING	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1821	cg42908326	1422	CAACGGGAGA GAAAAAGAGGAA GG[A/C]AACTTAT TTCTTAACCTGCT ATTGG	A	C				SILENT- NONCODING	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3

1822	cg42908326	2357	ATTCCCCCTTTCTC TGTTGTTCTTCTT C/T]GTTGGTTTC CTGAAGTCCTAT TTGA	C	T				SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1823	cg42714160	874	GAGGAGGAAGA AAACAGGCCCGA GT[G]gap]AAGGT GCTGGAAAGGG AGGGAGGAC	G	gap				SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-123	
1824	cg43983244	2635	AGGAGAGGAAG GCCAAAAA AA[gap/A]TTGGA AAAGAGGGCGG GGGACCCCT	gap	A				SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:P43271 PAIRED MESODERM HOMEBOX PROTEIN 1 (HOMEBOX PROTEIN MHOX) (HOMEBOX PROTEIN K-2) (RHOX) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 217 aa.	2.20E-113	
1825	cg43917865	274	AGGCGCGCGG GGAGGGTCCGC CCG[G/gap]CCAG GGCCCCGGGCG CTCGCAGAGG	G	gap				SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:P28360 HOMEBOX PROTEIN MSX-1 (HOX-7) - HOMO SAPIENS (HUMAN), 297 aa.	1.10E-111 (4p16.1)	4
1826	cg42714192	94	TATTATCATCATC ATCATCATCATC[A/gap]TCATCGAA GTATTTACAGTC CAGAG	A	gap				SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-108	
1827	cg43988025	1278	TTCTGAGAACTG ACTAGAGAAGAC A[G/A]AAAAATAG CCCgATGTAGGT TTCGG	G	A				SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17
1828	cg43988025	1279	TCTGAGAACTGA CTAGAGAAGACA G[A/G]AAAAATAGC CCGATGTAGGTT TCGGT	A	G				SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17

1829	cg43988025	1320	GGTTTCGGTGTC CCCATATAGGCC C[<i>gap</i>]/CJGTCCAC ACAGGCTTGACT GGGTGGA	<i>gap</i>	C				SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17
1830	cg43268289	1110	TTCCTCCCTCTC TCCCTTTCTCCT CT/CJCCCTGCTT TCTTGAAAAGGA CTGAA	T	C				SILENT- NONCODING	homeobox	Human Gene Similar to SWISSPROT- ID:Q92988 HOMEBOX PROTEIN DLX- 4 (DLX-7) (DLX-8) - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.40E-90	17 (17q21.3)
1831	cg43268289	1218	TGTATGCCCTTTG GCCCTGCACAAC C[C]/TATTTGTGA GCAAAAGCAGAA GTGGA	C	T				SILENT- NONCODING	homeobox	Human Gene Similar to SWISSPROT- ID:Q92988 HOMEBOX PROTEIN DLX- 4 (DLX-7) (DLX-8) - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.40E-90	17 (17q21.3)
1832	cg43988195	2818	TTTTTTGGCTTT TAGTCCAGAAGG [A/ <i>gap</i>]/CCTCATC TCTGCACCTCTT ACTTGA	A	<i>gap</i>				SILENT- NONCODING	homeobox	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1833	cg43988195	2902	GGAATAAGAGGA TGTTGGGCACT GC[C/ <i>gap</i>]/AAGGG CAAGGTCAAAAA TCAGGGTT	C	<i>gap</i>				SILENT- NONCODING	homeobox	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1834	cg43988195	333	GAAGATGAATAC ACAGAGTCTTTT GT/ATTTCTCTAT CAAATGTGGTTT TTTTA	T	A				SILENT- NONCODING	homeobox	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1835	cg43988195	334	AAGATGAATACA CAGAGTCTTTT TT/ATTTCTCTATC AAATGTGGTTT TTTTAT	T	A				SILENT- NONCODING	homeobox	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12

1836	cg43988195	744	ATGAAGAGAAAA TCCACCTAGCTC A[A/T]GGGGCA GTGAAGATGAGG AAAGAA	A	T				SILENT- NONCODING	homeobox	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1837	cg43922794	199	GGGGAAGCAGC ATTTCAGCCCG AG[gap]/GJATCGC GGAGTCCCAATG AAACGGGC	gap	G				SILENT- NONCODING	hydrolase	Human Gene SWISSPROT-ID:Q14694 PROBABLE UBIQUITIN CARBOXYL- TERMINAL HYDROLASE (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) (KIAA0190) - HOMO SAPIENS (HUMAN), 798 aa.	0.00E+00	14
1838	cg43296921	110	GCACAATGGCTT TATTGTCACTG A[A/G]TGCGGA CCAGGCCTACAG CCCGAG	A	G				SILENT- NONCODING	hydrolase	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)
1839	cg43296921	153	AGCCCGAGGGA GGACCCAGTCA CA[G/gap]GGTTG AAAGGGGTGCTT GAGCCCTT	G	gap				SILENT- NONCODING	hydrolase	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)
1840	cg43296921	180	GTTGAAAGGGGT GCTTGAGCCCTT T[G/T]TTCCAGA AGAGCAGAGAAA ATCTC	G	T				SILENT- NONCODING	hydrolase	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)

1841	cg43927025	2499	TATAATTACTTTA GCTGCACTAACA [G/gap]TACAATG CTTGTTAATGGT TAATAT	G	gap			SILENT- NONCODING	hydrolase	Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa.	5.10E-224	10 (10q24)
1842	cg43923662	111	GATTCATCAAC ATACAAGCCAA C[AG]AAGATCCC ATTCAATTAGAT ATAC	A	G			SILENT- NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3- HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1843	cg43923662	153	TAGATATACCAC TCAAGAGATCT C[CT]AAAGATCT TCACATTTTCCCA TCTT	C	T			SILENT- NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3- HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1844	cg43923662	366	ATTCTGATAATT TCACGTCATGAA ATTATTAGTCTT TGATTTCTTTCC CA	A	T			SILENT- NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3- HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1845	cg43305744	955	GGAAGCTGTGGT CCGATAAGCCT G[G/gap]CGCAGC CTGTTTGTGGT GACAACC	G	gap			SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:Q61068 UBIQUITIN CARBOXYL- TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1) - MUS MUSCULUS (MOUSE), 526 aa.	1.10E-61	

1846	cg43951711	737	TATAATCAAAGG C TACTATTATTGAT IC/TACAATTTAT TTTAAAGTCAGG AAAA	T				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:Q92353 PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (EC 3.1.2.15) (UBIQUITIN- THIOLESTERASE) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 467 aa.	5.00E-58	18
1847	cg43969804	166	CCACTTTCCTG C GGGTATTGCTTT G[C/gap]CCCTGT GCCTCCACCCCC AGGAAGC	gap				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1848	cg43969804	307	TTCCCCAGGGAC C AACCATCCTCTC C[C/gap]TGTGTC CCCTGCCCCCCA CACTGAG	gap				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1849	cg43969804	53	GTTTAATGGGAC C CATCACCGTGAT A[C/G]CCCCATCAC AGCAGTCCCAG GCTGGA	G				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1850	cg43929210	169	CTAAGGAAACAG gap GACTTGGGCAAA A[gap/T]TTTTTTA TTATGAAGATAC AGATCT	T				SILENT- NONCODING	hydroxysteroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17- BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5

1851	cg43929210	175	AAACAGGACTTG GGCAAAATTTT T[gap]/T]ATTATGA AGATACAGATCT AAGAAC	gap	T				SILENT- NONCODING	hydroxysteroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17- BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5
1852	cg43998672	1777	CGGCCAAGGCC AGCGCTCCATGG CG[G/ gap]/CCCAG CGGGCTGGGGC GGGGCGGGG	G	gap				SILENT- NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1853	cg43998672	281	CAGTGAAGTCTT GCATGAGACTCC C[C/ gap]/ATCCAG CGGAGTTCTCCA AGCTGCA	C	gap				SILENT- NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1854	cg43998672	384	CGCAGAGGCTC ACTGGGAACCT TG[G/ gap]/CCTCA CCGGGCCTGGA TTGGGCATC	G	gap				SILENT- NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1855	cg43998672	553	AGTGGCTGGC CATAGGTGCACA TG[G/ gap]/CTCAC CGAGCCACTGCT GGGGAAGG	G	gap				SILENT- NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1856	cg42886248	195	TTAATATAACTAT CTGGTAATTATA C/T]CTATGTTTAC TAACAATTTTACA AC	C	T				SILENT- NONCODING	hydroxysteroid	Human Gene SWISSPROT-ID:P28845 CORTICOSTEROID 11-BETA- DEHYDROGENASE, ISOZYME 1 (EC 1.1.1.146) (11-DH) (11-BETA- HYDROXYSTEROID DEHYDROGENASE 1) (11-BETA-HSD1) - HOMO SAPIENS (HUMAN), 292 aa.	8.50E-151	1

1857	cg43955809	938	TTCCCCCCCCGCT TTTTTTTTTTTTT T/gap]TGACTTTG CCTTGGAGAGCC AGAGC	T	gap				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.90E-72	4
1858	cg43955809	939	TCCCCCCCCGCTT TTTTTTTTTTTTT T/gap]GACTTTTGC CTTGGAGAGCCA GAGCT	T	gap				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.90E-72	4
1859	cg43955809	697	GATGTAACCA ACTCCCCGCC C[C/A]AAAAAATT AAATAGTCACA TTGGT	C	A				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.9E-72	4
1860	cg43955809	892	AACTCAAGGAGT GAAATCAGGAG G[G/T]GTAATAA ATGTCCTCGCA TTCCC	G	T				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.9E-72	4
1861	cg41382080	146	ACACAATCATTG ACTATTAGAGGC C[A/C]GAGGAGA ATGAGGCCTGG CCTGGGA	A	C				SILENT- NONCODING	immunoglob_receptor	Human Gene Similar to SWISSPROT- ID:P08118 PROSTATE SECRETED SEMINAL PLASMA PROTEIN PRECURSOR (PSP-94) (BETA- MICROSEMINOPROTEIN) (SEMINAL PLASMA BETA-INHIBIN) (IMMUNOGLOBULIN BINDING FACTOR) (IGBF) (PROSTATE SECRETORY PROTEIN PSP94) (PN44) HOMO SAPIENS (HUMAN), 114 aa.	2.6E-60 (10q11.2)	10

1862	cg41382080	179	ATGAGGCCTGG CCTGGGAGCCC TGT[G/A]CCTACT AGAAGCACATTA GATTATC	G	A				SILENT- NONCODING	immunoglobulin receptor	Human Gene Similar to SWISSPROT- ID:P08118 PROSTATE SECRETED SEMINAL PLASMA PROTEIN PRECURSOR (PSP-94) (BETA- MICROSEMINOPROTEIN) (SEMINAL PLASMA BETA-INHIBIN) (IMMUNOGLOBULIN BINDING FACTOR) (IGBF) (PROSTATE SECRETORY PROTEIN PSP94) (PN44) HOMO SAPIENS (HUMAN), 114 aa.	2.6E-60	10 (10q11.2)
1863	cg43925670	155	ATTAAAAAGCA CTCCCAATACCC C[Gap/C]ATTCCA TAGGATTAAACAG CTAGTAT	gap	C				SILENT- NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
1864	cg43925670	241	CCAGGTATATGT ACATTTTTTAGG [C/G]ACTTAGACC TTATCTCCATAAA CAT	C	G				SILENT- NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1

1865	cg43925670	73	AAAGATAATGTT TATTTATTTTTC[ATTAAATTATAGAA GTTGTAGATGCA AAA	A	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.[pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
1866	cg43925670	74	AAGATAATGTT ATTTATTTTTC[ATTATTATAGAAG TTGTAGATGCAA AAT	A	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.[pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
1867	cg42701070	216	AACCATGGGAAG CAGGGGGCATG GC[C/gap]ACTGG ATCTGAAAGGGA CCGGCTAA	C	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P20592 INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXB (P78-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 715 aa.	0	21
1868	cg43933380	148	TTTAAAGTCCAAT TTTGAAAAGCTT[G/C]CAGAAATTC TTCTGAAATTACT TAA	G	C				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6

1869	cg43933380	149	TTTAAGTCCAATT TTGAAAAGCTTG[C/G]AGAAATTTCT TCTGAAATTACTT AAA	C	G				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1870	cg43933380	1521	CCGTTCAATTC ACATACACATTG TTT/gap]ACACCC TAATGTAACAGG TAGTTTC	T	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1871	cg43933380	200	TTACTGTATGCA TAAACTTACAAA A[gap/C]ACATAT GCTATACCAAGG CAGAGAA	gap	C				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1872	cg43933380	228	ATATGCTATACC AAGGCAGAGAAA A[G/A]AAAAAAG TGAAGTGGCTAC AAAGG	G	A				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1873	cg42489246	610	GTTGCAGTGAGC CAAGATCGTGCC A[C/T]TCCACTCC AGCCTGGGTGAT AGGTG	C	T				SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P48551 INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR-2) - HOMO SAPIENS (HUMAN), 515 aa.	1.7E-256 (21q22.1)	21
1874	cg43931810	552	CACACCATGAGG AGCGAGGGCTC AG[C/G]TCTCCC CAGGGCCCTGG AAATCCAT	C	G				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q14653 INTERFERON REGULATORY FACTOR 3 (IRF-3) - HOMO SAPIENS (HUMAN), 427 aa.	1.2E-240	19

1875	cg43956260	210	ATGAAAGAGGGCT GTATATCTCAAA ATT/AT/AAAAAA AAAAAGGATAA AAAAT	A			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1876	cg43956260	224	ATATCTCAAAATT AAAAAATAAA A/gap]GGATAAAA AATTAGCCTTGA GTTCT	gap			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1877	cg43956260	51	TTTTTTTTTTTT TTCCTCTTTCAA T/A/AAAAATTTTAT TTTAAGTCCTTA GTG	A			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1878	cg43956260	89	TAAGTCCTTAGT GAATATCTAAGA G/G/A/AAAAATATA AAGTGCCTTGGCT TTAGA	A			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14

1879	cg43082514	1381	TGATTGCTGTGT CCAACTCCAGTA C[TTCTCTTTAACTC AGGACT	gap	C				SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.5E-188	4 (4q35.1)
1880	cg43082514	2153	GTTGTTATTACAT CCTTGTCACACA [T/gap]TTTTTTTT TTAAATTTGTAAA GGTG	T gap	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1881	cg43082514	2162	ACATCCTTGTGG CACATTTTTTTTT [T/gap]TAATTTTG TAAAGGTGAAAA AAGCT	T gap	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1882	cg43082514	2163	CATCCTTGTGGC ACATT T/gap]AATTTTGT AAAGGTGAAAA AGCTT	T gap	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1883	cg43082514	2163	ATCCTTGTGGCA CATTTTTTTTTT gap/T]AATTTTGT AAAGGTGAAAA AGCTT	gap T	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1884	cg43082514	2201	GTGAAAAAAGCT TTTATGAGCTCA TIG/CITAGCAATC AGATTTTCCTGT GGATT	G gap	C				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1885	cg43983653	135	CAAATGTACATA TTTACACACGTC C[TCACACATGACT TAATGG	gap T	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)

1886	cg43983653	136	AAATGTACATATT TACACACGTCCT[gap/T]ATGTGTTT ACACATGACTTA ATGGT	gap	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1887	cg43983653	2064	GAGGTTGCCGG GTTCTTAAGGCA GC[C/gap]GGGCA CGGCCGGCGTG GACTGGGCA	C gap	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1888	cg43983653	261	GGCTTGAGGG GTGGTGGGCGC CGA[G/gap]CAAG GCACTGTATAAA TAAATGCAA	G gap	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1889	cg43983653	432	AGCTCCTCTGAG GCTGAGGGAGC AT[C/T]GCCCCGA AGGACCCCACTT TCCTTC	C T	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1890	cg42918267	59	TAAGCTAAAAAC AAAATCAACCGG GIA/T]CCCCAGCT TTTCAGAACTGC AGGGA	A T	T				SILENT- NONCODI NG	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	
1891	cg42918267	72	AAATCAACCGGG ACCCAGCTTTT C[A/G]GAACTGC AGGGAAACAGC CATCATG	A G	G				SILENT- NONCODI NG	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	
1892	cg42918267	82	GGACCCCAAGCTT TTCAGAACTGCA GIG/A]GAAACAG CCATCATGAGTG AGGTCA	G A	A				SILENT- NONCODI NG	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	

1893	cg3000751	184	TCACCCATCTCA GCAAGCCCAGAA GTT/CJATCTGCAA TATCTACGATGG CCTCG	T	C				SILENT- NONCODI NG	interferon	Human Gene Similar to SWISSPROT- ID:P01562 INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D) - HOMO SAPIENS (HUMAN), 189 aa.	8.20E-98	9
1894	cg3000751	199	AGCCGAGAAGTA TCTGCAATATCT A/C/TGATGGCCT CGCCCTTTGCTT TACTG	C	T				SILENT- NONCODI NG	interferon	Human Gene Similar to SWISSPROT- ID:P01562 INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D) - HOMO SAPIENS (HUMAN), 189 aa.	8.20E-98	9
1895	cg43510640	187	GATAGAGTACGT GGGATACAGGTC A/C/TGGGCAGA CTCCTGGCCTCA ATGATG	C	T				SILENT- NONCODI NG	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1896	cg43510640	227	CCTCAATGATGC CTCCTGATCTAT C/G/CJCTAGGCC TGGACGACCAAC ACTGGG	G	C				SILENT- NONCODI NG	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1897	cg44339782	187	GATAGAGTACGT GGGATACAGGTC A/C/TGGGCAGA CTCCTGGCCTCA ATGATG	C	T				SILENT- NONCODI NG	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1898	cg44339782	227	CCTCAATGATGC CTCCTGATCTAT C/G/CJCTAGGCC TGGACGACCAAC ACTGGG	G	C				SILENT- NONCODI NG	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1899	cg43978774	16	TTTTTTTTTTTTT TTTC/TCTCAT TAAAAATATTTAT TGAGC	C	T				SILENT- NONCODI NG	interferon	Human Gene Similar to SWISSNEW- ID:Q99873 PROTEIN ARGININE N- METHYLTRANSFERASE 1 (EC 2.1.1.-) (INTERFERON RECEPTOR 1-BOUND PROTEIN 4) - HOMO SAPIENS (HUMAN), 361 aa.	3.50E-50	3

1900	cg43922672	2259	CACCCAGCAAAA GGTTGTTCTCTAA A[A/G]TAAGGGC AGAGTCACACGG GGGCAG	A	G				SILENT- NONCODING	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0.00E+00	15
1901	cg43922672	2277	TCCTAAATAAG GGCAGAGTCACA C[G/T]GGGGCAG CTGATACAAATT GCAGAC	G	T				SILENT- NONCODING	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0.00E+00	15
1902	cg42271251	256	TTGTTCAAGAGT TCCCTATCACTC T[C/gap]TTTAATC ACTACTCACAGT AACCTC	C	gap				SILENT- NONCODING	interleukin	Human Gene Homologous to SPTREMBL-ID:Q14629 INTERLEUKIN 2/BCM FUSION PROTEIN - HOMO SAPIENS (HUMAN); 288 aa (fragment).	9.60E-120	4 (4q26)
1903	cg42908571	1039	TTTATGTAAGTC ATATTATATTTT T/gap]AAGAAAGTA CCACTTGAAACA TTTTA	T	gap				SILENT- NONCODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 INTERLEUKIN- 6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
1904	cg42908571	155	CTGAGGGCTCATT CTGCCCTCGAGC C[C/gap]ACCGGG AACGAAAGAGAA GCTCTAT	C	gap				SILENT- NONCODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 INTERLEUKIN- 6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
1905	cg42887911	900	ACAGTCCTTCCG TGAGGCCTGGG GG[G/A]CATCTGT GCCTTATTATA CTTATT	G	A				SILENT- NONCODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P20809 INTERLEUKIN- 11 PRECURSOR (IL-11) (ADIPOGENESIS INHIBITORY FACTOR) (AGIF) - HOMO SAPIENS (HUMAN), 199 aa.	2.50E-103	19

1906	cg43994858	323	CAGCAAATTGTC CCTGCTTTAGTC A[C/T]AGCAATTT TTCATGTCCTCT GTTGC	C	T				SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P24394 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN PRECURSOR (IL-4R-ALPHA) (CD124 ANTIGEN) - HOMO SAPIENS (HUMAN), 825 aa.	0.00E+00	16 (16p12.1)
1907	cg43987278	710	GAGTTGATCTGA TTGGCTAGTTCA G[G/gap]CCCAGC CTACCTGATTGG ACAGAGC	G	gap				SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1908	cg43987278	98	ACAGAGTAACAA AGATTTTCTTTA [A/gap]ATAAATGT ATTCAACGAAA ATGAA	A	gap				SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1909	cg43987278	99	CAGAGTAACAA GATTTTCTTTAA [A/gap]TAAATGTA TTTCAACGAAA TGAAC	A	gap				SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1910	cg43091826	1583	CTTCTAACCAAC CTGTCTCCAGCT G[C/gap]TCTGCA CACATGGACAGG GACCTGG	C	gap				SILENT- NONCODING	Interleukin receptor	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN- 15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)
1911	cg43091826	1621	GACAGGGACCT GGGAAAGGTGG GAG[A/G]GATGC TGAGCCCAGCG AATCCTCTC	A	G				SILENT- NONCODING	Interleukin receptor	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN- 15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)

1912	cg43091826	265	CCTGGGCAGCG CTCGCCCGGG AGT[G/C]CAGCG GTGTCCTGTGGA GCTGCCGC	G	C				SILENT- NONCODING	interleukin receptor	Human Gene Homologous to SPTRMBL-ID:Q13261 INTERLEUKIN-15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)
1913	cg43926168	40	ATTCGGTTTTT TTTTTTTTTTT TTGGCATTTC AGATTTTATTGTA AA	A	T				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT-ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa.	8.80E-94	2 (2q14.2)
1914	cg43278750	1578	AGTTCTCTAAAT GTTGCTTTTCTC A[G/A]CCTGTTTA TCCATATTTCAAT CCTT	G	A				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1915	cg43278750	1583	TCTAAATGTTGC TTTTCTCAGCCT GTT/CJTATCCAT ATTCAATCCTT GGAAC	T	C				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1916	cg43278750	1611	ATCCATATTTCAA TCCTTGGAAGT T/CJCCAGCTCCC ATGACTCTATGC CCAC	T	C				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1917	cg43278750	1613	CCATATTTCAAT CCTTGGAAGT C/CJTAGCTCCCA TGACTCTATGCC CACCA	C	T				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1918	cg43278750	1616	TATTTCAATCCTT GGAAGTGTCCAG C/TJTTCCCATGAC TCTATGCCACC AAGC	C	T				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	

1919	cg43278750	1617	ATTTCAATCCTT GGAAGTGTCCAG CT/CJCCCATGAC TCTATGCCACC AAGCT	T	C				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1920	cg43278750	1627	TTGGAAGTGTCC AGCTCCCATGAC TTC/GJTATGCCCA CCAAGCTCTTGA ATTT	C	G				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1921	cg43278750	1650	CTCTATGCCAC CAAGCTCTTGAA TTC/GJTCTCATT TCTTCACCTACA ACCT	T	G				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1922	cg41657511	1553	TTGAGCATT TTTGGATGGG A/gapJGGTGCGT GAGGTTCTCTCA GCCCAG	A	gap				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1923	cg41657511	1560	TTTTTTTTTAGG ATGGAGGTGC GT/AJGAGGTTCT CTCAGCCACAGG GGGGTG	T	A				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1924	cg41657511	1561	TTTTTTTTTAGGA TGGGAGGTGCG TTC/TJAGGTTCTC TCAGCCACAGG GGGTGC	G	T				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11

1925	cg41657511	1618	GTAAGGACAGCC TTCACGTGTGCCT TTC/TGAGCTGCT TTCCGCTCCCTG GGCTC	C	T				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1926	cg41657511	1698	TGGCAGGGATGT TCTAGAAATGGG G[G/gap]TTGGTT CCTCTAGCTACC CCAAATG	G	gap				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1927	cg43929155	1432	AACTGAACATTC CAGAGCGTGTAG TIG/TAAATCACGT AAAGCTAGAAAT GATCC	G	T				SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P21109 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1) - ORYCTOLAGUS CUNICULUS (RABBIT), 355 aa.	4.20E-55	2
1928	cg43933187	44	TTTTTTTTTTTT TTTTTTTTTTTTG TTCAATGTTTGA ACATTTTATTAA G	G	T				SILENT- NONCODING	isomerase	Human Gene SWISSNEW-ID:P11388 DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1531 aa.	0.00E+00 (17q21)	17
1929	cg43933187	458	TAGACACAGCCA AAGTGTTCCTT [C/T]GGCCTCTGA TGATTTGAGAAG ATGA	C	T				SILENT- NONCODING	isomerase	Human Gene SWISSNEW-ID:P11388 DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1531 aa.	0.00E+00 (17q21)	17
1930	cg43951261	5307	CTTGTAAGATTG TTATAGACTGCC GT[gap]GCATTA GCACAGATTTTA ATTGTCA	T	gap				SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0.00E+00	3 (3p)

1931	cg40915009	3857	GACCAGCCAGG GCAACATGGTGA AA[A/gap]CCCCA TCTCTACTAAAA AACAAAAA	A	gap			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1932	cg40915009	3875	GGTGAAAACCCCA ATCTCTACTAAA A[A/T]ACAAAAA TTAGCCAGGTGT GGCGG	A	T			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1933	cg40915009	3944	GCTACTTAGGAG GCTGAGGCAGG AG[A/G]ATCACCT GAACACAGGAG GTAGAGG	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1934	cg40915009	3950	TAGGAGGCTGA GGCAGGAGAAAT CAC[C/T]TGAACA CAGGAGGTAGA GGCTGCAG	C	T			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1935	cg40915009	3954	AGGCTGAGGCA GGAGAATCACCT GA[A/G]CACAGG AGGTAGAGGCT GCAGTGAG	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0	
1936	cg40915009	3958	TGAGGCAGGAG AATCACCTGAAC AC[A/G]GGAGGT AGAGGCTGCAGT GAGCCGT	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0	
1937	cg43993971	78	TTTTTACCTCCTCA CGTGGCATCTTTT A/GTTTTTCTACA TGGGATGTGAAC AAC	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:P06744 GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) (NEUROLEUKIN) (NLK) - HOMO SAPIENS (HUMAN), 558 aa.	3.6E-305	19 (19q13.1)

1938	cg43930054	587	TGGCTGGCAGA GGAGAGCTGGG GAG[G/gap]CTGC AGCCTTTACAGC AGACAGCAG	G	gap				SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)
1939	cg43969064	561	AGAAACACATTA GGGATCATATTC A[T/C]AGACAAAA ACCTTTACATTTT CTTA	T	C				SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q08752 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP- 40) (CYCLOPHILIN-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 370 aa.	1.3E-200	4
1940	cg44001328	215	TGTGGAAGATAA GAGTTAGAGACC T[C/A]GGCCTCCT GGTCAGTGGAG CCCTTG	C	A				SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.pcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1941	cg44001328	237	CCTCGGCCTCCTC GGTCAGTGGAG CC[C/gap]TTGGC CTCATGCCCTGGT GGGCTAAG	C	gap				SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.pcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1942	cg44001328	308	GGTAGGGGAGG CCTTGGCTTGGC CC[C/gap]AGCAG CTCCAGGGCCCT GAGTTCCT	C	gap				SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.pcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1

1943	cg44001328	334	AGCAGCTCCAG GGCCCTGAGTTC CT[G/gap]CCAGA GGCTGGAGAGC AGGCAGCTG	G	gap			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa. pcis: TREMBL-NEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1944	cg43958501	129	TCACATAGAAA GCTAAAGACAAA ATTGJACTGGTAC CAACATAGCCC TTAGG	T	C			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:P46926 PUTATIVE GLUCOSAMINE-6- PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6- PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0080) - HOMO SAPIENS (HUMAN), 289 aa.	1.6E-156	5
1945	cg43958501	19	TTTTTTTTTTTT TTTTTAA/TTTTGA AAATACTGGATT TAATAGAA	A	T			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:P46926 PUTATIVE GLUCOSAMINE-6- PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6- PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0080) - HOMO SAPIENS (HUMAN), 289 aa.	1.6E-156	5
1946	cg44004587	967	TGTTTATCACAG CCTACTAAAAAC A[C/gap]AGAGTT TCACTCATTTGTT CAAAAT	C	gap			SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1947	cg44004587	1036	GCAAAGATTAAA TTAAGTTTATT [G/gap]CTCGCTC TCATTTTACAATA ATCTC	G	gap			SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1948	cg44004587	1262	AAAGTCATTCTA AGTTTGTAAAGC A[G/C]ATAAATTT TTCTGTAATCATT TACC	G	C			SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	

1949	cg44004587	282	GTACAAATTTTAA CATTAAATATACA C/TATTCATAAT CTCATCTATTTAA CA	C	T				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1950	cg44004587	378	TTCCTGACTCTG TAGGACAGTGGT C/C/gap]TCAGTT GGGGTTGACT CTGTCCCC	C	gap				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1951	cg44004587	573	ACCGAGTGGGA CTCAATTCCCAT TTT/gap]ATGAAC ACCTCTGTGCTC ACTGJAA	T	gap				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1952	cg44004587	783	ATATCATTTAAT TCCCTTGAACCT gap/T]GCTCTGCT AGTTTAATCTGC TAATA	gap	T				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1953	cg43255138	882	CGTGTCATGGC GGGGTTCTCCA A/T/C]ACACTCAC ACTGTCCATGTT CITTT	T	C				SILENT- NONCODING	isomerase	Human Gene Homologous to SWISSPROT-ID:Q00688 RAPAMYCIN- SELECTIVE 25 KD IMMUNOPHILIN (FKBP25) (PEPTIDYL-PROLYL CIS- TRANS ISOMERASE) (EC 5.2.1.8) (PIASE) (ROTAMASE) - HOMO SAPIENS (HUMAN), 224 aa.	1.40E-118	19
1954	cg42711479	676	CTTGAGGAACT TCGGTTGCAGAT T/G/gap]AAGCAT TTCAGGTTGTGC ATTITGT	G	gap				SILENT- NONCODING	isomerase	Human Gene Similar to SPTREMBL- ID:Q16645 PEPTIDYL-PROLYL CIS- TRANS ISOMERASE - HOMO SAPIENS (HUMAN), 108 aa.	2.90E-54	2
1955	cg42711479	729	GATGCATGTAGT AGCCTTTCCTGA T/G/A]ACAGAACA CAGATCTCTTGT TCGCA	G	A				SILENT- NONCODING	isomerase	Human Gene Similar to SPTREMBL- ID:Q16645 PEPTIDYL-PROLYL CIS- TRANS ISOMERASE - HOMO SAPIENS (HUMAN), 108 aa.	2.90E-54	2

1956	cg43919187	986	CCAACCATGTCA AGATGATAACA A/TCTCGCTTAG TACAAGAGATGG ATGCA	T	C				SILENT- NONCODI NG	isomeras einhibitor	Human Gene Similar to SWISSPROT- ID:P49312 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED) - MUS MUSCULUS (MOUSE), 319 aa.	8.80E-78	5
1957	cg43145505	3397	TTAAACAGCATG CATTGAACTGAA A[A/gap]GATAAC TGAGAAAATGAA AGCTCAC	A	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa. [pcis:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3
1958	cg43918241	2846	ACCTAGAGAGAG AAAAAATGCTTT [T/gap]CTTTGTGA AAAATCTGAATT CCTGT	T	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
1959	cg43918241	3412	GCACACAAATGT TGCAAAAGTCAA A[A/gap]CCCCAT GAATTAAACCT ACJGGAA	A	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
1960	cg43918241	4823	TTCTGTATGTGT GTATATATATATA [gap/T]ATTATGTA CTTCTGGCAATT CTATC	gap	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3

1961	cg43983484	2863	GGGACTGTGGT GACTTCTGCTGC TG[gap]CCCCG CCCCTGCCCCCA GAGCGTCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1962	cg43983484	2959	TGTGTGTGAATC TGCTTTCCTCT G[C/gap]CTTCGG AGGAAATTGTA AATCCCTG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1963	cg43983484	2960	GTGTGTGAATCT GCTTTTCCTCTG C[C/gap]TTCGGA GGAAATTGTAA ATCCTGT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1964	cg43983484	359	GGCCGGCGGCGG GCCCGCCGCGG GGC[G/C]GCGGC GGCGGGGCGAC GGTCCCCCG	G	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1965	cg43983484	360	GCCGGCGGCGG CCCGCCGCGGG GCG[G/C]GCGCG GCGGGGCGCAG GTCCCCCGC	G	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1966	cg43917863	127	TATACATTGAGA TATGTTTGAAC A[C/gap]TTCCTAA GGCTACAAACA GAACAT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q08881 TYROSINE-PROTEIN KINASE ITK/TSK (EC 2.7.1.112) (T-CELL-SPECIFIC KINASE) (TYROSINE-PROTEIN KINASE LYK) (KINASE EMT) - HOMO SAPIENS (HUMAN), 620 aa.	0.00E+00	4
1967	cg43976564	205	CAACAAATGTA CGACAGGTCAGA A[A/G]CTTAAGTT ACAAATAGAGT CAATA	A	G			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q99683 MITOGEN-ACTIVATED KINASE KINASE KINASE 5 - HOMO SAPIENS (HUMAN), 1374 aa.	0.00E+00	6

1968	cg43976564	307	TAAAAAACATA AACTTTATACAG T[A/C]ATTGAAAT TACGCATTTCTA CTCAG	A	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q99683 MITOGEN-ACTIVATED KINASE KINASE KINASE 5 - HOMO SAPIENS (HUMAN), 1374 aa.	0.00E+00	6
1969	cg43916734	20924	CCTCATTGGAG GAAAAAAGCAT G[C/T]ATTCTAGC ACAACAAGATGA AATTA	C	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1970	cg43916734	20951	TTCTAGCACAAC AAGATGAAATTA T[G/A]GAATACAA AAGTGGCTCCTT CCCAT	G	A				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1971	cg43916734	20956	GCACAACAAGAT GAAATTATGGAA T[A/G]CAAAAGTG GCTCCTTCCCAT GTGCA	A	G				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1972	cg43916734	21059	TTAGCTTTTGTGTT GTTTTTTTTTIG ap/T]CCTTCTAAC ACTTGTATTGG AGGC	gap	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1973	cg43090990	2252	CCAGAGACAGG AAAGAAATTGCC TT[C/G]TCCCTGG GAACTGGTTCAA GAGACA	C	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10
1974	cg43090990	2718	ATTCCTATCTGT GGATGTGTAAT G[G/gap]CTGGGG GGCCAGCCCTG GATAGGTT	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10

1975	cg43090990	2726	CTGTGGATGTGT AAATGGCTGGG GG[G/gap]CCAGC CCTGGATAGGTT TTTATGGG	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10
1976	cg43956329	2485	GTAACACTACAGTG GCATTAGGACTT AIC/TJCGCTTAGA TGACAATAGTGC TCTTT	C	T				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa. pcls:SWISSPROT-ID:P14619 CGMP- DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1977	cg43956329	3342	TCTGTAAATGTC AGTGTCTGAACA G[A/gap]CAACAC AAATTCAAATCAT TATACG	A	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa. pcls:SWISSPROT-ID:P14619 CGMP- DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1978	cg43956329	3427	ATTAACCAAAC TCCTGTCCAATT TIC/GJACTTATAC AACATAGTCAGT CTAGA	C	G				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa. pcls:SWISSPROT-ID:P14619 CGMP- DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1979	cg44022982	3348	CAGGGAGGAGG GGAGGTGCAGG GAA[G/A]AGGGG CCGGCCTCAGCT GTCACCAG	G	A				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16584 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	11

1980	cg44022982	3469	GTCATCTGGGCA CAGGGCTCTCTG G[A/G]TGCCTTCC TGCTGCCCCAGC CAGGG	A	G				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16584 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	11
1981	cg42922283	4204	ATGGCTGCCCTC TGGCAGGGCAG GG[T/C]AGGGCA GTGACACTGTAG GAGCATA	T	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q99558 NIK, SERINE/THREONINE PROTEIN- KINASE - HOMO SAPIENS (HUMAN), 947 aa.	0.00E+00	17
1982	cg43299934	926	CTTCTCAATAGG ACTACAGTATGG A[G/T]AAAGAAAG GACTTTCTGGAG AGGAC	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92667 KINASE A ANCHOR PROTEIN - HOMO SAPIENS (HUMAN), 803 aa.	0.00E+00	17
1983	cg43336163	2707	CGTTGGAAGACT GAGTGCCCGGG GC[A/gap]CAGCA CAGAAAGCCGGC CCCACCGCC	A	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1984	cg43336163	2786	GTCTCCGCCCCAG CTCCAGTCCTGT G[A/T]TCCGGGC CCGCCCCCTAG CGGCCGG	A	T				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1985	cg43336163	2787	TCTCCGCCCCAGC TCCAGTCCTGTG A[T/A]CCGGGCC CGCCCCCTAGC GGCCGGG	T	A				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1986	cg43336163	3208	TCTCGGAGCCCC AGCCGGCTCCG CC[C/G]CCTTCG GCGGTTTGATA TTTATTG	C	G				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19

1987	cg43336163	3209	CTCGGAGCCCC AGCCGGCTCCG CCC[C/G]CTTCG GCGGTTTGGATA TTTATTGA	C	G			SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1988	cg44929725	5014	TCACCAAGGTCT CTGTGTCAAACC TTG/AJTGCCACT CTATATGCACCTT TGTTT	G	A			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
1989	cg42859664	338	AGTGTGGATGCT GGTGGCAGGAG TC[C/A]AGGACTG TGAAGAGCTGTC AGCATA	C	A			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa.	0.00E+00	15 (15q26.1)
1990	cg38810367	4136	AGGTTTCACCAT GATGGCCAGGC TG[A/G]TCTCGAA CTCCTAACCTCA AGTGAT	A	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P52333 TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3) (LEUKOCYTE JANUS KINASE) (L-JAK) - HOMO SAPIENS (HUMAN), 1124 aa.	0.00E+00	19 (19p13.1)
1991	cg43995263	191	AAGATTATAAATA CGAGGGGTAA G[C/gap]CCCACC TGAGGGCACAG AACCTTTT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)
1992	cg43995263	194	ATTATAAATACG AGGGGGTAAGC CC[C/gap]ACCTG AGGGCACAGAA CCTTTTCTC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)

1993	cg43995263	2249	ACGTTTCTGAGA ACTGGCTGGGG GC[C/gap]AGGAG GCGGACCACAC GGTGCGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)
1994	cg43969763	6070	TTAAGATATCATA TGGGTCAGGTCA [T/gap]TTTTTTT TCTGTGCTGGTT GCCAC	T	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1995	cg43969763	6079	ATATGGGTCAGG TCATTTTTTTTTT gap/T]CTGTGCTG GTTGCCACATCT TAGCA	gap	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1996	cg43969763	6135	CAAAAAACTAA GCAGTTTATAA C[C/T]GATATTTA CGTAAAGAAAAT CATAA	C	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1997	cg43918986	663	CCTGATAGAGGA A AGAGGTGGCAG GG[A/G]AAACTG CCAGCTCAAAG CCCTAGT	A	G			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q13308 COLON CARCINOMA KINASE-4 PRECURSOR - HOMO SAPIENS (HUMAN), 1070 aa.	0.00E+00	6 (6p21.1)
1998	cg43019995	3241	GCCCGTGGGAC CATGACTTAGGG AG[G/gap]TGGGA CCCACCCACCCC CATCCAGG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P53667 LIM DOMAIN KINASE 1 (EC 2.7.1.-) (LIMK-1) - HOMO SAPIENS (HUMAN), 647 aa.	0.00E+00	7 (7q11.23)

1999	cg44910735	226	GGGGTGCTCTCG GGCAGAGACCC CCG[G/C]GCTTG GGGCAGCTGAG GCGGCCGGG	G	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q13869 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE - HOMO SAPIENS (HUMAN), 1149 aa.	0.00E+00	9 (9q34.1)
2000	cg43257904	116	CGGGGGAGACA CAAAAGGACCC CC[C/gap]AAAT CCACATGGGT GCTGGGAAC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2001	cg43257904	141	CAAAATCCACAT GGGTGCTGGG AA[C/gap]CCCA AATCCAGTGGAA GGCACATC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2002	cg43257904	2476	CGGACTCTCGTT ATTGGCTCTGCG G[G/gap]ACTCAG CCTCCACCCCT ATTGGGT	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2003	cg43257904	267	AATTAGAAGTA TCCCAAAGCCA A[gap/A]GAGGA ACCAAATGATGG AGGAGAC	gap	A				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2004	cg43257904	318	AGGGGCTCAG TCCTTGCGGGG GT[C/gap]CCCCA ATTCCAGAAGAA CTGGAAA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)

2005	cg43257904	38	TTTTTTTTTTTT TATTTTTTTTTT /GJCCCAGCAGAA TTCTGTGCTTCT TGG	T	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2006	cg43257904	482	TGAGATTGGCTC CCTGGTGGCTTG G[G/gap]CGGG CCTAAGGCACAA GGCGGGCT	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2007	cg42879455	2335	ATAGTGGCTTCT GAGCAAAGGCC AA[A/G]AAATTAT TGTGCCTGAAAT TTCCCG	A	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0.00E+00	X (Xq21.3)
2008	cg43016269	6151	TACATCATCTGG CCAGGCATGGTC G[gap/C]TTACGC CTGTAATCCTAG CACTTIG	gap	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q28021 RHO-ASSOCIATED KINASE - BOS TAURUS (BOVINE), 1388 aa.	0.00E+00	
2009	cg43931272	1166	TTAGGGATAAAA CACTAACTCTAG T[G/C]CCCTTAAC GGCAATAGCAA CITTT	G	C				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2010	cg43931272	1452	CCTCACTCAGAG CAGCCACACACA G[T/G]GGCCGTT GACGCTGGAAC CTCGGGC	T	G				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	

2011	cg43931272	307	GGCTAATTTTAT ATTTTAGTAGA A/GJATGGCGTT CACCATGTGGAC CAGA	A	G				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2012	cg43931272	959	TCTCAGTACTCC CACTCAATTTT [gap/T]CCCTACT GAGATGAGGGA AGCAAT	gap	T				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2013	cg44003408	253	GGACTGGAGACT GATGCATGAGG GG[G/C]CTACGG AGGCGCAGGAG CGGTGGTG	G	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P53355 DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1) - HOMO SAPIENS (HUMAN), 1431 aa.	0.00E+00	
2014	cg44001122	4440	AGTGTGGGT TTGTTTTTCTTT A/GJAGAAAAAGA AATGTACACCAC TCCT	A	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31152 EXTRACELLULAR SIGNAL- REGULATED KINASE 4 (EC 2.7.1.-) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK) - HOMO SAPIENS (HUMAN), 557 aa.	4.40E-307	18
2015	cg43957153	131	GGACCGGCGG CGGCGGCGCG GCA[G/C]CGCGG GCGCGGTAGGG TGTTTAACT	G	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)
2016	cg43957153	132	GGACCGGCGG GGGCGGCGCG CAG[C/G]GGCGG CGGCGTAGGGT GTTTAACT	C	G				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)
2017	cg43957153	81	AAGTGACGATAC TTTTGGCGCGG C[C/gap]GGTTGC TGTTCTTCTCT GGCTCCG	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)

2018	cg44004766	3864	CAGATTCGAAAT TCTGTGCCATGG C[AG]TATATGTT CAAATTCAAACC ATTTT	A	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2019	cg44004766	4255	TGTATAGTAGGG ATAAAACACTAA CT[gap]TAATGT GTATTCATTTTAA ATTGTT	T	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2020	cg44004766	4256	GTATAGTAGGGA TAAACACTAAC TT[gap]AATGTGT ATTCATTTTAAAT TGTTC	T	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2021	cg43952792	322	CGCCGGGCCGG GGACACCCCGG CGC[C/ gap]GCC CCTCGGTGCTCT CGGAAGGCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2022	cg43952792	351	CCCTCGGTGCTC TCGGAAGGCC AC[C/ gap]GGCTC CCGGGCCCGCC GGGACCCCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2023	cg43952792	367	AAGGCCACCG GCTCCCGGCC CGC[C/ gap]GGGA CCCCCGGAGC CGCCTCGGCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2024	cg43952792	377	GGCTCCCGGCC CCGCCGGGACC CCC[C/ gap]GGAG CCGCCTCGGCC GCGCCGGAGG	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)

2025	cg43952792	383	CGGGCCCGCCG GGACCCCGCG AGC[C/gap]GCCT CGCCCGCGCCG GAGGAGGGCG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2026	cg43952792	388	CCGCCGGGACC CCCCGGAGCCG CCT[C/gap]GGCC GCGCCGGAGGA GGCGGGGGAG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2027	cg43952792	559	TATAAAGTTTGT GATCGTTGGCG GA[A/C]ATTTTGG AATTAGATAAT GGGCTG	A	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2028	cg43971741	2104	TGAGCACAGTTA TGGCAGAGAAGT TTT[gap]CTCCGC ACCAGAATTATC CACAGCA	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2029	cg43971741	2108	CACAGTTATGGC AGAGAAGTTTCT C[C/gap]GCACCA GAATTATCCACA GCAACTT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2030	cg43971741	2133	CGCACCAAGAAT ATCCACAGCAAC TTT[gap]GGCTGA GCCCCACTACAC ACAGAGA	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2031	cg43971741	2161	CTGAGCCCCACT ACACACAGAGAA ATT[C]CATCAACC TGACTTAAGAGT TTTCA	T	C			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9

2032	cg43971741	2162	TGAGCCCCACTA CACACAGAGAAA TTC/TATCAACCT GACTTAAGAGTT TTCAA	C	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2033	cg43971741	2196	GACTTAAGAGTT TTCAAGATGTCA A[A/gap]CTTCAG GCTGATCAGCAG ATGGGAT	A	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2034	cg43971741	2234	CAGCAGATGGG ATGTGAAAAATA CT[A/gap]CCCTA TTCTATCATTTGC TGTGCT	A	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2035	cg43971741	2508	ATTATAGTTTCAT GTCATTGAAAGT TTT/gapJAAATTGG TTTCATTAAAGA TCAAT	T	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2036	cg43971741	2516	ATGTCATTGAAA GTTTAAATTGGT TTT/gapJCATTTAA AGATCAATATAC TAGGTC	T	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2037	cg43971741	2521	ATTGAAAGTTTA AATTGGTTTCATT TTT/gapJAAAGATC AATATACTAGGT CTGCCCT	T	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2038	cg43119489	2360	GGTCTCAGCGG CCGGCAGACGT GAG[G/gap]CGCT TCCGAGCGCAG GCCTCCGCCG	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00537 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.70E-282	

2039	cg43119489	2376	AGACGTGAGGC GCTTCCGAGCG CAG[G/gap]CCTC CGCCGCCACAG CCGCCCTCCG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00537 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.70E-282	
2040	cg43123314	2399	TGGACATTCCTA GGAAACCCAGA GG[G/gap]TGGAG GTGGGGGCCCC ACGGCTAA	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q16875 6- PHOSPHOFRUCTO-2-KINASE (EC 2.7.1.105) / FRUCTOSE-2,6- BISPHOSPHATASE (EC 3.1.3.46) BRAIN/PLACENTA-TYPE ISOZYME (6PF-2-K/FRU-2,6-P2ASE) - HOMO SAPIENS (HUMAN), 520 aa.[pcds:SPTREMBL-ID:Q16875 FRUCTOSE 6-PHOSPHATE,2- KINASE/FRUCTOSE 2,6- BISPHOSPHATASE (EC 3.1.3.46) (FRUCTOSE-2,6-BISPHOSPHATE 2- PHOSPHATASE) (FRUCTOSE-2,6- BISPHOSPHATASE) - HOMO SAPIENS (HUMAN), 520 aa	1.80E-281	
2041	cg43921754	153	CCGCGCCACCC CCGGCCCCGCG CCA[gap/G]CAGC CCCTCGCCGCG CGTCCAGCGT	gap	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2042	cg43921754	207	CGGCCAGCAGC CTCCCCATACGC AG[G/gap]TCCTG CTGGACCGCCC CGTCGCGCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2043	cg43921754	285	AGCTCCGCCGC CCCGAAACTTTC AC[C/gap]GCGAG CGGGAATATGG GATGTATA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)

2044	cg43921754	292	CCGCCCCGAA CTTTCACCGCA GC[G/gap]GGAA TATGGGATGTAT AAATCAA	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2045	cg43922705	178	GAGAGCCTCTCG GCAGCGGGG GG[G/gap]TCCTC TCCTCCAGAAC AAAGGCAC	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P27987 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)
2046	cg44019155	1267	AATCCACGTTTA TTTTTCCTGTGT CTTCGAAAGTGT CTATGTAATGAC ATTGA	T	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2047	cg44019155	1317	CTCTCTGAAACT GTCATTTTGAGT C[gap/T]GTTTCA CCTTGCAGGATG CTCACAC	gap	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2048	cg44019155	1317	CTCTCTGAAACT GTCATTTTGAGT C[gap/T]GTTTCA CCTTGCAGGATG CTCACAC	gap	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2049	cg44019155	1363	CACACATCTCCC TCTCCACCTTTT T[gap]GCCCTTAA ATTCATTAAAG CAATTGC	T	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2050	cg43241753	1017	CCACAGCCCCTT TCTCTGCTTTTC [C/T]TTTATTTC GCTACCCATCCA GTGG	C	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9

2051	cg43241753	2525	GCTGCACCGGC CGCTTTCCCCCA CC[C/gap]GTGCC GGAGGCCCTTC CCTGCGCTT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9
2052	cg43241753	2530	ACCGGCCGCTTT CCCCACCCGT GC[C/G]GGGAGG CCTTCCCTGCGC TTGCGGC	C	G			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9
2053	cg43947749	1615	CTTCCATCTGGG AGCCCCAAGAG GG[G/C]CTGGGA AGGGGGGCCAT AGCCCATC	G	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2054	cg43947749	1616	TTCCATCTGGGA GCCCCAAGAGG GG[C/G]TGGGAA GGGGGGCCATA GCCCATCA	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2055	cg43947749	2070	AGGTCTACTCC TCCTCACCCAC C[C/gap]TGGAGG GCCAGGGGAGT GGAGAGAG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2056	cg43932396	923	CCCAATGCCACA TTGCGCATAGCT G[C/T]AGAAGTCC TTAACATTTCCT ACGT	C	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262 (14q32.3)	14

2057	cg43932396	409	ACAGGGAGTCA GGGAGGGCCTG GGG[C/gap]GACA GCGGAAAGGTTA AGCGTCGAA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)
2058	cg43932396	480	AGAGATCATCTG AGGGGAGGCT CC[C/gap]GGTGG GACAGTCACCAA GAACTGTG	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)
2059	cg43957447	2146	ATGTTGTCATTG ATATAAACCTGT T[gap/T]GGTTCA GCAAAACAACTA AAATGAT	gap	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49336 CELL DIVISION PROTEIN KINASE 8 (EC 2.7.1.-) (PROTEIN KINASE K35) - HOMO SAPIENS (HUMAN), 464 aa.	1.80E-260	
2060	cg43930359	1473	GCATGAGGAGATG GGAGGGCGGGA CT[G/gap]GGCCG CCCAGCCCCCTTG ACTCCAGC	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.[pcds:SWISSPROT-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.	4E-255	
2061	cg43930359	1511	CCTTGACTCCAG CCTCGACCGCCA G[G/gap]CCCCCAG GCCAGAGCCAC CCAATGAA	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.[pcds:SWISSPROT-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.	4E-255	
2062	cg43965549	1595	CCATGTTTGCTC TAAATTAAAGACA G[gap/G]CATTGA TCTCCTGGAGGC TGGTTCT	gap	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)

2063	cg43965549	1803	CAGGTGACGTGA TTCTAAGGCAGG A[A/gap]TTTGAG AGTTCACAGAAG GATCGTG	A	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
2064	cg43965549	2199	AAACATTTTATAC TGACATGCTAT G/gap]CTGAAGA CATTCAAAACGT GATGTT	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
2065	cg43965549	2282	ATTTTGTACATC CCAAAGGATGAG [A/C]ATGTGACCT TTAAGAAAAATG AAAA	A	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2066	cg43965549	2283	TTTTTGTACATCC CAAAGGATGAGA [A/C]TGTGACCTT TAAGAAAAATGA AAAC	A	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2067	cg43965549	2286	TGTACATCCCAA AGGATGAGAATG T[gap/T]GACCTTT AAGAAAAATGAA AACTTT	gap	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)

2068	cg43965549	2485	AGTAGTCTTATG TAAAGTATGTTTT [T/gap]ACATTATG CAAAATAAACCC AATAC	T	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2069	cg43926820	475	TCTCAGCATGAA CTCCTGAGTGAA G[C/G]CTCTCCTC AGCGTGACTCAG GAACA	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P51956 SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 3) (HSPK 36) - HOMO SAPIENS (HUMAN), 459 aa (fragment).	1.40E-251	13
2070	cg43329822	119	CTGGCACCTCTG GAGAGGGCAGA GC[C/gap]TCCTC AGAAGAGCTGG CCTGAGGAA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23677 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE A (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 461 aa.	1.30E-250	15 (15q14)
2071	cg43292279	1658	CCGAGCCTGAAC TGAGCCCCAGC GG[G/gap]CTGGC GGGCCTTTTCC TGC GTCCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2072	cg43292279	1985	CTGTCCTGCCCG TGAGGGTGGG GG[G/gap]ACCGG GCCCCCTCTCTAG GGACCCCT	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2073	cg43292279	2181	GCCCAACCGCC TTGTGAGATGGA AT[C/T]GTAATAA ACCACGCCATGA GGACAC	C	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15

2074	cg43292279	2214	ACCACGCCATGA C GGACACGCCCG CC[C/gap]GCCTC GGCGCTTCCTCC ACCGAAAA	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.12) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2075	cg43928793	1815	TTCTGTGCCGAC C CAGCCCCCAGG AC[C/gap]TCCGG AGCGCCCTGCA GGCCCGGGC	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:Q15831 SERINE/THREONINE-PROTEIN KINASE 11 (SERINE/THREONINE- PROTEIN KINASE LKB1) - HOMO SAPIENS (HUMAN), 433 aa.lpcis:SWISSPROT-ID:Q15831 SERINE/THREONINE-PROTEIN KINASE 11 (SERINE/THREONINE- PROTEIN KINASE LKB1) - HOMO SAPIENS (HUMAN), 433 aa.lpcis:SPTREMBL-ID:Q15831 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 433 aa.lpcis:TREMBLNEW-ID:G2754827 SERINE THREONINE KINASE 11 - HOMO SAPIENS (HUMAN), 433 aa.	4.70E-237	
2076	cg43069976	120	GGTCCCTGGAG G CTCCGCACTTGG CG[G/gap]CGCAA CCTGCGTGAGG CAGCGCGAC	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.lpcis:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1

2077	cg43069976	1592	AAATGCTGTAGT GTTGAATACTTG GTTCJTCCATGAG CCATGCCCTTTCT GTATA	T	C			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa. pcds:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
2078	cg43069976	1593	AATGCTGTAGTG TTGAATACTTGG TTTCJCCATGAGC CATGCCCTTTCTG TATAG	T	C			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa. pcds:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
2079	cg43069976	1813	TCTAAATCTTGG GAGAAAAAATAA TTG/AJTAGGAAA AAAATATTTATGC AGGA	G	A			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa. pcds:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1

2080	cg43957648	211	GAGCAGACACA GTACCTGATCCA AC[A/G]CCACAA GGCAAATCTATG GCCATCA	A	G			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2081	cg43957648	413	CCAGGCGTAGCT CATGAGGGCCA CG[C/gap]CGGCG GCTGGAGCCCC CGTGAGCAA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2082	cg43957648	414	CAGGCGTAGCTC ATGAGGGCCAC GC[C/gap]GGCGG CTGGAGCCCCC GTGAGCAAT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2083	cg43957648	418	CGTAGCTCATGA GGCCACGCCG GC[G/T]GCTGGA GCCCCCGTGAG CAATACTG	G	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2084	cg43957648	426	ATGAGGGCCAC GCCGGCGGCTG GAG[C/gap]CCCC GTGAGCAATACT GCTGGGCCA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2085	cg43957648	78	AGGCTCTTATTG AAAGTGGCAGG GG[C/gap]CTCTC AATGTTCTATGA AAACTAAC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2086	cg43957648	79	GGTCTTTATTGA AAGTGGCAGGG GC[C/gap]TCTCA ATGTTCTATGAA AACTAACA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2

2087	cg43257603	3364	AACTCCAGGTCT AACAGCTGACC C[G/gap]AGTGAT GGGGAATTTATC CGTGACC	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2088	cg43257603	3368	CCAGGTCTAAAC AGCTGACCCGA GT[G/gap]ATGGG GAATTTATCCGT GACCAATT	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2089	cg43257603	3384	GACCCGAGTGAT GGGGAATTTATC C[G/T]TGACCAAT TTATCCTTGACC AATAA	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2090	cg43257603	3386	CCCGAGTGATG GGGAATTTATCC GT[G/T]ACCAATT TATCCTTGACCA ATAACC	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2091	cg43257603	3426	GACCAATAACCT AATTGCTCTATTC C[G/T]GAGTTATA AAAGTCCCCATC CTTAT	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2092	cg43257603	3427	ACCAATAACCTA ATTGCTCTATTCC G[G/T]AGTTATAA AAGTCCCCATCC TTAT	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2093	cg43257603	3478	AGCTCTACTGGA ATTTTCATACAC G[G/gap]TAAATG CAGAAAGTTACTA AGTATTA	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)

2094	cg43257603	3627	ATCAAGGTGACT AAGAAATCAGT TIGCJTGTAAATA AAACAAGCAGC ATAAA	G	C			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2095	cg43984889	1176	TCTAGAAAGTTC TATTAGTCGTGA TACJTCGTCTTG TTTTGCTTTGTAT TTTG	A	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.[pcis:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	X
2096	cg43984889	696	CTGGGACTAAAT CATCAGGGCATG G[C/gap]CACCTG ATGCTCTCCACT TTCAGGG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.[pcis:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	X
2097	cg43984889	697	TGGGACTAAATC ATCAGGGCATGG C[C/gap]ACCTGA TGCTCTCCACTT TCAGGGT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.[pcis:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.8E-221	X

2098	cg42508800	132	CATCGCGGACTC TGCCAGACTCT T[A/C]GAGCCGG GGCACCCCTCAAA CCCCAG	A	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q16654 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 4) - HOMO SAPIENS (HUMAN), 411 aa.[pcis:SP TREMBL-ID:Q16654 PYRUVATE DEHYDROGENASE KINASE ISOFORM 4 - HOMO SAPIENS (HUMAN), 411 aa.	1.6E-220	7 (7q21.3)
2099	cg43947829	389	TCATTCCAACAG CTTTACCAGGCT TTC/GJGCCAACG CAATAAGTTACA CACTCA	C	G				SILENT- NONCODI NG	kinase	Human Gene TREMBL-NEW- ID:G2978628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	
2100	cg38438124	1574	GCCTCGGACAG ACATGAACATTG GA[G/T]GGACAG AGGTGGCTTCG GTGTAGGA	G	T				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS.MUSCULUS (MOUSE), 405 aa.	2.8E-216	10
2101	cg43917871	1157	AATCAGCCTATT ATAATTTTTTTTTT T/gap]ATGACTGA ACTACTATAAAT CCACA	T	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2102	cg43917871	1201	ATCCACAAGCAA CGGTTGAGACAC GIG/TJTGCTTCTG AAGTGTTTCACC CCTCC	G	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)

2103	cg43917871	1234	GAAGTGTTTCAC CCCTCCCGCCA G[G/gap]CGCAAG CTGCATCAAGGA GAGGGTG	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2104	cg43917871	1241	TTCACCCCTCCC CGCCAGGCGCA AG[C/gap]TGCAT CAAGGAGAGGG TGGACTCCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2105	cg43990838	21	TAGATTTTTTTT TTTTTTT[A/T]TG TTGACACAAAT CTTTTATTC	A	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q03426 MEVALONATE KINASE (EC 2.7.1.36) (MK) - HOMO SAPIENS (HUMAN), 396 aa.	1.4E-203	12 (12q24)
2106	cg43945404	1579	TAGTAATCATTG GATGCATGATGG G[G/gap]CAGGGC CGGTGATGGTG CCTCCCCC	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2107	cg43945404	1586	CATTGGATGCAT GATGGGCGCAGG GC[C/gap]GGTGA TGGTGCCTCCCC CTTGCTGG	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2108	cg43945404	1661	CTTTCACCGCTC ATTATGTAGTCT G[G/gap]CTACAG CCCTCAAAAACA GCTTATA	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2109	cg43945404	1670	CTCATTATGTAG TCTGGCTACAGC C[C/gap]TCAAAA ACAGCTTATACT CTTAAGA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11

2110	cg43933472	1413	GTGACTAAAGCA ACAGTAAGCAGT A[gap]/AJGGTGCA CTGAAGTACATA CTGCCGC	gap	A				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2111	cg43933472	1565	TCCAAACGGCTC AAAGGAGTCAAA G[T/C]GGATAAG CCAAGACGGGC TGGAGAC	T	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2112	cg43933472	634	GATGCTGACATG CTGTAGAAGGAA A[A/C]AGAATTGT ATACTTTCTCATT TAAA	A	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2113	cg42923882	233	CACACATGGGG CTCCCCAGGCAA GG[C/gap]CACCT GCTGACAGAGGT GAAGCGCA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92961 MAP KINASE KINASE MEK5B - HOMO SAPIENS (HUMAN), 448 aa.	1.8E-196	
2114	cg43929089	149	AATGAACCAAAT TACCCAAACAAA A[T/G]AAACATGG CAATATAAAAAT GTAA	T	G				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa; pcis:SWISSPROT-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa.	1.6E-192	
2115	cg44131795	251	CCACAGGAATTA ACGGAAGAAAGTG T[A/G]TACAAATTT TTGAGGTATGCT CTTTA	A	G				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2760825 PROTEIN KINASE C- BINDING PROTEIN BETA 15 - RATTUS NORVEGICUS (RAT), 498 aa.	1.1E-191	

2116	cg43917159	2170	CCATAAGCAGAA CAAGAACCAAT C[A/gap]AACGTC TTAACGCGTATA GAGAGAT	A	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.2E-191	16 (16p13.3)
2117	cg43917159	2172	TAAGCAGAACAA GAACCAAATCAA A[gap/A]JCGTCTT AACGCGTATAGA GAGATCA	gap	A			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.2E-191	16 (16p13.3)
2118	cg43917159	2397	TGCAGAAATGTTG TTGGTTACTGTT G[C/gap]TCCCGG AGCCCTCAACT CGTCCCG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2119	cg43917159	304	AAGCAATTCTAC CTGCCCTTGGCCT C[C/T]CAAAGTGC TAGAATTACAGG CATAA	C	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2120	cg43917159	320	CTTGGCCTCCCA AAGTGCTAGAAT T[A/G]CAGGCATA AGCCACCACGC CTGGCC	A	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2121	cg42703622	1554	GGAAACTTAGTG TGCCTTGAAAA G[G/gap]CCGCAA GTTGCTTACTCC GAGTAGC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12
2122	cg44932781	121	AGACCAAATGCA GAGAAGCCGGT AG[G/gap]AACCC GAGGCCACGGA GGCTGCTGG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78356 PHOSPHATIDYLYNOSITOL-4- PHOSPHATE 5-KINASE TYPE II BETA (EC 2.7.1.68) (1- PHOSPHATIDYLYNOSITOL-4- PHOSPHATE KINASE) (DIPHOSPHOINOSITIDE KINASE) (PTDINS(4)P-5-KINASE) - HOMO SAPIENS (HUMAN), 416 aa.	2.50E-185	17

2123	cg43934426	936	GCACTGGCAGC CTGCTGTGCAGG GG[C/A]AGCAGC ATCCACAGGGG GCATCCAG	C	A				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G1778153.MAP KINASE 3B - HOMO SAPIENS (HUMAN), 347 aa.	3.20E-183	
2124	cg43987006	123	CCATGATTCAGG GGCACAGCTGC CC[C/gap]AGCAG ACACACACTTTC ATACGCAC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P21425 RIBOSOMAL PROTEIN S6 KINASE I (EC 2.7.1.-) (S6K) (P70-S6K) - RATTUS NORVEGICUS (RAT), AND ORYCTOLAGUS CUNICULUS (RABBIT), 502 aa.	3.10E-176	11
2125	cg43933478	47	TTTTTTTTTTTTT TTTTTTTTTTTTT[G TTTGAAGAGATT CCTGTCATTTAA TTA	G	T				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.[pcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	7.80E-173	12
2126	cg44131752	1527	ACATGTTTCCAC TTAATACCAGAG A[C/gap]CCCCCC CCTTCCCTCC CCTTCCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
2127	cg44131752	1535	CCAGTTAATACC AGAGACCCCC CC[C/gap]TTCCC CTCCCCCTTCCC CTCCCCCT	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
2128	cg44131752	1604	ATTGCAATAAAA CAAACCTTTCTC T[G/T]CACAACA CACCAAAGCTTT ATTCA	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16

2129	cg44000392	245	CTAGACCGATCT CCGGGAGCCCC CG[G/gap]AGTAG GCGAGCGGCGG CCGCCAGCT	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.10E-172	7
2130	cg44000392	265	CCCCGGAGTAG GCGAGCGGCGG CCG[C/gap]CAGC TAGTTGAGCGCA CCCCCGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2131	cg44000392	266	CCCGGAGTAGG CGAGCGGCGGC CGC[C/gap]AGCT AGTTGAGCGCAC CCCCCGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2132	cg44000392	289	GCCAGCTAGTTG AGCGCACCCCC CG[C/G]CGGCC CAGCGCGCCGC GGCGGGCGG	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2133	cg44000392	290	CCAGCTAGTTGA GCGCACCCCCC GC[C/G]CGCCCC AGCGCGCCGCG GCGGGCGC	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2134	cg43291463	1258	GATCAAGAACAA AAAAAATAGCAG C[T/gap]TTTTTTT TTCTGTACAGAC GTATAG	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q25197 PROTEIN-TYROSINE KINASE - HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS), 1477 aa.	6.5E-172	15 (15q25)

2135	cg43291463	1616	CCTTGACTCCAA GCCTGTCCGCCA G[A/G]CTGCTTC GGGGCCCATGG CCACCAG	A	G				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q25197 PROTEIN-TYROSINE KINASE - HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS), 1477 aa.	6.5E-172	15 (15q25)
2136	cg43007055	1516	TTTGTTGGAGTG GTGCCAGGTACT G[G/gap]TTTTGG AGAACTTGTCTA CAACCAG	G	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2137	cg43007055	1568	GATTGATTTTAAAT GATGCTTTTTT T/gap]ATTTTACT TTTTTTTAAGCAC CAAA	T	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2138	cg43007055	1583	TGTCTTTTTTTAT TTTACTTTTTTT /gap]AAGCACCAA ATTTTGTTGTTT TTT	T	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2139	cg43007055	1601	TTTTTTTAAGCAC CAAATTTTGTGTG gap/T]TTTTTTTT TCTCCCTCCCC ACAG	gap	T				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2140	cg43007055	1611	CACCAAATTTTG TTGTTTTTTTTT gap/T]CTCCCTC CCACAGATCCC ATCTC	gap	T				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)

2141	cg43007055	1611	CACCAAATTTTG TTGTTTTTTTTT gap/TCTCCCTC CCCACAGATCCC ATCTC	gap	T			SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2142	cg43007055	2474	GTCTTTGAGAAT AAAGGAAAAAAA A[gap/AJTCTTCA GATGCAATGTT TTGTGTA	gap	A			SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2143	cg43007055	350	GTGCCGCTGCC GCTGTTGCCGCC GC[C/gap]GCTGC TGCTGCTGCTCG CCCCGTCG	C gap	gap			SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2144	cg43925513	189	TGAATTATTATT CCTCTCTTCCAT C/gap]AGATGAG GCTTATCGTGTC AAATCC	C gap	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.[pcis:SWISSPROT- ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.	1.2E-165	14

2145	cg43925513	346	TGGAAGGACTGT GTTGTGCAGCTG C[A/gap]CATAGC TATAATTATTATAA GTCTGC	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.[pcls:SWISSPROT- ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.	1.2E-165	14
2146	cg43336176	2028	TGCCCTCAGT GAGTGGCAGG GC[C/gap]GGGG GTGGTCCAGCC CTGCCCGGGC	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16205 MYOTONIN PROTEIN KINASE - HOMO SAPIENS (HUMAN), 625 aa.	1.1E-164	19
2147	cg43982923	1494	TCCGACTTCTGT CCGCCCTAGGC CC[C/gap]GGGAC CCCCGGCCTCC AGGCTGGGG	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2148	cg43982923	1505	TCCGCCCTAGGC CCCGGGACCCC CG[G/gap]CCTCC AGGCTGGGGCC TGGCCTATT	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

2149	cg43982923	1519	CGGGACCCCG GCCTCCAGGCT GGG[G/gap]CCTG GCCTATTTAAGC CCCCTCTTG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2150	cg43982923	1551	CTATTTAAGCCC CCTCTTGAGAGG G[G/gap]TGAGAC AGTGGGGGTGC CTGGTGCG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2151	cg43982923	1585	TGGGGGTGCT GGTGCGCTGTG CTC[C/gap]AGCA GTGCTGGGCCC AGCCGGGGTG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2152	cg43982923	1600	CGCTGTGCTCCA GCAGTGCTGGG CC[C/gap]AGCCG GGTGGGGTGC CTGAGCCCG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2153	cg43982923	1605	TGCTCCAGCAGT GCTGGGCCCAG CC[G/A]GGGTGG GGTGCCTGAGC CCGAATTT	G	A			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

2154	cg43918763	76	ATACTGCGTTCC ATCCCGACCCG GG[G/gap]CCACG GTAAGTGGGCCCT GTTTCCCC	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P24941 CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) - HOMO SAPIENS (HUMAN), 298 aa. pcds:SWISSPROT-ID:P24941 CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) - HOMO SAPIENS (HUMAN), 298 aa.	1.2E-158	12 (12q13)
2155	cg43921600	115	CTGGCTCTTGGA AATTGAGCGGAG A[G/gap]CGACGC GGTTGTTGTAGC TGCCGTG	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06493 CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1) - HOMO SAPIENS (HUMAN), 297 aa.	2.6E-158	10 (10q21.1)
2156	cg43933460	98	GACGGTTTCTGA GCGTTGGCCTTT G[G/gap]CACGCG CTACCCCTTTT GCTTTGG	G	gap				SILENT- NONCODI NG	kinase	Human Gene SP TREMBL-ID:Q63185 EUKARYOTIC INITIATION FACTOR 2A PROTEIN KINASE - RATTUS NORVEGICUS (RAT), 620 aa.	2.3E-155	7
2157	cg43257282	1399	CCCCAGAAAAG GCCGGGTGACA CC[G/gap]GGGG GCTCCAGCCC GTGCACCCCTG	G	gap				SILENT- NONCODI NG	kinase	Human Gene Homologous to SP TREMBL-ID:Q15130 CDC2-RELATED KINASE - HOMO SAPIENS (HUMAN), 316 aa.	2.9E-147	16
2158	cg43958362	161	TTTTGAAAAGTC ACAAAAAGGGT A[C/gap]CCCCAA ACTCAGGTATAC CAAGTAA	C	gap				SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2159	cg43958362	2286	CCCGGAACCGC GGGTCCCAAGG AGC[C/gap]TGCG GAAGGAGTCGG AGCACCAGGA	C	gap				SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12

2160	cg43958362	322	CTCCCGGGAAC TGAGCTGCGTAT A[A/C]AGAAGTCT GCTTTGGTCCAA AGGAC	A	C			SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2161	cg43958362	716	TCTAGACGTGGT GACTTAAAAAAT G[G/gap]CCTTAA GGCTGCAGAGC CAGCCACC	G	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2162	cg44016530	214	CATGTTTTTTTT TTTTTTTGTGTTT /AJTAGAGTTTTTT AACATAAAGTTTT A	T	A			SILENT- NONCODI NG	kinase	Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.70E-129	12
2163	cg43265203	982	CAACATCACTGG AAGAAATACCTA T[C/T]GTTAAACC CTGATATACATT CTTAA	C	T			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.[pcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2164	cg43265203	54	GGATTATTTTTAA TTTTTCAATCTG A/gap]AAAAAAA AAACCCAAACA AAAAA	A	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.[pcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	

2165	cg43285203	65	AATTTTCAATCT A GAAAAA A/gap]CCCAAAAC AAAAAA ACTAT	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.[pcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2166	cg43285203	73	ATCTGAAAAAA AAAAACCCAAA C[gap/A]AAAAA AAACAAAGTATC CTCATAT	gap A			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.[pcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2167	cg42866488	1761	AGTCGCTCTCAT GAAGCCCTTAGG G[gap/G]AGAGCA CCTGTTGTGTGC CTGACAC	gap G			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.[pcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2168	cg42866488	2065	TTGGGGAGAGCT C GGCAGTGTGCG GA[C/gap]GCTGA TAACATTTTCCC AATAATTGA	gap C			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.[pcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16

2169	cg42866488	2449	TGGAATTACTGA AAGTCTGTGGCC C[<i>gap</i>]/T/AAGAGA GAGACACAAGTG GCCTTAA	gap	T				SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.[pcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2170	cg42866488	2691	TTTGCAATAAA GGCTCTGGAAG CA[<i>AT</i>]/AAAAAAA AAAAAAA AA	A	T				SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.[pcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2171	cg42866488	2692	TTGCAATAAAG GCTCTGGAAGCA A[<i>AT</i>]/AAAAAAA AAAAAAA	A	T				SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.[pcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2172	cg42925992	133	GGAGGGAGGCG GGGGGCACCTG GGG[C/ <i>gap</i>]/CCGC CATGAACCCCGG CTTCGATT	C	gap				SILENT- NONCODI NG	kinase	Human Gene Homologous to SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	5.10E-105	
2173	cg43918705	1032	CTCACCAACGA AGGTATCAGCT A[<i>T</i>]/ <i>gap</i>]/TTTTTT TTAAATTCAAAA GAATA	T	gap				SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.[pcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1

2174	cg43918705	1152	CAACATTTTAGG ATTAGGGATAC C[T/C]GCTTCCTC TTTTCTTGCAA GTTTT	T	C			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.lpcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2175	cg43918705	1728	ATCTAGTTAAATT TCCCATTGTGAT T/AJTATTTTCTT GAATACTTTTTC AT	T	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.lpcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2176	cg43918705	2392	AGGCCAGCAAAT ACAGAGGTGGTT T[G/A]ATCAAACA GCTCTAGTATGA AGCAA	G	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.lpcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1

2177	cg43918705	2839	ATTCAGTGATGT TGGATGTATATC A[A/G]TTATTAG TAAATAATCTCAA TAAA	A	G				SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa. [pcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2178	cg43965859	147	GCTGCGCTCAG GCCAGGAGGAC CTC[T/G]AATCAG GACGGGGTGGG GCGGGGCT	T	G				SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P00568 ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE) - HOMO SAPIENS (HUMAN), 194 aa.	2.40E-98	9 (9q34.1)
2179	cg43965859	73	TTTAGTGCTCAG CTGTCCATGAAA A[C/A]AGGATAAG CGGCTTCCTCCG TCTGT	C	A				SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P00568 ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE) - HOMO SAPIENS (HUMAN), 194 aa.	2.40E-98	9 (9q34.1)
2180	cg43952004	165	GGGAGTCTTGA GGCTGAGTGCG TA[ap/G]CTTCA AATCCAGCACTA ATTCTCTCA	gap	G				SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14
2181	cg43952004	229	GGTCTTCATAGA TTGGTGGCTTGA G[C/gap]CCTGCA ATTAATTATAATC CCTTGC	C	gap				SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14
2182	cg43952004	231	TCTTCATAGATT GGTGGCTTGAG CC[C/gap]TGCAA TTAATTATAATCC CTTGCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14

2183	cg43970923	1814	CCCAGCTATCCC CGCTCTGACCTT G[ap]/G[ATTTTC ATTCTTATGTTTT TCCTCT	gap	G			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:P97841 GUANYLATE KINASE ASSOCIATED PROTEIN - RATTUS NORVEGICUS (RAT), 666 aa.	1.40E-92	
2184	cg44924345	157	TTTTGTCGTTCC AAAGTACAAAA G[ap]/A[AAAAAA AAATCAAAGGCA TTTCATC	gap	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P52623 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - MUS MUSCULUS (MOUSE), 260 aa (fragment).	7.10E-92	1
2185	cg44924345	166	TCCAAAGTACAA AAAGAAAAAAA A[ap]/A[TCAAAG GCATTTTCATCTC CATGGTG	gap	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P52623 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - MUS MUSCULUS (MOUSE), 260 aa (fragment).	7.10E-92	1
2186	cg43966625	652	CACAGCGGCGG GGAGCGGCGG TGG[A/G]GGGG CGGTGCTGGGC CCAGGGCCG	A	G			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE-ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.[pcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-89	17
2187	cg43266014	219	ACGTGGAGGATC ACTCGGTGGATA A[A/T]TAAGGATA AGTTGAGCGAG GGCGIG	A	T			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P23919 THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE) - HOMO SAPIENS (HUMAN), 212 aa.	1.00E-87	
2188	cg43983647	440	AAATTCCTTCTCT TCTCCTGAACTG C/TTGACTTTCAA AAATTCACAGAA TGA	C	T			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q62920 PROTEIN KINASE C- BINDING PROTEIN ENIGMA - RATTUS NORVEGICUS (RAT), 520 aa (fragment).	1.10E-86	4

2189	cg43919577	1068	ACAAGCAGTGCA CAGTGGCCGG CA[G/gap]GTACT TAAGTACCTTAT CCTAATCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2190	cg43919577	1069	CAAGCAGTGCAC AGTGGCCGGC AG[G/gap]TACTT AAGTACCTTATC CTAATCCT	G	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2191	cg43919577	117	GACTTTACATTTA CAAGTAGAAACA A/GICATGTGTTA TCTGTGGGTAAG GTAG	A	G			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2192	cg43919577	416	TTAAGAACAGCA TTCCTTTTGGAC A[G/A]TATGTCAT AGACCCCAATTTT TAATA	G	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2193	cg43971367	2030	GAGCGGCAGGA GAACGTCTGGAG GC[G/gap]GCACT GTTGCCGATCCG GGTCTGGA	G	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P54352 ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 517 aa.	1.60E-75	
2194	cg43980968	1675	CCCAGTGCCAC AGGTGGCAGGA GC[C/gap]TGTCC AGGACTCTGCA TTGCTGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P27515 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 501 aa.	9.50E-75	

2195	cg43984445	247	AGGGAGCCCG ATCACAGCCTGA AC[A/T]TCATGGT ATTGGTTACAGA TTCCTT	A	T				SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q16854 DEOXYGUANOSINE KINASE PRECURSOR (EC 2.7.1.113) (DGUOK) - HOMO SAPIENS (HUMAN), 277 aa. lpcis:SPREMBL-ID:Q16854 DEOXYGUANOSINE KINASE (EC 2.7.1.113) - HOMO SAPIENS (HUMAN), 277 aa.	8.70E-73	2
2196	cg43246312	890	CGTGAATGGCCA GAGCTACTCTTC A[A/C]TTGCTGAA CAATGTCAAAA GAATT	A	C				SILENT- NONCODI NG	kinase	Human Gene Similar to SPREMBL- ID:Q90269 INTRACELLULAR TYROSINE KINASE DOMAINS OF PLATELET-DERIVED GROWTH FACTOR RECEPTOR SUBTYPE ALPHA - BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO), 457 aa (fragment).	4.20E-62	11
2197	cg43246312	939	TTGACACTTGCT GAACAAATCTTT A[A/C]AAGTCAGA ACTTCTGATGGA TTAAA	A	C				SILENT- NONCODI NG	kinase	Human Gene Similar to SPREMBL- ID:Q90269 INTRACELLULAR TYROSINE KINASE DOMAINS OF PLATELET-DERIVED GROWTH FACTOR RECEPTOR SUBTYPE ALPHA - BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO), 457 aa (fragment).	4.20E-62	11
2198	cg43988142	201	GCCCCGACCCA GCCCCCTTAAGC C[A/G]GCCAGGC AGGGTCCCCCG ACACCT	A	G				SILENT- NONCODI NG	kinase	Human Gene Similar to SPREMBL- ID:O09132 A6 PROTEIN TYROSINE KINASE HOMOLOG - MUS MUSCULUS (MOUSE), 350 aa.	3.00E-61	3
2199	cg43988142	386	GTGGCAGGGAG CGGAAGGTGGG CAG[C/gap]CCCA CAGTCCACACGT GGCCGGCCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene Similar to SPREMBL- ID:O09132 A6 PROTEIN TYROSINE KINASE HOMOLOG - MUS MUSCULUS (MOUSE), 350 aa.	3.00E-61	3

2200	cg43918784	361	AAACGGGTAAC GTACCTGTTAA TTC/AJTCCTGGT GGCAACTTTTAA AATCT	C	A				SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2201	cg43918784	509	TCCATAAATAA TTAACATTTTCA A/GJGTAGAAAT CTTGAAGTTCTA AAGG	A	G				SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2202	cg43918784	706	AACTCTTCGGT ACAATGGATTCC TTC/TJGGTTTCTG ATTTGTGGGTAT CCGAA	C	T				SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2203	cg43979971	1998	TAAAAAAATAAT TTTTAAACTTA A/CJAACACTACG AGATCTGATTTA TTCT	A	C				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2204	cg43979971	285	GCCGCGACAGC AGCGCCGGCCCC CGG[gap/C]AGCT CCCGCGGCCCC GGCCCCGGCC	gap	C				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2205	cg43979971	321	GCCCCGGCCCC GGCCCCGGCCCC CGG[C/gap]CCCG GGGCACAGGC TGTCGGCTGG	C	gap				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2206	cg43979971	324	CCGGCCCCCGG CCCGGCCCGCG CCC[C/gap]GGCG GCACAGGCTGTC GGCTGGCCCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2

2207	cg43928048	1310	CTAAACTATATAT GTATTTTTCCTCA T/CJAGGAAAGCA CAAGGAGAAGAC AGAA	T	C				SILENT- NONCODING	kinase	Human Gene Similar to SWISSPROT- ID:P20505 30 KD PROTEIN KINASE HOMOLOG (EC 2.7.1.-) (PROTEIN B1) - VACCINIA VIRUS (STRAIN COPENHAGEN), 300 aa.	5.30E-55	
2208	cg43105476	234	AGATGTTGCTTA AATATATTCATAA [G/A]CCTGTTGTA AGATTTTCACTTA TGC	G	A				SILENT- NONCODING	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
2209	cg42714770	146	GTCATGAAGTCG ACAGCTTCCGGA G[G/gap]CTGCGA GGCTCGCAAGAA ATGCCCA	G	gap				SILENT- NONCODING	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16- INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)
2210	cg42714770	317	GACATTTACGGT AGTGGGGAAG GC[A/T]TATATCT ACGTTAAAGGC AGGACA	A	T				SILENT- NONCODING	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16- INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)
2211	cg42714770	450	TCGGTGACTGAT GATCTAAGTTTC C[G/C]GAGGTTT CTCAGAGCCTCT CTGGTT	G	C				SILENT- NONCODING	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16- INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)
2212	cg42714770	454	TGACTGATGATC TAAGTTTCCGGA G[G/gap]TTTCTC AGAGCCTCTCTG GTTCTTT	G	gap				SILENT- NONCODING	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16- INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)

2213	cg42714751	61	AGATGGGCAGG GGGCGGTGCGT GGG[G/T]CCCAG TCTGCAGTTAAG GGGGCAGG	G	T			SILENT- NONCODING	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16- INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	2.60E+53	9 (9p21)
2214	cg44021336	191	ACACACCTGTGG GGCAGCTGAAC A[G/A]AAGAAG GATGCCCCAGGAT AGCTAT	G	A			SILENT- NONCODING	kinase receptor	Human Gene SWISSNEW-ID:P35590 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1138 aa. pcis:SWISSPROT-ID:P35590 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1138 aa.	0.00E+00	1
2215	cg43241731	301	GAATCTGCGCCC CAGAGAGTCCC GG[G/gap]AGCGC CGCCGGTCGGT GCCCCGGCGC	G	gap			SILENT- NONCODING	kinase receptor	Human Gene SWISSPROT-ID:Q16620 BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B) - HOMO SAPIENS (HUMAN), 822 aa.	0.00E+00	9
2216	cg43917080	209	GATACACCGGGT GTGGGATTACA A[A/C]TAGGACCA ACAATGTGTGCG GGGCA	A	C			SILENT- NONCODING	kinase receptor	Human Gene SPTREMBL-ID:Q01974 PROTEIN-TYROSINE KINASE TRANSMEMBRANE RECEPTOR ROR2 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 943 aa.	0.00E+00	9
2217	cg43917080	232	AAATAGGACCAA CAATGTGTGCGG G[G/gap]CACAGA CGGCTGCCTGT GGGTCTGT	G	gap			SILENT- NONCODING	kinase receptor	Human Gene SPTREMBL-ID:Q01974 PROTEIN-TYROSINE KINASE TRANSMEMBRANE RECEPTOR ROR2 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 943 aa.	0.00E+00	9
2218	cg44021449	3336	CACACAGTAGCT GTTAGCCACACAG G[G/gap]AGAGGG CATCGGGGCCAT TTGGCCG	C	gap			SILENT- NONCODING	kinase receptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15

2219	cg44021449	3359	GGCAGAGGGCA TCGGGGCCATT GG[C/gap]CGGCT CTGGTGGCCACT GAGCTGGC	C	gap			SILENT- NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15
2220	cg44021449	4345	CTGTTAGGACA TTTCCAAGCTGT TTAGJGTGCTGT TTAAAATAGAAAT AAAA	A	G			SILENT- NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15
2221	cg43322545	2984	GGGAAACTCC ACCTCCCACT T[C/]CCACCCCA CGCCTTATCCCC ACTTG	C	T			SILENT- NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. [pcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.]	0.00E+00 (19q13.1)	19
2222	cg44024023	641	CTGCTCCAGG GATGCTGGGAC GTG[ap]GJCGGT GCCTGCTAAGTG CTCAGCTGT	gap	G			SILENT- NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29317 EPHRIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 976 aa.	0.00E+00	
2223	cg44024023	669	GTGCCCTGCTAAG TGCTCAGCTGTG T[G/ap]CGTCTC GCAGGGAAGA GGCCCCAG	G	gap			SILENT- NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29317 EPHRIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 976 aa.	0.00E+00	

2224	cg44025829	1915	AGGAAGATTGACGTTGTTGTCAT T[G/T]TCCAGCTG GGACCTAATGCT GGCCT	G	T			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:Q04771 ACTIVIN RECEPTOR TYPE I PRECURSOR (EC 2.7.1.-) (ACTR-I) (SERINE/THREONINE-PROTEIN KINASE RECEPTOR R1) (SKR1) (ACTIVIN RECEPTOR-LIKE KINASE 2) (ALK-2) (TGF-B SUPERFAMILY RECEPTOR TYPE I) (TSR-I) - HOMO SAPIENS (HUMAN), 509 aa.	7.90E-283	2
2225	cg43263845	277	GAAGACCCAGG GAACTGGATATC TA[G/T]CGAGAAC TTCCTCCGGATT CCCCGG	G	T			SILENT- NONCODING	kinasereceptor	Human Gene TREMBLNEW-ID:G247985 ACTIVIN RECEPTOR, ACTRIIB=TRANSMEMBRANE PROTEIN SERINE KINASE - XENOPUS LAEVIS, 510 aa.	3.30E-204	2
2226	cg43954819	1423	GTGAGCATCCTG GCAGGTGCCCC AG[G/T]ATGCCAC GCCTGGAAGGG CCGGCTT	G	T			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2227	cg43954819	1573	GTCTCACTCGTT CTGTTACCCAGG G[C/gap]TCTGCA GCACCTCACCTG AGACCTC	C	gap			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2228	cg43954819	1808	CTGGGGAAAGG GCTGGCTGCAAT TG[C/gap]AGCTC ACTGCTGCTGCC TCTGAAAC	C	gap			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2229	cg43954819	2795	TGCAAAAATAAC CAAGTCCTCCGA A[G/gap]GCATCT CACGGAACCGTA GACTAGG	G	gap			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13

2230	cg43954819	2798	GCAAAAATAACC AAGTCCTCCGAA G[G/gap]CATCTC ACGGAACCGTAG ACTAGGA	G	gap				SILENT- NONCODI NG	kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2231	cg43954819	46	CGGAAGGCGCG GAGCTGGGAGT GGC[A/T]CAGCC ATGGCTGTGAGA AGGGACTC	A	T				SILENT- NONCODI NG	kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2232	cg43954819	48	GAAGGCGCGGA GCTGGGAGTGG CAC[A/C]GCCAT GGCTGTGAGAA GGGACTCCG	A	C				SILENT- NONCODI NG	kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2233	cg43989555	1630	AGGCCAGCTG CCTTGGGCTGG GGC[C/gap]TGCG GAGGGGAAGCC CACCCACAAT	C	gap				SILENT- NONCODI NG	kinaserec eptor	Human Gene Similar to SWISSPROT- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa. pcis:SPTREMBL- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa.	1.20E-99	11
2234	cg43980494	897	CTCACAAGTCCC TGGGAAGACAG GG[C/T]ATGGGC TTACAGAGAGGA GAGGGGG	C	T				SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2235	cg43980494	1446	TGGTCCGAAATA TAAGCCGAGCTC A[G/T]CATCTTGC CACACACGTGAC ATGGC	G	T				SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16

2236	cg43980494	376	GGGGACACAGG AACACGATGACA TG[G/gap]CCAGG GCCACAACCTCT TCTGTCTGT	G	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2237	cg43980494	383	CAGGAACACGAT GACATGGCCAG GG[C/gap]CACAA CTTCTTCTGTCTG TGGGGAAG	C	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2238	cg43980494	384	AGGAACACGATG ACATGGCCAGG GC[C/gap]ACAAC TTCTTCTGTCTGT GGGGAAGA	C	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2239	cg43980494	481	AGGGGGACACT GGCTGCATTCCC CC[G/C]CCCCCA GGAAGCACCTCT AGGCCCT	G	C			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2240	cg43980494	489	ACTGGCTGCATT CCCCCGCCCCC AG[G/gap]AAGCA CCTCTAGGCCCT GGACCCCT	G	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2241	cg43980494	515	AAGCACCTCTAG GCCCTGGACCC CT[C/G]GCTCAC CCTGGCCCCCTAA GACTCCA	C	G			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2242	cg43980494	559	GACTCCATCTCT TCTCTGCCCTCTG G[C/gap]CCTCCT GGCTCTTCTCTCC TGCTCCC	C	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16

2243	cg43980494	648	GTTCAGGGCCTG ACCCCAACCCCC C[<i>gap</i>]/GJATACCA CCTTATGAAGGT ACAACCT	<i>gap</i>	G			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2244	cg43980494	768	TCCTTCCTCTCC TCCCTCCCCCTG G[A <i>gap</i>]/AAAAA AAAAAAGGAAA AGAAAGC	A <i>gap</i>	<i>gap</i>			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2245	cg43980494	781	CCTCCCCCTGGA AAAAA A[<i>gap</i>]/AGGAAA GAAAGCACCAAC TCCCCGG	<i>gap</i>	A			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2246	cg43925424	232	GCGGGGCGGTA GCTCCGGCGCC CCT[C/A]GCTGGT GACTGCTGGC CGTGCCIC	C	A			SILENT- NONCODI NG	kinesin	Human Gene SWISSPROT-ID:Q07868 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	1.90E-304	14
2247	cg43987378	2380	TTTTTTTAAATA AAGGTTTATTAT G/C/CATTGCCC AAGAAGGCAGAT ACTT	G	C			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.50E-254	6
2248	cg43088603	1956	AAATCCATTTC AAATTTATTGATG [G/C]ATTCATGTT GTTCTTCTTTTAT TTT	G	C			SILENT- NONCODI NG	kinesin	Human Gene Similar to SWISSPROT- ID:P33174 KINESIN-LIKE PROTEIN KIF4 - MUS MUSCULUS (MOUSE), 1231 aa.	1.70E-79	4 (4q24)
2249	cg44002977	231	GCTAGCTACTCT AGAGGACCACA GG[G/A]TGCAGA GAGGGTGTCTCT GAGGGTCC	G	A			SILENT- NONCODI NG	kinesin	Human Gene Similar to SWISSPROT- ID:Q07868 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6

2250	cg44002977	406	TGTGAGGGGCTGT GGGGGTGGGG GA[C/gap]CCAGC AGACCTGGGG CCGGGTTGA	C	gap				SILENT- NONCODI NG	kinesin	Human Gene Similar to SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6
2251	cg43946310	3902	ACTCCTTGCTTC CTGATGCTGGGC A[A/gap]TGAGGC AGATAGCACTGG GTGTGAG	A	gap				SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2252	cg43946310	4427	AGATTGCATTTT ATTAAAGCATTT C/GJCTACCAGCA AAGCAAATGTTG GGAA	C	G				SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2253	cg43946310	4440	ATTAAAGCATTT CCTACCAGCAAA G[C/GJAAATGTTG GGAAAGTATTTA CTTT	C	G				SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2254	cg43983535	143	GAATTAGCACCA TCTGAATACAGA A[G/AJGAATTCTA TGATACATGCACA AATTA	G	A				SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0.00E+00	6 (6q22)
2255	cg44009224	5282	CTCCCCAGCTCG AGATCATCTTC A[C/AJTCAGGACA CAAACCCAGACAG GTTTA	C	A				SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0.00E+00	

2256	cg43958558	283	AGGTTTAGATTC TTTTTTTTTTTTTTT gap/TAAATCTGCC CCTTTCAGATTA TATCA	gap	T				SILENT- NONCODI NG	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa; pcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)
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2257	cg43958558	283	AGGTTTAGATTC TTTTTTTTTTTTTTT gap/TAAATCTGCC CCTTTCAGATTA TATCA	gap	T				SILENT- NONCODI NG	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.lpcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)
2258	cg43970746	127	GGGAGGAGGGG AAGTGAGGCC CAG[C/gap]CCCCA CAACCCCTCCCC GCCCACCCCC	C	gap				SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:P48634 LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) - HOMO SAPIENS (HUMAN), 2142 aa.	0.00E+00	3
2259	cg43921887	335	CATTCAGCATGA TTCCACCTGGGC A[T/C]GAGCTGG AAAAGAGCTCAG TCITCA	T	C				SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa.	0.00E+00	14
2260	cg43298284	1921	TGAGTTGCACAG CTATGAAGGCTG TT[G/A]CACTGCAC GAATGGAAGAG GCACCT	G	A				SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6

2261	cg43298284	2363	CGGTGGCTCGC GCCTGTGGTCCC AG[C/gap]ACTTT GGGAGGCCAAA GCGGTGCTG	C	gap			SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2262	cg43298284	2394	GGGAGGCCAAA GCGGTGCTGAG ATT[G/A]CAGGTG TGAGCCACCCTG CCCAGCC	G	A			SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2263	cg43298284	2506	ACTTGGCTGCAT AAATGTGGTACA A[G/C]CATTCTGT CTTGAAGGGCAG GTGCT	G	C			SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2264	cg42479188	1420	TCCCCTGAGACC TTACTCCTTCCA G[C/T]CCCAAATC ATTACTTTTCTG TGGT	C	T			SILENT- NONCODI NG	MHC	Human Gene Homologous to SWISSPROT-ID:P13765 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DO BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 273 aa.	3.40E-147 (6p21.3)	6
2265	cg43966144	99	CACATCATTTGGG GGGTCAAGGGA CC[C/gap]GGGCA ATATAGTATTCT GCTCAGTG	C	gap			SILENT- NONCODI NG	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147 (6p21.3)	6
2266	cg39425214	678	GGCAGCGGGAC CCGCCAGAGCC CTC[C/G]ACCCG GGAGAGTCCCA GGCGCCTTT	C	G			SILENT- NONCODI NG	MHC	Human Gene Similar to SWISSPROT- ID:P16215 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CH28 ALPHA CHAIN PRECURSOR - PAN TROGLÖDYTES (CHIMPANZEE), 346 aa.	4.70E-55	
2267	cg42928872	3016	GACAGGGGTTT CTTCTGGGCATT AC[A/G]TCGCATA GAAATCAATAAT TTGTGG	A	G			SILENT- NONCODI NG	misc_cha nhel	Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	11

2268	cg42928872	3073	GGATCTGTGTTT TAATGAGTTTCA C[A/G]GTGTGATT TTGATTATTAATT GTGC	A	G			SILENT- NONCODI NG	misc_cha nnel	Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0	11
2269	cg43984759	158	CGTCGAGTGACA GCGGCCTGGG GG[G/gap]CAGGG GGGGCGGGGGC GGCCGGGATC	G	gap			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2270	cg43984759	3297	GCTACAGGGAAT GATTGGTCATGG G[G/gap]AAGTCT CTGGGCCATAAG CCACGAT	G	gap			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2271	cg43984759	3324	AGTCTCTGCGCC ATAAGCCACGAT C[C/A]CAGCGCA AAACCCTTACTC AAATGT	C	A			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2272	cg43984759	3379	ATTGACTTCGGT ATTCATAGTAC C[T/C]GAGATTTT ATTTGAGATAC CATCA	T	C			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2273	cg43984759	3388	GGTATTTTCATAG TACCTGAGATTT T[AT]TTTGGAGA TACCATCAGGGT GAGTT	A	T			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20

2274	cg43957213	130	GGCAAGATTCAG TCCCTGACCGCA A[G/gap]GCACTT ACAGTCTAGTTG GGAAGGG	gap			SILENT- NONCODI NG	misc_cha nnel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcis:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcis:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669-aa	0	1 (1p36.1)
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2275	cg43957213	131	GCAAGATTCAAGT CCCTGACCGCAA G[G/gap]CACTTA CAGTCTAGTTGG GAAGGGA	G	gap			SILENT- NONCODING	misc_cha nnel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcis:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcis:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa.	0	1 (1p36.1)
2276	cg42684570	221	AACCTAAAAGCA AAGTTGTGAAAG A[G/A]AAGCAGAA TTCCAAAGTCCC TTATT	G	A			SILENT- NONCODING	misc_cha nnel	Human Gene SWISSPROT-ID:P46098 5- HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN- GATED ION CHANNEL RECEPTOR) - HOMO SAPIENS (HUMAN), 478 aa.	1.8E-260	11 (11q23.1)
2277	cg40367355	1773	AGGGCAATTGGA ATAATGTCCTGT T[A/G]GATAAACA GACATTTAGCAA TGCTG	A	G			SILENT- NONCODING	misc_cha nnel	Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa.	4.10E-199	21
2278	cg44963814	1142	GGGGCCAGCCC CTCCCCGCCCTCC TC[C/T]CTGCCTG GCGGCAGGGGT CGCGATG	C	T			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)

2279	cg44963814	1152	CCTCCCCGCCTC CTCCCTGCCTGG C[G/gap]GCAGGG GTCGCGATGATG GGCTGGA	G	gap			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2280	cg44963814	1220	TTCTGGGACCCA CTCCGACTCCCC C[gap/C]TCCCCG GCATCATTTCCC CTCCCGC	gap C	C			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2281	cg44963814	1285	CCTGGGGTCCC CCCTCCCTGTAA TG[C/G]ACTCCTG CCCCGGCCCAA CCTCGCC	C	G			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2282	cg44963814	797	CCGCCTCAAGGA AGAGCCAGCCG TA[A/gap]TGGGG ACTCTCCAGGCA CCGCCTGC	A	gap			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)

2283	cg44963814	805	AGGAAGAGCCA GCCGTAATGGG GAC[T/C]CTCCAG GCACCGCCTGC CCCCAGCG	T	C				SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa. pcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2284	cg44963814	854	GTGGGGGTGGC CACTCCTGGGCC CC[ap/C]AGAAA GCCTCAGAGTCC TGCCGACG	gap	C				SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa. pcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2285	cg43328088	392	TGCTTGAGGAAG GTCTTGAGAAA C[G/C]CTCACTCC CTCTAAACTTTTA GCTT	G	C				SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SWISSPROT- ID:P35526 CHLORINE CHANNEL PROTEIN P64 - BOS TAURUS (BOVINE), 437 aa.	2.70E-99	1
2286	cg43309398	221	GCTCTTGGTCCA GCTGGTCGCGG GG[G/ap]CGCTG CGGTCTAGCCG GGCGCGGCG	G	gap				SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.10E-67	15 (15q24)
2287	cg43309398	236	GGTCGCGGGG CGCTGCGGTCTA GC[C/ap]GGCG CGCGGGCGGC GCGCAGAGA	C	gap				SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.10E-67	15 (15q24)
2288	cg43978512	1658	ATCCTTCCCCG CATGTTTCATAGA C[G/A]GACAGAC TTCTACTTTTCAGT CGCTA	G	A				SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SWISSPROT- ID:Q15700 CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN 110) - HOMO SAPIENS (HUMAN), 870 aa.	6.20E-53	10

2289	cg43978512	1702	GTCGCTAGAAA GAGCTGAGTCTG G[C/T]GTCCCCTC AGGCGGCCAGC TGCAGT	C	T			SILENT- NONCODI NG	misc_cha nnel	Human Gene Similar to SWISSPROT- ID:Q15700 CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN 110) - HOMO SAPIENS (HUMAN), 870 aa.	6.20E-53	10
2290	cg43013507	1808	TCGCACGCCCG AGGCCGGCCT CCG[G/gap]TCCC GCTTCCAGTTTC CTTGAAGCG	G	gap			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2291	cg43013507	1987	GATTCAAGACAG TCTTTTGTAAC G[G/gap]CACACG CCCACGCCCTTC CTCTATA	G	gap			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2292	cg43013507	2037	AACCCCCAGAGA CAGGCTGGGC AG[C/gap]GCCAA GGCGGTCTCGC GCGGGACTT	C	gap			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2293	cg43013507	2089	TACAGCAGTGTC TTATCCAGCAGC C[gap/G]ATTGGA TGTAACGTTTTG CTTTGGG	gap	G			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2294	cg44929972	1659	TTAAACTCTAGA CACAGTTTAT CTT/CJTGGAATAA CTTAGATAACTTT TGTA	T	C			SILENT- NONCODI NG	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.70E-214	7

2295	cg44929972	2199	GTAACACTGATT TTATCTGCTGTA TIG/AJAGACTTTG TGCATTTTACTTT GAAA	G	A				SILENT- NONCODI NG	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.70E-214	7
2296	cg43940300	227	CTTTGCTTTTCT GTCAGAATAGCT T/CACAAACATA CTAGTACTATTTA TTT	T	C				SILENT- NONCODI NG	ngf	Human Gene Similar to SWISSNEW- ID:P78543 BTG2 PROTEIN PRECURSOR (NGF-INDUCIBLE ANTI- PROLIFERATIVE PROTEIN PC3) - HOMO SAPIENS (HUMAN), 158 aa.[pcIs:SWISSPROT-ID:P78543 BTG2 PROTEIN PRECURSOR (NGF- INDUCIBLE ANTI-PROLIFERATIVE PROTEIN PC3) - HOMO SAPIENS (HUMAN), 158 aa.[pcIs:SPTREMBL- ID:P78543 NGF-INDUCIBLE PC3 ANTI- PROLIFERATIVE PROTEIN - HOMO SAPIENS (HUMAN), 158 aa.	3.10E-82	1
2297	cg44022292	2240	ATGGTTGCCATG ATCTACCGCTTT TIG/gap]CGCCCC TGCTGACTCCGG CGTCGGG	G	gap				SILENT- NONCODI NG	nuc_rec pt	Human Gene SPTREMBL-ID:Q15625 STEROID RECEPTOR (TR2-11) - HOMO SAPIENS (HUMAN), 603 aa.	0.00E+00	12
2298	cg43971768	182	TAAGAAGAAAGA GAAATGGTTAAG T[A/G]CTTAAACT GTCCACTGACAC CTGCT	A	G				SILENT- NONCODI NG	nuc_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2299	cg43971768	23	TTTTTTTTTGT CAGAGCAAAG[GT] TCATTTTATTGT AATGAAATTTTA	G	T				SILENT- NONCODI NG	nuc_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2300	cg43971768	277	TTGTTAGATGAA GCAAGCCGTCCT G[C/T]TCCCGCA CAGCCTGTGAAA CCTCCA	C	T				SILENT- NONCODI NG	nuc_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15

2301	cg43971768	330	TTGCCCACTTTCA AGGTCAGTGCCC C[A/G]CAGAGCC TGGCCTGTTGTT GACCAT	A	G				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2302	cg43971768	343	GGTCAGTGCCC CACAGACCCTGG CC[T/C]GTTGTTG ACCATAACACTA GCTTIG	T	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2303	cg43991048	204	TAATAATTTTTC GTGCTACTAATG gap/A]AAAAAAA AATTAAAGCCTG CACTG	gap	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
2304	cg43991048	214	TCAGTGCTACTA ATGAAAAA A[gap/A]TTAAAG CCTGCACTGGAA ATTJACA	gap	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
2305	cg43921419	2593	AACCCCGGCCAT CCATCACAAAGG C[gap/C]AACCTG GGAGAGTAACTA TTTTGGG	gap	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0.00E+00	19
2306	cg43921419	3208	ACAATCGGCCCA TCACCGAGCCCC C[C/gap]GGCGCC AGGCCAGCTC CCCCTCTG	C	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0.00E+00	19
2307	cg43249083	282	TTTGCACCGGGA GCTCCAGATTGG C[C/T]ACCCCGC AGCGCTGCGGA GCCGGCA	C	T				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P20393 V- ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00 (17q11.2)	17

2308	cg43992723	5608	TGCTCTTTCAAAA GACACCTGCCTT A[gap/G]TGCAAG GGGAAACCTGTG AAAGCTG	gap	G				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0	4 (4q31.1)
2309	cg43992723	5636	CAAGGGGAAAC CTGTGAAAGCTG CA[G/C]TCAGAG GGAGGAGTTTTT CTTACAT	G	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2310	cg43992723	5651	GAAAGCTGCAGT CAGAGGGAGGA GT[T/C]TTTCTTA CATAATTGCAA TTTCAG	T	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2311	cg43992723	5848	GTTTCAGACTTAG TTTTTATAAAATG [G/A]GAATTCTGA CTTACTTAACCA GGT	G	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2312	cg43992723	6085	TGGTACAGTTCA TAATTCACCAA A[gap/A]GTTTCATA TAATTTAAAGAA CACTA	gap	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2313	cg43992723	6102	TCACCAAAGTT CATATAATTAA [G/A]AAACACTAA ATTAGTTTAAAT GAA	G	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2314	cg42507196	172	TCGTCCTGGGA CTGCACCTGCTC C[C/gap]GTCGGG TCGCCCCGGCTTC ACCGGAC	C	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:P03372 ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.lpcis:SWISSPROT-ID:P03372 ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.	0.00E+00	6 (6q25.1)

2315	cg43961967	2285	AAGACCACCTTC CCTTCCTCAGCA G[G/gap]CCAAAC ATGGCCAGACTC CCTTGCT	G	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2316	cg43961967	2383	TCCTTTGAGGCC CCAACTCAAGTG T[gap/G]CACCTC CTTCCCAGCTC CCCCAGG	gap	G				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2317	cg43961967	2414	CTTCCCCAGCTC CCCCAGGCAGA AA[gap/A]TAGTT GTCTGTGCTTCC TTGGTTCA	gap	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2318	cg43961967	2484	TGCTTCTACTGT GACACTTATCTC A[gap/G]CTGTTT ATAATTAGTCGG GCATGA	gap	G				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2319	cg43961967	455	TGCCACTCCCTG GCCCCCTCCACC G[G/C]CCGCCCC CCTTGGGGCGG AGGGCAT	G	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2320	cg43961967	469	CCCTCCCACCG GCCGCCCCCTT GG[G/C]GCGGAG GGCATGGTGTGA AAGGCCA	G	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2321	cg43961967	474	CCACCGGCCGC CCCCCTGGGG CGG[A/gap]GGGC ATGGTGTGAAAG GCCAAGTGC	A	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)

2322	cg43961967	476	ACCGGCCGCC CCCTTGGGGCG GAG[G/C]GCATG GTGTGAAAGGCC AAGTGCTG	G	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2323	cg43961967	532	GGTATCATGGGT GCTGTGCCCTAG G[G/gap]CCTGGG TGGCAGGGGGT GGGTGGCC	G	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2324	cg43917579	1583	CTGCCTGGCCTG TTTGGACTTTGG G[G/gap]CACAGC CTGTCACCTGCTC TGCCCTAA	G	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2325	cg43917579	1745	CGCCTCCCACCA GGCTCTCAGG AC[A/G]CCCCTGC CACACCCACG GGGCTTGG	A	G				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2326	cg43917579	4478	TCCCGTGGGG CACCCAGGAGG GCC[C/gap]TGCC GGAATGTGCAGC CTGTGGGTA	C	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2327	cg43917579	4527	GTAGTCGGCTG GTGTCCCTGTGG TG[G/C]AGCTGG GGTGCCTGATCT GGTGCTC	G	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2328	cg43917579	50	GCCCGCCGCC GCTGCCCTGCGC CGC[A/C]GGCCG GGGATGAGTTAG TCGCAGAC	A	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9

2328	cg43917579	4951	GCATCTGGAAG GTAAAAA A[A/gap]TCTATTT TTGTACAAATGT AATTTT	A	gap			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2330	cg43917579	58	CCCGCTGCCTG CGCCGCAGGCC GGG[G/C]ATGAG TTAGTCGCAGAC AAGGACAC	G	C			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2331	cg43917579	77	GCCGGGGATGA GTTAGTCGCAGA CA[AT]GGACACC AAACATTTCTG CCGCTC	A	T			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2332	cg43987181	253	CACACAAAAAAG TGCATCTAAATG A[T/gap]TTTTTTT TTTAAAAAACAAAT GTCTT	T	gap			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.lpcis:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

2333	cg43987181	2434	GAGTTCACTGGG ACTCTTCCCTCC TTC/TGGCGTGG CGTCATACGTGG CCCTCA	C	T				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.lpcIs:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6
2334	cg43987181	264	GTGCATCTAAAT GATTTTTTTTTT ATTJAAAAACAAT GTCCTTAATTCCT CAT	A	T				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.lpcIs:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

2335	cg43987181	747	TTTCATAAAAA GACAAAAGCATA A[T/AT]TGAGAAAT TAGAGGGATTTT AGTTA	T	A				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa. pcds:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6
2336	cg43315956	1813	GCCAAAGGGG GACCAGAAATCC CC[C/gap]ATGCG AGCTGTTTGAGG ACTGGGAT	C	gap				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2337	cg43315956	3757	TACAAACTTTTC CAATTTTAAAAA [gap/A]TCAGCCA TTTCATGCAACC AGAAAC	gap	A				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2338	cg43315956	4535	CATGCTGATAT TGGGATTTTTTT [T/gap]CCAGCCT TCTTGATGCCAA GGGGCT	T	gap				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2339	cg43315956	4709	AGTTCTCATTAA GCACTAGTGAA [gap/T]TTTTTTT TTTGATATATTAG CAAG	gap	T				SILENT- NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3

2340	cg43315956	4720	AAGCACTAGTGG AATTTTTTTTTT gap/T]GATATAATT AGCAAGTCTGTG ATGTA	gap	T				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.30E-244	3
2341	cg43935583	1599	TGTCAGCCAAAT TTGGAGGTCAAG C[G/A]TAATGTCC TTCTGATAAATAA AGCC	G	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2342	cg43935583	1605	CCAAATTGGAG GTCAAGCGTAAT G[T/C]CCTTCTGA TAAATAAAGCCC TTGCT	T	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2343	cg43935583	1646	AGCCCTTGCTGA AGGAAAAGCAAC C[T/A]AGATCACC TTATGGATGTCG CAATA	T	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2344	cg43935583	1658	AGGAAAAGCAAC CTAGATCACCTT A[T/C]GGATGTCG CAATAATACAAA CCAGT	T	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2345	cg43935583	1666	CAACCTAGATCA CCTTATGGATGT C[G/A]CAATAATA CAAACCAAGTGTA CCTCT	G	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2346	cg43949686	415	AAACAGAAGCAG ATAAAAAAAAAA A[ap/A]GATGCA GGACTCCTTCAG TTCTTCA	gap	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.40E-167	

2347	cg43949686	6483	TCGATGCGTATT CTGTGGCCGCC ATC/TTCGCGCAG GGTGGTGGTATT CTGTCA	C	T			SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.40E-167	
2348	cg43996179	140	TTTTGGTCACTG GTTTCATTTTTT [C/T]CTTGCTCTA AACCACCTCTTC TCTG	C	T			SILENT- NONCODI NG	nucl_rec pt	Human Gene Homologous to SWISSPROT-ID:Q14739 LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) - HOMO SAPIENS (HUMAN), 615 aa.	1.10E-120	
2349	cg43996179	266	GTGCTGGTGGAT GAGTGGGCACAT G[C/gap]CCCCAC CTGGGGTGGTG GAGCCGCT	C	gap			SILENT- NONCODI NG	nucl_rec pt	Human Gene Homologous to SWISSPROT-ID:Q14739 LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) - HOMO SAPIENS (HUMAN), 615 aa.	1.10E-120	
2350	cg43933695	3029	ATTTTCGCTTTTA ACAGAGCAGCTT [C/G]CTGCTAGC GGAGGCAGGC AATTAC	C	G			SILENT- NONCODI NG	nuclease	Human Gene SWISSPROT-ID:P54277 PMS1 PROTEIN HOMOLOG 1 (DNA MISMATCH REPAIR PROTEIN PMS1) - HOMO SAPIENS (HUMAN), 932 aa.	0.00E+00	
2351	cg44128653	618	CCTGGTTCAATC GATCCTCTGGCT T[C/gap]AGTGGC TGGGACTACAGG CATTTAT	C	gap			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa. pcls:SWISSPROT- ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.40E-203	19

2352	cg43944393	1834	AAGAGAGAGGG AGATAAAGGGG GA[G/T]ACAAAAG ATGTACAGAAAT GATTTC	G	T				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa. pc s:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2353	cg43944393	1869	GTACAGAAATGA TTTCCTGGCTGG C[C/gap]AACTGG TGGCCAGTGGG AGGTGATG	C	gap				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa. pc s:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2354	cg43944393	1971	AGAGAGCCACCA GGAAGGCGCAT CT[T/gap]AGCAG ATGGGAGGAACT GCTGAGAG	T	gap				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa. pc s:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2355	cg43944393	1977	CCACCAGGAAG GCGCATCTTAGC AG[A/gap]TGGGA GGAAGTCTGAG AGAAGATG	A	gap				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa. pc s:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11

2356	cg43944393	1989	CGCATCTTAGCA GATGGGAGGAA CT[G/A]CTGAGA GAAGATGGGCA GAAAGCTG	G	A			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa. pcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2357	cg43944393	297	CGAGCTTAGGAC CGCCTGCCCGG GG[C/gap]AACCC CGAACCAAGCTT TAGCCGCC	C	gap			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa. pcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2358	cg43944393	317	CGGGGCAACCC CGAACCAAGCTT TA[G/gap]CCGCC GAGGCCGCGTG TCCCAAAGG	G	gap			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa. pcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2359	cg43942083	400	GTTGAATAGGAG CCCTAACTGTAG TT[A]ACTTCTTT CACAGCAGGGA AGGAAG	T	A			SILENT- NONCODI NG	nuclease	Human Gene Similar to SWISSPROT- ID:P07898 RIBONUCLEASE PANCREATIC PRECURSOR (EC 3.1.27.5) (RNASE 1) (RNASE A) (RNASE UPI-1) (RIB-1) - HOMO SAPIENS (HUMAN), 156 aa.	9.20E-83	
2360	cg43943773	113	ATTTCATATGTAA CAAAGATAAGGA [C/T]GTGTGCAG GTATAAAACAGA GGCAG	C	T			SILENT- NONCODI NG	nuclease rh1b	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19

2361	cg43943773	197	CTCATTATCCCT GAGGGGTAGGG GC[G/C]GGGGAG GAGAGGAGTCA CAGGCAGT	G	C				SILENT- NONCODI NG	nuclease nhib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2362	cg43943773	228	GGAGAGGAGTC ACAGGCAGTTCA CC[C/A]ACACCTG GAAAATCGATGA CTTCAT	C	A				SILENT- NONCODI NG	nuclease nhib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2363	cg43943773	312	GAAGTCATGAGA AGAAGGCCCTTC TT[G/C]CCAGGG ATGATGTTTCTC AGTATC	T	G				SILENT- NONCODI NG	nuclease nhib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2364	cg42685908	176	TACAAATATTTT ACATTTAATAGT C/AJATGAAAAAG AAAAGAACTTGA AAAA	C	A				SILENT- NONCODI NG	oncogen e	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2365	cg42685908	193	TTAATAGTCATG AAAAAGAAAAGA A[C/G]TTGAAAAA ACAACTTCAACT CTGTA	C	G				SILENT- NONCODI NG	oncogen e	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2366	cg42685908	223	AAAACAACCTC AACTCTGTACAA A[T/G]GTTAATAT CAAGGAGCAGCT GAAGC	T	G				SILENT- NONCODI NG	oncogen e	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2367	cg42685908	320	TTATTAAATATC CTTGTCCTTTTC C/gapJATGATATA CACATATTTTTC TCTT	C	gap				SILENT- NONCODI NG	oncogen e	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2

2368	cg42685908	383	TATTATGTATTTT TAATGACAGCTT A/C]CTTAACAAC ATTCACTCTGGTG CTTT	A	C				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2369	cg42685908	92	AGTTATACAAC TTAAACATTGAAT [G/T]AATCATTCT TATCAAATACAT CAAG	G	T				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2370	cg43947181	2974	TTCAATTGCATC ATCACTGACCTG T[T/gap]AGAAATTT AACCCGGAAACA TCGCAA	T	gap				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2371	cg43947181	3937	TCATGCTTTTGA ACATCTTTT [T/gap]TTCATTGA AACAAATTCAAG TTCCT	T	gap				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2372	cg43947181	3938	CATGCTTTTGA CATCTTTT T/gap]TCATTGAA ACAAATTCAAGT TCTTG	T	gap				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2373	cg43947181	3939	ATGCTTTTGAAC ATCTTTT T/gap]CATTGAA CAAATTCAAGT CTTGG	T	gap				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10

2374	cg43988571	2942	CCACGGGACACC CCCAGCCTCAG GTG[C/gap]ACTG ACCTGCTGCCCTG CCCCCAGCC	C	gap			SILENT- NONCODING	oncogene	Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52-SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.[pcls:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52-SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	0.00E+00	10 (10q24)
2375	cg43939230	341	GTAATAGAGGTC TTTGTAGATGGG T[A/G]CTGTATCC CATGGCAGCCCT TGCTG	A	G			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q99907 LATENT TRANSFORMING GROWTH FACTOR-BETA-BINDING PROTEIN-2 - HOMO SAPIENS (HUMAN), 1821 aa.	0.00E+00	14 (14q24)
2376	cg42716300	189	CTGCGGGAAGG TGCGGGGAGCG GAG[G/C]CATGG CCTCCGGTGCCT ATAACCCG	G	C			SILENT- NONCODING	oncogene	Human Gene SWISSPROT-ID:Q04864 C REL PROTO-ONCOGENE PROTEIN (C- REL PROTEIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	2 (2p13)
2377	cg43298442	232	TTTTTTTTTCCA CACAGCAGATGT [A/gap]TCCAAAC ACATAAAAATCT CTACAG	A	gap			SILENT- NONCODING	oncogene	Human Gene SWISSNEW-ID:Q99583 MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT) - HOMO SAPIENS (HUMAN), 582 aa.	0.00E+00	
2378	cg44008321	156	GTTGCTGATATT TATTCAAACGTC ATT[C]CCATACAA TAAAGAACTCTG CTTTT	T	C			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q63406 OST ONCOGENE - RATTUS NORVEGICUS (RAT), 872 aa.	0.00E+00	

2379	cg44008321	279	GGGAGGGTCA CACAAGGCGC GCA[G/gap]CTGT GCGACGAGACG GAGCACCGC	G	gap				SILENT- NONCODING NG	oncogene	Human Gene SPTREMBL-ID:Q63406 OST ONCOGENE - RATTUS NORVEGICUS (RAT), 872 aa.	0.00E+00	
2380	cg43957159	507	AGCTAGTAAACA GACAAGCCTGTC G[G/A]ACTTTGAA ACCAACTTGACC GGGTC	G	A				SILENT- NONCODING NG	oncogene	Human Gene TREMBLNEW- ID:G2736087 ERYTHROBLASTOSIS VIRUS ONCOGENE HOMOLOG 2 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	2.30E-260	21 (21q22.3)
2381	cg43997978	111	TCCAGGTTTTT AATTTCCCTGA A[T/gap]TTTTTTT TTAAACAACAAA ATTGGC	T	gap				SILENT- NONCODING NG	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2382	cg43997978	120	TTAATTTCCCTG AATTTTTTTTTTg ap/TJAAACAACAA AATTGGCAAGAA GAAA	gap	T				SILENT- NONCODING NG	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2383	cg43997978	716	ATTTAAAGGCA GTAGGGTGCTGT G[G/gap]CTGCAG CCTCTCCTCCAA GACGGAT	G	gap				SILENT- NONCODING NG	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2384	cg43997978	764	GATGTTGCAGGG GAGGGCCGTTA GG[G/gap]CAAGA ACCCAGCAGCTG CGTGGATG	G	gap				SILENT- NONCODING NG	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2385	cg43997978	822	ATATACCCAGT AGTGTTCAAGGA CIA/gap]AGGCC TCTGATCCCTAT GGCTTGG	A	gap				SILENT- NONCODING NG	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1

2386	cg43917532	511	CCTCCCCACCTT CCCCACCTCCC C[gap/C]ACCTC CCCATAGCGCC CCTCCCG	gap	C				SILENT- NONCODING	oncogene	Human Gene SWISSNEW-ID:P01106 MYC PROTO-ONCOGENE PROTEIN (C-MYC) - HOMO SAPIENS (HUMAN), 439 aa. [pcis:SWISSPROT-ID:P01106 MYC PROTO-ONCOGENE PROTEIN (C-MYC) - HOMO SAPIENS (HUMAN), 439 aa.	4.20E-236	8 (8q24.12)
2387	cg43988569	383	CTGCTGGAAGAG GAAATCCCGG GG[G/gap]CCGCC GGCCCTCTTCG ACAGCTAC	G	gap				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q13249 ABL BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 390 aa.	5.00E-213	2
2388	cg43959113	84	ACCAAGGGAG AGGGACGGCC CAT[T/C]GCCAAT CTGTCCAGCCC CCCGGG	T	C				SILENT- NONCODING	oncogene	Human Gene SWISSPROT-ID:P53539 FOSB PROTEIN (G0/G1 SWITCH REGULATORY PROTEIN 3) - HOMO SAPIENS (HUMAN), 338 aa.	6.00E-182	19
2389	cg44008545	1334	TAAACACTTAA CCAGTTACCCAA A/TATCTGATTAG AAGTATAAGGTG CTC	A	T				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92905 JUN ACTIVATION DOMAIN BINDING PROTEIN - HOMO SAPIENS (HUMAN), 334 aa.	4.30E-179	
2390	cg43298230	1927	AACCCGTCCTCT CCCGAGTTTTC A/T/GJAAGTGAAGC CCACTCGCAAGT TGGAG	T	G				SILENT- NONCODING	oncogene	Human Gene SWISSPROT-ID:P54843 TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-MAF) - MUS MUSCULUS (MOUSE), 370 aa.	1.60E-158	
2391	cg44010709	1277	AATGCAGAGCCC CTCAGGATGGG GT[gap/G]CCCCG TCAGGGGCTGG ACGGTCGTG	gap	G				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2392	cg44010709	163	CCGGGTCGTCTC CTGCAAGGTTGC C[C/gap]CGGTGG GTCTGACGCCCA GCTGGCG	C	gap				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)

2393	cg44010709	164	CGGGTCGTCCTC TGCAAGGTTGCC C[C/gap]GGTGGG TCTGACGCCACAG CTGGCGT	C	gap				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2394	cg44010709	191	GTGGGTCTGAC GCCCAGCTGGC GTC[C/gap]GGGA GCCGGGTGGA GTCCTGGAGG	C	gap				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2395	cg44010709	224	GGGTGGAGTCC TGGAGGGAGGC GAA[gap/G]CGGG ATGTGGAGGGG GCCTGGAGTG	gap	G				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2396	cg44010709	267	CTGGAGTGGGG GGAGGGGCGGG TGA[G/C]GCGAG GCCCGGCCCGC CACAGTCCT	G	C				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2397	cg44010709	273	TGGGGGAGGG GCGGTGAGGC GAG[G/gap]CCCG GCCCGCCACAG TCCTGCCCTCT	G	gap				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2398	cg44010709	68	AACCTTACTTGT TTTTGGGAGGAG TA/GTTAATGGGT GGGAGGGTGA GAGGG	A	G				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)

2399	cg43918770	5017	GCGGACCACTG ACCGCTCCCCAG CG[G/gap]CAGAA GGCCTGGTCCC CTGTGGTTC	G	gap				SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.60E-140	5
2400	cg43918770	8967	TACTTTAAAGGA GTGAGCCAGAA GG[C/gap]CAAGG AGTTCGTGTGCT TCCCTCCIG	C	gap				SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
2401	cg43966629	1072	ATCCTAGTTTCC CTAACTGCCTCC T[C/A]CACAGGG AGGAGTGTGG GATCCCC	C	A				SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2402	cg43966629	1089	TGCCTCCTCCAC AGGAGGAGTG TT[G/gap]GGATC CCCCCTACCCCTG TGCCCCCG	G	gap				SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2403	cg43966629	17	TTTTTTTTTTTT GAA[T/G]GATATT TAACCTTTTCTTAA AAAAA	T	G				SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2404	cg43966629	199	CAGTGTGTATAT TCTATTTCATCAG G[G/A]AGAGTTG GGTGAGGACGT GGTGATG	G	A				SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2405	cg43966629	25	TTTTTTTTTTTT GAATGATATT[A/ G]ACTTTTCTTAA AAAAAAAATCTTA A	A	G				SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1

2406	cg43964295	980	AAACATCTGACG TCGTACAAAAA A[A/gap]TTCATC AGTATTCTGGG ACAGAA	A	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2407	cg43964295	1351	AACAACAAAAAT ACAATTAAAAA A[A/gap]TAAATAA TAAAGTCATTG TGATCG	A	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2408	cg43964295	1614	GCTGCAAGGG ACACACAACCAG GG[G/gap]TACTG TTGACTAGCTT TTGCATAG	G	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2409	cg43964295	1960	GCTTCTCTCTC TGCTACACAGC T[G/A]TACGCCG GCTGCTTGGCAA ACCGGG	G	A			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2410	cg43964295	2071	TAGACATTTTGG AGTCTTGTTCT C[G/A]TAATCCTT GATGGGGACCG TGTTGG	G	A			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2411	cg43964295	623	GAATACTCCCTA AATGCAGTAGAT T[A/gap]AAAAAA AAATCAAATCTA CAAGTG	A	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20

2412	cg43964295	633	TAAATGCAGTAG ATAAAAAA [A/gap]TCAAATCT ACAAGTGGTTCA GTATT	A	gap			SILENT- NONCODING	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2413	cg43964295	633	AAATGCAGTAGA TTAAAAA [gap/A]TCAAATCT ACAAGTGGTTCA GTATT	gap	A			SILENT- NONCODING	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2414	cg43964295	73	ATTCACACTTGC TGTTGAATAACA A[G/C]GGAATCAA GGCTCCCTAGA TGGGG	G	C			SILENT- NONCODING	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2415	cg43964295	697	GAAAGAAATCA GAATTTACAAAG T[A/C]AGATTGGT GTGCTTCCAAGT TCACA	A	C			SILENT- NONCODING	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2416	cg43317357	87	TGGGTCGACAG CTGGAGGGCA GGA[T/C]TGGGG GGAAGCTGCTG GGCGCAGCC	T	C			SILENT- NONCODING	Human Gene Homologous to SWISSPROT-ID:P98083 SHC TRANSFORMING PROTEIN - MUS MUSCULUS (MOUSE), 578 aa.	1.30E-106	
2417	cg43297056	228	CGCTTTGTTTTT TTTTTTTTTCT /A]AAGAGAGAGG CAATTTTATTCTT CC	T	A			SILENT- NONCODING	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103 (20q13.1)	20
2418	cg43297056	268	TTTATTCTTCCAA AAAAATGCACCA A/gap]GAGAGGG TGAGCACAGGA GCACCCC	A	gap			SILENT- NONCODING	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103 (20q13.1)	20

2419	cg43297056	482	AACAGGGCAGC ACATGGCCCTGT TG[C/gap]CTCCA CCTGAGAGTCTG GGGAGGGG	C	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SPTRMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103	20 (20q13.1)
2420	cg44129020	155	CTGCATAGGTCC AGGCCCGGGT GG[C/gap]CCCC AAAGGCTCCCT CCTTCCCA	C	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS- INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.lpcis:SWISSPROT-ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS-INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.	1.60E-99	
2421	cg44129020	519	GCCGGCGTGGG CGGCGGCGGCT GCG[T/C]GGTGG TGGCGGGCGTC ACTGCCGGG	T	C			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS- INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.lpcis:SWISSPROT-ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS-INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.	1.60E-99	

2422	cg43922882	91	TGCTACCAAGGC AGTAATATTTTC [C/T]ATATGAACC AGACCAAATACC CTTT	C	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	6.40E-91	
2423	cg43922882	94	TACCAAGGCAGT AATATTTTTCAT [A/T]TGAACCCAGA CCAAATACCCTT TAAT	A	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	6.40E-91	
2424	cg43292762	1409	CAGGCGTCACCA TCCACCTTCCCT T[gap/T]CTACAA GGACTCCATTGG ATCTGCA	gap	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2425	cg43292762	1442	GACTCCATTGGA TCTGCAAGAACAA C[T/gap]TGGACC TTTGGGTTCTTT CTGGGGG	T	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2426	cg43292762	1443	ACTCCATTGGAT CTGCAAGAACAC T[T/gap]GGACCT TTGGGTTCTTTC TGGGGGG	T	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2427	cg43292762	1490	GGGATATTTC TAAGGCATGTGG C[C/gap]TTTATCT CAACGGAAGCC CCCTCTT	C	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2428	cg43292762	1811	GAAATTCATAC TTCTCTCAGATG G[G/gap]AACAGT AAAGAAAGCAGA ATCAACT	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)

2429	cg43292762	1884	TTGAAAAGACCA AGACTTTTGTCT GTA/TTCAGTGG TTTACAGCTAC CACCC	A	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2430	cg43292762	1885	TGAAAAGACCAA GACTTTTGTCTG ATT/AJCAAGTGGT TTTACAGCTACC ACCCCT	T	A				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2431	cg43292762	1816	GGTTTACAGCT ACCACCCTTAGG G[G/gap]TAATTG GTAATTACCTGG AGAAGAA	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2432	cg43967603	212	TCGACTTTTTTT TTTTTTTTTCTG TJCCAGCTGGC ACATTTATTGGC ATT	G	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:Q99471 C-MYC BINDING PROTEIN MM-1 - HOMO SAPIENS (HUMAN), 167 aa.	4.80E-77	12
2433	cg43967603	282	ATCACCGGAAG CCACGCCCAAAG G[G/gap]TGTCCC TCTGCCCCATT CTGCAAA	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:Q99471 C-MYC BINDING PROTEIN MM-1 - HOMO SAPIENS (HUMAN), 167 aa.	4.80E-77	12
2434	cg43101925	378	TCCTGGGAATT CACTTCTCTTCC TTC/TCCCTCATGG AAGATGCAAGTA AAAGG	C	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:P28574 MAX PROTEIN (MYN PROTEIN) (MYC-BINDING NOVEL HLH/LZ PROTEIN) - MUS MUSCULUS (MOUSE), 160 aa. pcis:SWISSPROT- ID:P28574 MAX PROTEIN (MYN PROTEIN) (MYC-BINDING NOVEL HLH/LZ PROTEIN) - MUS MUSCULUS (MOUSE), 160 aa.	2.00E-72	14 (14q23)

2435	cg44029157	1010	CCACCCCTTACTT CCTGGCCTCTTC T[G/gap]GGCTAC TGCCACTGTGTG CCTTCTG	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17082 RAS-RELATED PROTEIN R- RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.10E-66	
2436	cg44029157	1012	ACCCTTACTTCC TGGCCTCTTCTG G[G/gap]CTACTG CCACTGTGTGCC TTCTGCC	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17082 RAS-RELATED PROTEIN R- RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.10E-66	
2437	cg43975131	2054	GAAGGGAAGTGA AAAGCAGTAGAA G[A/G]AACAGTCA GAGATGCCTCAC TGATA	A	G				SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2438	cg43975131	2081	ACAGTCAGAGAT GCCTCACTGATA G[G/A]CAGGAGG CCGAACAGGTAA ACCCCA	G	A				SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2439	cg43975131	578	AGCCTGACTCCT GCTGGGCACAG CC[C/gap]ACCCT GCTGGGCACAG TGACTGGAG	C	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2440	cg43975131	589	TGCTGGGCACA GCCACCCCTGCT GG[G/gap]CACAG TGACTGGAGGT CCAGGCTG	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2441	cg43975131	880	CTCCCTGAGGCT GAGACGTGAAG GT[G/gap]CCCCAG TCTGGGCCGTGA CTCACTCT	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)

2442	cg43280482	2797	TGGCATAATCACC CCGCACTGTGG GG[C/gap]CAGGC ACCACTAGCCTG GCTCAAAT	C	gap				SILENT- NONCODING	oncogene	Human Gene Similar to TREMBLNEW- ID:G2952331 ARG/ABL-INTERACTING PROTEIN ARGP2A - HOMO SAPIENS (HUMAN), 666 aa.	3.90E-62	8
2443	cg43941861	604	ACCAATTTCTGAC CTGCAGTTGCAG A[A/C]TAGGTGTG ACTTGCAATTTAA AATAA	A	C				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P01100 P55-C-FOS PROTO- ONCOGENE PROTEIN (G0S7 PROTEIN) - HOMO SAPIENS (HUMAN), 380 aa.	2.60E-61	14
2444	cg17903042	1163	GCCGCGCAGAG CGGCCGCGGGG GGG[G/gap]CGCT GGCACAAACCC GGGAGAAAA	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P04628 WNT-1 PROTO-ONCOGENE PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 370 aa.	7.90E-61	
2445	cg43943100	1164	TGCAAACTCTAG GACTATTATATAA [gap/T]GTAAAAAT CTCTCTTGATGAT ACTGG	gap	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2446	cg43943100	1164	TGCAAACTCTAG GACTATTATATAA [gap/T]GTAAAAAT CTCTCTTGATGAT ACTGG	gap	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2447	cg43943100	1180	TATTATATAAGTA AAATCTCTCTT G/CJTGATACTGG AAAGTGATTAGA ATGT	G	C				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2448	cg43943100	1182	TTATATAAGTAA AATCTCTCTTGT G/CJATACTGGAA AGTGATTAGAAT GTGC	G	C				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6

2449	cg43943100	1219	GATTAGAATGTG CAAACGTGATATA G[gap/C]TAGCTT TCATCCGCCTCT TAAAGGG	gap	C			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2450	cg43943100	1278	CAGGAAAGTCCA TTTAAGATGTTG GT[A]AGGTTTAA CAAAGTTGGAAT GCTGG	T	A			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2451	cg43943100	1279	AGGAAAGTCCAT TTAAGATGTTGG T[A]TGGTTTAAC AAAGTTGGAATG CTGGC	A	T			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2452	cg43943100	1364	CTCAGAGCTACA ATGCATTTAGTA T[A]gap]TTAAAGC AGCTGACATGAT GACTTT	A	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2453	cg43979706	1456	CCCCATGTCAGG CGGAGCGGAA GG[C/gap]CCACC GTGCCAGAGGG TGGGCACCA	C	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	
2454	cg43979706	1814	ATTTAAGTCCCT GGGCTGCCCCC TT[G/gap]GGTG CCCCCGCTCC CAGGTTCCC	G	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	
2455	cg43979706	893	GCCCCGGTTCTG TCAGGGTCCCTA A[G/A]GGAGGAC ACTCAGGGCCTG TGGCCA	G	A			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	

2456	cg43268513	633	CCTCTGCCCTGTG ACCGCGCGCCC GG[C/gap]CGCTA GACTGACTTCGC GCAGCGGT	C	gap				SILENT- NONCODI NG	oncogen e	Human Gene Similar to SWISSPROT- ID:P04628 WNT-1 PROTO-ONCOGENE PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 370 aa.	7.70E-51	2
2457	cg43307658	2271	GGGCCAGCCC CCAACCCACAGG CA[G/C]GGAGGG GCATCCCTCCCT GCCGGCC	G	C				SILENT- NONCODI NG	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2458	cg43307658	2337	GGATGAAACCA CAGGATTCCG GA[T/C]GCCAGA CCCCATTTTATA CTTCACT	T	C				SILENT- NONCODI NG	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2459	cg43307658	2472	GCTGAATAAAC AAGGTTTTCTA C[A/T]AAGTGGCT CTGCATGCGGC CTGCTG	A	T				SILENT- NONCODI NG	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2460	cg43307658	2474	TGAATAAACAA GGTTTTCTACA A[A/T]GTGGCTCT GCATGCGGCCT GCTGGC	A	T				SILENT- NONCODI NG	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2461	cg43096761	208	AATAGGCATACA TAAGCAATTATG TIG[A/T]TTATATT CTACTCCTTTCT GAAAC	G	A				SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:Q16853 COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (SERUM AMINE OXIDASE) (SAO) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	17

2462	cg43096761	24	TTTTTTTTTTTT TTTTTTTTTT[G/T] TTTGGGCCCAAT TATTGTTTATTT	G	T			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:Q16853 COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (SERUM AMINE OXIDASE) (SAO) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	17
2463	cg44028217	36	TTTTTTTTTTTT TGAGGCTCTGAG [G/A]GTTTATTGT CTGCCCCAGTGA GGCT	G	A			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
2464	cg44024803	166	AACATAGTTCTG ATTTTGAAGTGT T[gap/G]AGTGGA ACTCAAACAGAA ATGATTA	gap	G			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:P31513 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 3 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 3) (FMO 3) (DIMETHYLANILINE OXIDASE 3) (FMO II) - HOMO SAPIENS (HUMAN), 531 aa.	4.60E-294	1 (1q23)
2465	cg43271573	1938	TAATGCTAGAGA ATGATAACTAAG A[C/T]TTCTGTGC ATTGAAGGTTG TTGGA	C	T			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:Q01740 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) - HOMO SAPIENS (HUMAN), 531 aa.	5.30E-293	1 (1q23)
2466	cg42849556	2051	CCACAATAAAA AAACCTATCAT C[gap/A]TTACAAA ACAAGACACCC AAGTCC	gap	A			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:P19878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) (P67-PHOX) - HOMO SAPIENS (HUMAN), 526 aa.	2.80E-287	1 (1q25)

2467	cg43948982	294	TTTAAATGACAAT GGAAATTTGATA T/CACAAAATG GAAGGTAATA GAAA	T	C				SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:Q15800 C 4 METHYL STEROL OXIDASE (EC 1.-.-)- HOMO SAPIENS (HUMAN), 293 aa.	1.90E-169	4
2468	cg43269428	511	CGCATCAGGTAG ACATGATCATGT G/C/AJATTTCTTT TCCACGCTGCAA ATCAC	C	A				SILENT- NONCODI NG	oxidase	Human Gene Homologous to SWISSPROT-ID:Q63448 PRISTANOYL- COA OXIDASE (EC 1.3.3.-) - RATTUS NORVEGICUS (RAT), 700 aa.	1.20E-105	
2469	cg43972840	1584	AGCCCCAGCTTA TCTCCTCCTCCG C[G/gap]CTGTGT AAATGCTCCAGC ACTCAAT	G	gap				SILENT- NONCODI NG	oxygehas e	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.60E-168 (16p13.3)	16
2470	cg44010395	387	TGAGGATGCTGA AGGCAGGGCT GA/T/CJCCCTTCG CCCCCTCTGAAG TTTAGG	T	C				SILENT- NONCODI NG	oxygehas e	Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa. pcls:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.	5.20E-151 (22q12)	22
2471	cg43916857	5785	AAAAGAAGATTT TCTTTAGCAAGA A/A/TJAAAGAGGT CATGTCAATTTGT JAATA	A	T				SILENT- NONCODI NG	peptidas e	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17
2472	cg43916857	5788	AGAAGATTTTCT TTAGCAAGAAAA A/A/TJGAGGTCAT GTCATTTGTTAAT AAGT	A	T				SILENT- NONCODI NG	peptidas e	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17
2473	cg43916857	6366	GGAAACAAGAC TTTCCCAGCTTG T/G/AJTTACCTAG AAGCGTGAATGT ATAGG	G	A				SILENT- NONCODI NG	peptidas e	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17

2474	cg43948682	359	CAATTAAAAAAT CATAAAGACTG A[G/A]TGTGCA ATAAAATATCAAA GAGG	G	A				SILENT- NONCODING	peptidas	Human Gene Similar to TREMBLNEW- ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa.	5.00E-75	10
2475	cg43254736	278	GAGCCAGGAGC CCGGGATGCGG AGA[T/C]GGCC TCGGTCTCCACA TCCTGGCG	T	C				SILENT- NONCODING	peptidas	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.10E-67	
2476	cg42923012	237	AATTTGTGTGTC CTTAGGCAAGC C[C/gap]ACCCCC TGTCTGAAGCTC AGTTTC	C	gap				SILENT- NONCODING	peptidas	Human Gene Similar to TREMBLNEW- ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa.	1.00E-65	X
2477	cg41626506	291	GGAAACAGTCG TCCTGCTGATT C[G/C]GATTGCG TGTGTTTGAA AGAGT	G	C				SILENT- NONCODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00 (3q26.3)	3
2478	cg41626506	3179	AGCACAGCGAG CGCTCTCATTCT GA[C/gap]CTTTT TCCTCTTCTCAG CCAACG	C	gap				SILENT- NONCODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00 (3q26.3)	3
2479	cg41626506	3180	GCACAGCGAGC GCTCTCATTCTG AC[C/gap]TTTTT CCTCTTCTCAGC CAACTGC	C	gap				SILENT- NONCODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00 (3q26.3)	3
2480	cg444913844	216	CGAGCCGAGGC CTCCTGCAGTGT TC[C/T]GCACAGC AAACCGCAGCT ATGGCT	C	T				SILENT- NONCODING	peroxidase	Human Gene SWISSPROT-ID:P04040 CATALASE (EC 1.11.1.6) - HOMO SAPIENS (HUMAN), 527 aa.	2.70E-296 (11p13)	11

2481	cg42691989	331	CTAAGGCTCCTC AGGACTGGATG GA[G/T]TAGGAG ATCTGTGTGTTG AGCAGTT	G	T				SILENT- NONCODING	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.90E-101	14 (14q24.1)
2482	cg42691989	332	TAAGGCTCCTCA GGACTGGATGG AGT[G]AGGAGA TCTGTGTGTTGA GCAGTTC	T	G				SILENT- NONCODING	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.90E-101	14 (14q24.1)
2483	cg43951241	365	CTCAGGGGAGG CCCGCCACAA GG[C/gap]TTCG GGCCCCCTCCTC ATAGAGACA	C	gap				SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2484	cg43951241	372	GAGGCCCGCCC ACAAGGGCTTCG GG[C/gap]CCCTC CTTCATAGAGAC ACCACCCG	C	gap				SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2485	cg43951241	375	GCCCGCCACAC AGGGCTTCGGG CCC[C/gap]TCCT TCATAGAGACAC CACCCCTGA	C	gap				SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2486	cg43951241	519	AGGAAGAAGGA GGCTGGTGGTG TGT[A/T]GTGTGG GCATGTGGGAG ATGCTGGC	A	T				SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	

2487	cg43951241	886	GGCCCTTGCATG ATGGGCAGGG GT[<i>gap</i>]/A/GGGGT AGGGTGGGGTG GGCATCAGT	<i>gap</i>	A				SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2488	cg43917453	13	TTTTTTTTTTT /TTGAAATCAGA AGTTTAATATGA CAC	G	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2489	cg43917453	1467	ATGAACCGATT CCCTCCACCCGT A/ATCTGGATT TTCCACAAATCT CTCTT	A	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2490	cg43917453	164	ATTTCGATTAATT AAATCCAGATA G/AJAGAGAAAGTA ATTTTGGAAAG AAAT	G	A				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2491	cg43917453	1642	TCCTGACAACAT CCGTGGGGTGG GG[G/ <i>gap</i>]/CTCCC CTGAGGCCCT GAGGCTGCC	G	<i>gap</i>				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2492	cg43917453	1662	TGGGGGCTCCC CTGAGGCCCT GAG[G/ <i>gap</i>]/CTGC CGCTCACTGGG GAAGGCCCTT	G	<i>gap</i>				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2493	cg43917453	270	ATTTTGGCATCA TTCTGTCCGCTC A/G/TTAGGCCGT GTTCCCTCTGGT AGGC	G	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7

2494	cg43917453	656	CGCAGTGGTG CAGGTCGCCCT GATC/TTCCTCT CCCGGAGGGA AATGCTCG	C	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2495	cg43917453	661	TGCGTGCAGGTC GCCCTGATCTCC TTC/gap/TCCCGG GAGGGAATGCT CGCAGCC	C	gap				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2496	cg43917453	90	CCGGAGGTTTCT CTTCAACATAA G/GT/AGTTAGAA ATTACAAAGTAGG CATAT	G	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2497	cg43920534	1087	CTTGGTTTTCGG CTTTTTCCTT [gap/A]AAAAAAA AAGGCCACTGAA ATGTA	gap	A				SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
2498	cg43920534	1097	CGCTTTTTCCTCC TTAAAAAAA gap/A/GGCCACT GAAATGTATAA ATGTC	gap	A				SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
2499	cg43958187	3119	CTATCAAAATAC ATGTATGTTTCA G/G/gap/JATATTT GACCTGTCAATTA AAAAAAA	G	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q05209 PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1) - HOMO SAPIENS (HUMAN), 780 aa.	0.00E+00 (7q11.23)	7
2500	cg43930478	41	GGCCATTGAGG GGAGCCCCATGG GG[G/C]CAGGAA GGCGGCTGTGA GGCGCCCC	G	C				SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q15171 PROTEIN PHOSPHATASE 2A 74 KDA REGULATORY SUBUNIT (DELTA OR B HOMO SAPIENS (HUMAN), 570 aa.	1.10E-306	6

2501	cg43928335	1725	GCTTAAATAATG ATTTAACAAGGA A[G/T]ACGAGTAA AAACAATCCCA TTTCA	G	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.20E-302	11 (11q22)
2502	cg43088901	2091	CCCTCCATCCCC CTTTACCCCTCTTT [G/C]CTGCAGAG AACTTAAGCAA AGGGG	G	C				SILENT- NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa. pcis:SWISSPROT- ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2503	cg43088901	2345	AGCCGGGGCCT TATCGGGCTCCA GC[C/gap]ATCTC ATGAGGGGAGA GGAGACGGA	C	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa. pcis:SWISSPROT- ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2504	cg43088901	2387	GGAGACGGAGG GGAGTAGAGAA GTTT[gap]ACAC AGAAATGCTGCT GGCCAAATA	T	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa. pcis:SWISSPROT- ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2505	cg43302847	2299	ATGCTCATGTCC CTGTCCCCAGGC C[C/gap]AGCCCT CCTCAGGGGA GTTGAGGT	C	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)

2506	cg43302847	2419	CTGGGTGGCCAT CCTACCCAGCGT G[<i>gap</i> /G]CCCAGG CCGGGAAGAGC CACCTGGC	<i>gap</i>	G				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
2507	cg43302847	2518	AAGCGACTCTCC TGTTTGGAAACGG C[<i>gap</i> /A]AAAAAA AAATTTTTTTTTTC TCTTTT	<i>gap</i>	A				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
2508	cg44012067	105	TTTAAATTTTTT TTTTTTTTTTTC TTTCAACTTGCT CAGTGCTTTATT GAA	C	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P30305 M PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 566 aa.	1.00E-285	20
2509	cg43984117	145	TATAGAGGGGAC GGCGCAGGCGG GG[C/ <i>gap</i>]CCCCC TGCTGACCCCTCT CTCTGGGG	C	<i>gap</i>				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2510	cg43984117	188	CTCTGGGGGTCTC TCCTATGGCGGG G[C/ <i>gap</i>]CCTATT GCTTGAGTGGG GGAGGAGC	C	<i>gap</i>				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2511	cg43984117	190	CTGGGGGTCTTC CTATGGCGGG CC[C/ <i>gap</i>]TATTG CTTGAGTGGG GAGGAGCCA	C	<i>gap</i>				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	

2512	cg43984117	295	CTCCCCACAGAA C TGCCCCAGGCTGT G[C/gap]CCCCAG CCCCAGCTGCTC CACCTCC	gap			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2513	cg43984117	299	CCACAGAATGCC C CAGGCTGTGCC CC[C/gap]AGCCCC CAGCTGCTCCAG CTCCTTCC	gap			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2514	cg43984117	324	CAGCCCCAGCT C GCTCCACCTCCT TC[C/]TCTCTGT CCAGGGAGCAG ACCTCT	T			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2515	cg43984117	95	TAAATAGCTGG C GGAGGGGGTG AG[C/gap]CCCCAG CCTAGCCCCACC ATGGGGCT	gap			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2516	cg43984117	98	AATAGCTGGGA C GGGGGTGAGC CC[C/gap]AGCCT AGCCCCACCATG GGGCTATA	gap			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2517	cg43139469	1922	CTCAAGCCTGGA C GTCTGAGGCTTG C[C/gap]TACAAG AGGAGAGAAAGT AGATAGG	gap			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7.00E-259 5 (5q31)	

2518	cg43139469	402	GCTCAGGGTTTC TGCAGTGTCTTT T[gap]/TGGTGAC TTGTTAGCAGCC AGTGGCT	gap	T				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7.00E-259	5 (5q31)
2519	cg43980696	528	CCCCCAGTGAA AGCTGGGCTGG GC[A/T]GGGAGT CCTCAGAAAGCCA CTCTGGC	A	T				SILENT- NONCODING NG	phosphatase	Human Gene SPTREMBL-ID:Q28647 PROTEIN PHOSPHATASE 2A0 B' REGULATORY SUBUNIT ALPHA ISOFORM - ORYCTOLAGUS CUNICULUS (RABBIT), 500 aa.	9.10E-250	11
2520	cg43918944	2303	TGAATGAATTTTA TCATCTATGATA T/A/GAGTGAGAT AATTATGGGAGT GGTA	T	A				SILENT- NONCODING NG	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
2521	cg43918944	2374	TCCTTGATTGTG TTGCACATAGAT A/T/CJGGTAGTCT GCTCTGTATATT TTTCC	T	C				SILENT- NONCODING NG	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
2522	cg43336281	99	CTTTCTGGCATC TTGGGACTTGTC C[C/gap]TAAGAA TAGGGAAGACAG TCATCTCT	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2523	cg43336281	131	TAGGGAAGACAG TCATCTCTGTCCT G[G/gap]AGCAAA GCTCCCCCTTGC ACAGGAA	G	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2524	cg43336281	141	AGTCATCTCTGTC CTGGAGCAAAAGC T[C/gap]CCCCCTT GCACAGGAACAC AACTCCC	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22

2525	cg43336281	1631	AGCGACTATGTT TAAGGTTTTTTTT [T/gap]GTAAATAA GAGACCTTAAGC AATGC	T	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2526	cg43336281	2528	AGAGCCCCGCT GTCGGGCCAG GCA[C/A]CACTAG GTGGCAGTCGC AGCTCCIG	C	A			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2527	cg43336281	299	AGAATGCACAGG ACTCTGGGGCT G[C/gap]CCCCCT TGAGCTACAGAG GCAGAAT	C	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2528	cg43336281	326	CCCCTTGAGCTA CAGAGGCAGAA C[G/A]AACCAAA ACACTGCTTCCT TTAAC	G	A			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2529	cg43336281	394	CATTAGCTTGG GACGAGGCTAG GC[C/gap]TAAGA AGGCCAGAGC TGTCCTCCC	C	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2530	cg43336281	830	ATCTCCCCAGGA CACGCCGGCTC AC[C/T]TGACCC ACAGCGTTCTAG GAGGTC	C	T			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2531	cg43336281	97	GCCTTTCTGGCA TCTTGGGACTTG T[C/gap]CCTAAG AATAGGGAAGAC AGTCATC	C	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22

2532	cg43988504	2416	CAGTTTCCAGG AATAGGCATTTG C[C/gap]TAATTC CTGGCATGACAC TCTAGTG	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lcds:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2533	cg43988504	3028	CCAGGCTGTAAG CATTCTGAGCTG G[G/gap]CTTGTT GTTTTTAAGTCC TGTATAT	G	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lcds:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2534	cg43988504	60	GGCCTCGGGC TAAGAGCGCGAC GC[G/gap]GCCTA GAGCGGCAGAC GGCGCAGTG	G	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lcds:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2535	cg43988504	61	GCCTCGGGCT AAGAGCGCGAC GCG[G/gap]CCTA GAGCGGCAGAC GGCGCAGTG	G	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lcds:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2536	cg43988327	1820	CAGCCAGCCACA TTTCCCTGTGTC TT[G/gap]GCTAGA GCCACCAATTAGA CTCAGAC	G	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P11117 LYSOSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP) - HOMO SAPIENS (HUMAN), 423 aa.	1.90E-233	11 (11p12)

2537	cg43983327	1821	AGCCAGCCACAT TTCCCTGTGTCT G[G/gap]CTAGAG CCACCATTAGAC TCAGACA	G	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11117 LYSOSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP) - HOMO SAPIENS (HUMAN), 423 aa.	1.90E-233	11 (11p12)
2538	cg44004203	103	AATATAGAAATCC CACTAGCAGCTT T[G/gap]CTTAGT GATCAAGACGTT TTTGGGA	G	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2539	cg44004203	1659	TACTAAATGTGA TCTAAGAGAATA T[G/C]GTTCCACC CAGTGTGGAGC CATGAA	G	C				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2540	cg44004203	1660	ACTAAATGTGAT CTAAGAGAATAT G[G/C]TTCACC CAGTGTGGAGC CATGAAA	G	C				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2541	cg44004203	1728	ACATAAAGATGC CATTGTAGTAGA A[A/gap]TGCACA AATGCATGTAAT AACTGCA	A	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2542	cg44004203	1827	ACTCAGACTTCG TTCAAAGTGACA G[gap/G]AACGAG GGGAGTGGAGT GCAAAGGA	gap	G				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	

2543	cg44004203	2018	GGGTAGGAGGG CAACAAACACAT CC[C/T]TAGGTGA AGGAGTGTAAT ACAGAT	C	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2544	cg44004203	659	CCTCTTTTGTG ATCACCTTCTGG C[C/gap]TTGCGG AGATGACAAACC TGTTCTG	C	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2545	cg43984194	249	TAGCCCCAAGAT TGAGATTCTTAT G[gap/G]AATACA CTGTATTATTAC CTGCAAT	gap	G				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P35813 PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) - HOMO SAPIENS (HUMAN), 382 aa.	1.9E-208	14
2546	cg43984194	252	GCCCCAAGATTG AGATTCTTATGA A[T/C]ACACTGTA TTATTACCTGCA ATACT	T	C				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P35813 PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) - HOMO SAPIENS (HUMAN), 382 aa.	1.9E-208	14
2547	cg43307343	460	AAAATTTATAGCTC GCAGAAATATTCT[C/T]AAGTCATGA ATATTAGGTGTC TGTC	C	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P17706 T- CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa.	3.6E-207 (18p11.3)	18
2548	cg43969460	167	CCTGGACTCGGAG GGAAGGCCGAG AG[G/gap]ACACG GACGGTGGCCA CACCACGCT	G	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	

2549	cg43969460	187	GAGAGGACACG GACGGTGGCCA CAC[C/gap]ACGC TGCAGTGAAGGC CCAAGTGTG	C	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	
2550	cg43969460	215	GCTGCAGTGAAG GCCCAAGTGTGA TIG/C]GCAGAGA AAGAGGGAAGT TGGAGA	G	C			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	
2551	cg43933809	1541	CATTAGTCTTTA AAAAA gap/A]GGATTCTT ATTAACCAACAT ACTTA	gap	A			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2552	cg43933809	2090	GCAGTAAGTAAT ACAATGTGCCAA TIC/T]CATAAAAT GTAAGTTAACAG GTTC	C	T			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2553	cg43933809	2378	TTGTTAATACTAA CCCTTAAAAAA A/gap]GAAATAGG AAAAGAAAGGCT GCAAT	A	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)

2554	cg43933809	3189	AATAGTTGGTGA ATGCTGTAAAG C/T/CJCTTCCCAT ATTTCACTTTAA AAAT	T	C			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2555	cg43933809	3190	ATAGTTGGTGAA TGCTCTGTAAAGC TTC/TTCCTCCATA TTTCACTTTAA AATG	C	T			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2556	cg43917813	1566	TGAAATTTAGTA CACTATGTTCTA G[gap/G]GTCAGT CTAACAGTTTGC CTGCTGT	gap	G			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11082 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 309 aa.	5.3E-174	8
2557	cg43917813	1892	TAAATTACTGTTT TATGTTGATCTG C/TATATTTCTGT ATATTTGTCATG ACA	C	T			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11082 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 309 aa.	5.3E-174	8
2558	cg43269274	15	TTTTTTTTTTTT TTC/TTCCTTTTA CTATTTTATTTT ACAC	C	T			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10

2559	cg43269274	164	AACTAACAGACA AAAAGAAAAAA A[<i>gap</i>]GTAGTA CCACGTTGCAAA ATCTGCA	A	<i>gap</i>			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2560	cg43269274	208	ATCTGCAATCC CAGAGTCCACA G[C <i>gap</i>]TTGAAG ACAACCTCCAGG GGCAGGG	C	<i>gap</i>			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2561	cg43269274	22	TTTTTTTTTTT TCTCCTTTT[C/A CTATTTTATTTT ACACTATAAAA	T	C			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2562	cg43269274	40	CTCCTTTTACTAT TTTTATTTTACA[C[<i>gap</i>]TATAAAA ACAAGAACAACA ACAAC	C	<i>gap</i>			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2563	cg43269274	53	TTTTATTTTACAC TATAAAAACAA[G/C]AACACAAC AACAAACCAGTAA CATA	G	C			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2564	cg43269274	635	CATGTCCTTACA AACCCTGTAGGG T[G/T]ACTTTCCC AACTAGACGGTG ATCAG	G	T			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10

2565	cg43269274	816	CCCACGTTGCTG CAGGTATTTATT G[C/G]CTTATGCT TGAAATGAAAAG GCGAA	C	G			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2566	cg43972150	119	AACAGCCAGCCA TGGCCTGCTGGA A[G/gap]CCAGGG GACAATTCTTCA TACACAG	G	gap			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2567	cg43972150	299	CATGGCGGAGG CAAGTGTGGAT GT[G/gap]GGGAC AGGCCATGTCCC CAAAGCCC	G	gap			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2568	cg43972150	302	GCGGAGGCAAG TGCTGGATGTGG GG[gap/G]ACAGG CCATGTCCCCAA AGCCCCCTA	gap	G			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2569	cg43972150	47	TTTTTTTTTTTT TTTTTTTTTTTTT GJTAAAGCCAC GCTAATAATTAC CCC	T	G			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2570	cg43972150	809	GAAATCCCAGAC CCTCTGCTCACT C[C/gap]TCACGG GGACAAGCTATG AGATGCC	C	gap			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17

2571	cg43967897	119	GCGCGGAGGC GGTGGCGCGG CTG[C/gap]CCGG GGCCAACATGAC CAGGCTCTG	C	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2572	cg43967897	121	GCGGAGGCGG TGGCGGCGGCT GCC[C/gap]GGGG CCAACATGACCA GGCTCTGAA	C	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2573	cg43967897	197	GGACAGACTCG CTGGGCTCCG GAG[G/gap]CAGT GATTCCAAGCTG CTCGCGCAC	G	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2574	cg43967897	234	AGCTGCTCGG CACGCTGCTGCC AA[G/gap]CTGCA GGATGGTGCAC GTAGCCAGG	G	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2575	cg43272594	938	CCGGACCCCGC CCAGGCAGGGA GCTG[A]CTGTGA GTCCAGCTGAG GCCCCACCC	G	A				SILENT- NONCODING	phosphatase	Human Gene Similar to SPTREMBL- ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa.	1.4E-79	19

2576	cg43985274	912	CTTGGCTGGACC TGGAGGCCCTG CC[C/gap]AGCCC TGCTCTGCCCCAG CCCAGCAG	C	gap			SILENT- NONCODING	phosphatase	Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. pcis:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. pcis:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70	
2577	cg43948077	1216	ACCCCTCCACCC CATTCCCACCCA ATTG]CCCACCCCT TCTCCATGACCA AAAAT	T	G			SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2578	cg43948077	342	TAGTCTTGAGC TCTGAATAACAA G]G]GCTCTCAA TTGAGGGGGGA AAGAGC	A	G			SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2579	cg43948077	352	GCTCTGAATAAC AAGAGCTCTCAA TT]G]GAGGGG GAAAGAGCCTCC AAACTG	T	G			SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2580	cg43948077	359	ATAACAAGAGCT CTCAATTGAGGG G]G]GAAAGAG CCTCCAAACTGA CACTA	G	T			SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2581	cg43948077	369	CTCTCAATTGAG GGGGGAAAGAG CC]T]GCCAACT GACATCTAAAA TTCCTC	T	G			SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1

2582	cg43948077	373	CAATTGAGGG GGAAAGAGCCTC CA[AT]ACTGACA TCTAAAAAATTCCT CTTAG	A	T				SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2583	cg43948077	376	TGAGGGGGGAA AGAGCCTCCAAA CT[gap/T]GACAT CTAAAAAATTCCT CTTAGAGA	gap	T				SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2584	cg43948077	381	GGGGAAAGAG CCTCCAAACTGA CA[T/gap]CTAAAA ATTCCTCTTAGA GACACCA	T	gap				SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2585	cg43948077	390	AGCCTCCAACT GACATCTAAAA TT[C]CCTCTTAG AGACACCAAGTTA CTTCC	T	C				SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2586	cg43948077	393	CTCCAAACTGAC ATCTAAAAATTC CT[C]CTTAGAGA CACCAGTTACTT CCAAA	T	C				SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2587	cg43948077	413	ATTCCTCTTAGA GACACCAAGTTAC TT[gap]CCAAAC AAATCTTTTCCTT TTTAAT	T	gap				SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2588	cg43948077	472	CCCAACTGGTCA TATCCTTTTGAAA A[gap/A]CTGCCT TCATAATACACTT AAAAGT	gap	A				SILENT- NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1

2588	cg43948077	488	CCTTTGAAACT GCCTTCATAATA C/A/CJCTTAAAG TAATGCCCTTAGA GTAGA	A	C				SILENT- NONCODING	phosphatase inhibitor	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2590	cg43931444	1926	TTTGTAGCTGTT TAAAAA A[A/gap]AAGGTA GCTGTGATACAA ACCCAG	A	gap				SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT- ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2591	cg43931444	1927	TTGTAGCTGTT AAAAA A[A/gap]AGGTAG CTGTGATACAA CCCCAGG	A	gap				SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT- ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2592	cg43931444	1928	TGTAGCTGTTA AAAAA A[A/gap]GGTAGC TGTGATACAAAC CCCAGGA	A	gap				SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT- ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9

2593	cg43931444	612	CGCAGTAGACAG AGACAGACCGA GA[<u>gap</u>]/GJAGGAA GGGAGAGACAG AGGGGGCGC	gap	G				SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT-ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2594	cg43950308	662	TTATGTTACATCA AGGCAGCCATG C[C/ <u>gap</u>]/AATAAA ATGGAAGGCTAT GAAAGCA	C	gap				SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P46019 PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) - HOMO SAPIENS (HUMAN), 1235 aa.	0 (Xp22.2)	X
2595	cg43950308	806	AGGTGGCCCTTG TCAAGGCTACTG C[C/ <u>gap</u>]/GCCAGG AGGATCTTTGCA TCTTTAG	C	gap				SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P46019 PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) - HOMO SAPIENS (HUMAN), 1235 aa.	0 (Xp22.2)	X
2596	cg43996195	357	GGCACGGGCTC CAGCTCTTGTGT AA[G/A]/AAAGAAC AGGAATGAGAAC AGCTTT	G	A				SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	
2597	cg43947998	1288	AATAGGGGGAG AAGAGAATGGTG GG[G/T]/TTTTTTT TCCCCCTTAAAA TGTAAT	G	T				SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:Q131265 METHYLTHIOADENOSINE PHOSPHORYLASE (EC 2.4.2.28) (MTA PHOSPHORYLASE) (MTAPASE) - HOMO SAPIENS (HUMAN), 283 aa.	2.8E-152 9 (9p21)	

2598	cg43958858	2869	TTCTGTTTGCTG TTTTTTGTTTTG [gap/TTTTTTTTT CTCCAGAGCACT TTGGT	gap	T			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.lpcis:SWISSPROT- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME- ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)
2599	cg43958858	2877	GCTGTTTTTTTGT TTTTGTTTTTTTTTg ap/TCTCCAGAG CACTTTGGTCTA GACTA	gap	T			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.lpcis:SWISSPROT- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME- ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)
2600	cg44016415	248	AGAAATGAGAAA AAAATAGCAAGC G[C/gap]CAGGGC CAATTAAGCATC CTCTCC	C gap	gap			SILENT- NONCODING	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2601	cg44016415	249	GAAATGAGAAA AAATAGCAAGCG C[C/gap]AGGGCC AATTAAGCATCC CTCTCC	C gap	gap			SILENT- NONCODING	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X

2602	cg44016415	283	TTAAGCATCCCT. CTCCCGTTTTT C[T/gap]GAATAC AACACAGTGATC CTCACCG	T	gap				SILENT- NONCODI NG	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2603	cg44016415	296	TCCCGGTTTTTC TGAATACAACAC A[G/gap]TGATCC TCACCGTAACCC CTACACA	G	gap				SILENT- NONCODI NG	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2604	cg43282997	619	CGAGACAGGAG GCTGAACCCCG GAG[G/gap]CTGC AGCCAGGGAGG AGGCAGTGGG	G	gap				SILENT- NONCODI NG	polymera se	Human Gene SWISSNEW-ID:P55199 RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) - HOMO SAPIENS (HUMAN), 621 aa.	5.5e-314	
2605	cg43282997	715	GGGAGGGCCGA GGTGGGCTTGC AGC[C/gap]ACCC GCCAGGGCCAG ACGTCTGCAG	C	gap				SILENT- NONCODI NG	polymera se	Human Gene SWISSNEW-ID:P55199 RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) - HOMO SAPIENS (HUMAN), 621 aa.	5.5e-314	
2606	cg43993893	318	CAAAGGTTAAGA AATAAATTAAGA C[T/gap]CCTATT GGGTTGTGTCTG CCAGGGA	T	gap				SILENT- NONCODI NG	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178 (8p11.2)	8
2607	cg43993893	321	AGGTTAAGAAAT AAATTAAGACTC C[T/gap]ATTGGG TTGTGTCTGCCA GGGAGGA	T	gap				SILENT- NONCODI NG	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178 (8p11.2)	8

2608	cg43993893	337	AAGACTCCTATT GGGTTGTGCTG C[gap/G]CAGGGA GGATACAGGCCT CATTCGC	gap	G				SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. pcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
2609	cg43935562	2098	CAGTCAGTTCAT CCCTACCCTGGC C[C/T]AGATGATC ACTGATCTTGTC ATTAT	C	T				SILENT- NONCODING	polymera se	Human Gene TREMBLNEW-ID:G300898 A1 REPLICATIVE POLYMERASE ACCESSORY PROTEIN 38 KDA SUBUNIT - HOMO SAPIENS, 315 aa.	4.7E-166	13 (13q12.3)
2610	cg43938941	182	GACAATGATGGA GGCTCAGATCAC A[C/T]TGCACCTC TTAGTCTTCCA ACTTG	C	T				SILENT- NONCODING	polymera se	Human Gene SPTREMBL-ID:Q19869 SIMILAR TO S. CEREVISIAE SERINE- RICH RNA POLYMERASE I SUPPRESSOR PROTEIN - CAENORHABDITIS ELEGANS, 685 aa.	1.9E-160	13
2611	cg43916712	2631	GAGATTATGTTG TGCTCTTTATTG C[C/gap]AAAAAT AAACACTTTTAA AAGACA	C	gap				SILENT- NONCODING	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
2612	cg43916712	3207	ACTAACCAGGAG AGAAGTCTAGTT G[G/gap]TTCCCT ACAGGTGCACTG GAAACAC	G	gap				SILENT- NONCODING	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
2613	cg43916712	4335	TTGGCGTACGGC ATCTCGCCAGG G[G/gap]CCACCA GCCTCCGCGTCT GCTCCGC	G	gap				SILENT- NONCODING	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	

2614	cg43988515	577	AGAAACATTAAA CACTATGACACA TIGTACCTTTT AGCTATTTTAAAT AGTC	G	T				SILENT- NONCODING	polymera se	Human Gene Similar to SPTRMBL- ID:Q92811 RNA POLYMERASE II COMPLEX COMPONENT SRB7 - HOMO SAPIENS (HUMAN), 144 aa.	1.80E-70	12
2615	cg43935115	1077	TCCACAATACTT AGCACTTGTCCTC C[gap/C]AAGTGT AAACACTTCCCA JGGCGTG	gap	C				SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2616	cg43935115	1192	TAAGAAATTCAG GCCAGTTGTGGT G[Gap]CTCATG CCTGTAATCTCA CCAGTTT	G	gap				SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2617	cg43935115	1466	TCTCCATTAAAA AAAAA A[Gap]GGCATTTC AAACTAACAGCG GTTTA	A	gap				SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2618	cg43935115	314	GTTTCCCCCAG ACTGAGATCAAG TIGTACTTCACT GCAGTGGCTCAA GAGTG	G	A				SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2619	cg43935115	810	GTAGCCCTGTCA TTGGGCACACAA C[AC]ACCACAGT TCATACAGCAA TGGGC	A	C				SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2

2620	cg43948227	94	A A C T C T T A T G A T C A A A A A G G C C A C [A/T] T T T T T A A G A T T G T A T T A C T T G A T T	A	T				SILENT- NONCODING	polymera se	Human Gene Similar to SWISSNEW- ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.[pcis:SWISSPROT-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5
2621	cg43969348	422	T A G C T G C T A A C A A T G C C T T G G G T C T T C G A G G G C A A C C C A G G T C C C C A T G G T G C	C	G				SILENT- NONCODING	polymera se	Human Gene Similar to SPTRMBL- ID:Q15370 RNA POLYMERASE II TRANSCRIPTION FACTOR SIII P18 SUBUNIT - HOMO SAPIENS (HUMAN), 118 aa.	3.90E-59	16
2622	cg43924683	161	T A C A A A A C C C C C C A T C C A G A T A T A T T [gap] C A C G T T A A C A A T T C T G A G A T A A C T G	T	gap				SILENT- NONCODING	polymera se	Human Gene Similar to TREMBLNEW- ID:G300899 A1 REPLICATIVE POLYMERASE ACCESSORY PROTEIN 36 KDA SUBUNIT - HOMO SAPIENS, 325 aa.	1.40E-54 3 (3q27)	
2623	cg42534568	104	C G A G G G G A T G C G C G C C A G C A A C C C C [C/gap] A G C T C T C C C C A G A G A G G G C C C G G C C	C	gap				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00 (12p13)	12
2624	cg42534568	132	C T C T C C C C A G A G A G G G C C C G G C C G A [G/C] G C T G G A G C G G A G C C T G A C G C C A G G C	G	C				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00 (12p13)	12
2625	cg42534568	2529	G G T A A G T G G C T T T T T G T A C T G T A G T T [gap] C A G A T A G A G A T A T T T T G G G T A T A T T	T	gap				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00 (12p13)	12

2626	cg42534568	2546	ACTGTAGTTCAG ATAGAGATATTT [G/gap]GGTATAT TTTCAAGATACA TGTGT	G	gap				SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2627	cg42534568	2556	AGATAGAGATAT TTTGGGTATATTT [T/gap]CAAGATA CATGTTGTATTTA TGGAA	T	gap				SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2628	cg42534568	2585	GATACATGTTGT ATTTATGGAAGA AATGTGTTGGT CCTGATGGTTT TCTGT	A	T				SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2629	cg42534568	2617	GTCCTGATGGTT TTTCTGTGTTACT [T/gap]ATATTAGA GTCAGAGATCTT GGTAT	T	gap				SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2630	cg42534568	88	TGACGTCAGGG CCAAGCGAGGG GAT[G/gap]CGCG CCAGCAACCCCG AGCTCTCCC	G	gap				SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2631	cg44938709	758	AGACCGCGAAC CGGAGGAGCG CGG[G/gap]CCCC ACCCTAAAGAGG GCGCAGCCG	G	gap				SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P17658 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (HBK2) - HOMO SAPIENS (HUMAN), 529 aa.	1.00E-287	12 (12p13)
2632	cg42937321	132	GGTGCCACAC GCTGCTGAACCA CG[G/gap]CTACG CGGAGCCCCCG CGCAGGCCG	G	gap				SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)

2633	cg42937321	137	CCACACGCTGGT GAACCACGGCTA C[G/gap]CGGAGC CCCGCCGCGAGG CCGCGAGC	G	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2634	cg42937321	149	GAACCACGGCTA CGCGGAGCCCC GC[C/gap]GCAGG CCGCGAGCTGC CGCCCCGACA	C	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2635	cg42937321	151	ACCACGGCTACG CGGAGCCCCGC CG[C/gap]AGGCC GCGAGCTGCCG CCCGACATG	C	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2636	cg42937321	1820	CTTGGTCTGCCT ATGCCCTTGTTT T[gap/T]ATACATT TCCAGACCATTC ATCAAG	gap	T			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2637	cg42937321	3084	ACCTTACTACAA GGGACCTTCAG GC[C/gap]TTTCT CTTTAAAAAAA AATACA	C	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)

2638	cg43333426	1740	TCAGGACAGAGC CAACCTGGCTC C[A/G]TGGACCTT CTGGAGGAAGG TGGGG	A	G				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSNEW-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.lpcsl:SWISSPROT- ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.	4.40E-241	
2639	cg40991967	78	CAACAGGGCCTC GGTACCCTCAC C[C/T]AGCATATC CAAACTCTTGCA TCAAA	C	T				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P48048 ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 1 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 1) (ATP- REGULATED POTASSIUM CHANNEL ROM-K) (KIR1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.80E-205	11 (11q24)
2640	cg43008113	161	CTGCGGCGTTG GCCTTGGCTTTG GC[C/T]TTGGCG GCGGCGGTGGA GAAGATGC	C	T				SILENT- NONCODING	potassiu m_chann el	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.lpcsl:TREMBLNEW-ID:G2811120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.80E-180	1
2641	cg43008113	1806	AGTGTAGTTCTG AAACTAAGACTA T[A/gap]GATATTT TGTTCTTTTGAT TTCTC	A	gap				SILENT- NONCODING	potassiu m_chann el	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.lpcsl:TREMBLNEW-ID:G2811120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.80E-180	1

2642	cg43917554	1297	GTCCCCACTCAA CTGACTCATACC TIG/TJTTCGGC TGCATCACTATG TGCCC	G	T				SILENT- NONCODING	potassium channel	Human Gene Similar to SPTREMBL- ID:Q16558 MAXIK POTASSIUM CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 191 aa.	1.80E+00	5
2643	cg43262191	2044	TCTGACCCCAACC CTGGGCCACTG CC[C/gap]TGCTC CAGAGAGTGGA CCTTGACTC	C	gap				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2644	cg43262191	3158	TTCCCATTTTCTC AGCCTCTTCTCA C/gapJTGCTCCA GAGAGGTGGT GCCTGG	C	gap				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2645	cg43262191	3174	CTTCTCACTGCC TCCAGAGAGGTG G[G/A]TGCCTGG GTTGAGAGACAC AGCTGC	G	A				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2646	cg43262191	3258	AAGGAGGTCATT CATCAACAAATA TTA/GJTATTGG AGACCGACTTTG TGCAA	A	G				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3

2647	cg43262191	3914	ATGGCAATTAA CCACATTTGGAA G[G/gap]CACTGC CTTCAGCTGAGT TTATGAA	G	gap				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.pcls:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2648	cg43951366	174	CCCTCAGACAGC AAAGCCTACCCC C[gap]C[GCGCCG CGCCCTGCCCCG CCGCTGCG	gap	C				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.pcls:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)

2649	cg43951366	197	CCCGCGCCGCGC CCCTGCCCGCC GCT[G/C]CGATG CTCGCCCGCGC CCTGCTGCT	G	C			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.lpcis:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)
2650	cg43951366	198	CCGCGCCGCGC CCTGCCCGCGC CTG[C/G]GATGC TCGCCCGCGCC CTGCTGCTG	C	G			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.lpcis:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)

2651	cg43951366	2441	TTTGAAATTTTAA AGTACTTTTGGT T/CJATTTTCTGT CATCAACAAAA ACA	T	C				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.jpcls:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)
2652	cg43951366	2676	CTTGGATTAA TCTGTAAATCA GATJAGAAATTT TACTACAAATTGC TTGTT	A	T				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.jpcls:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)

2653	cg43951366	2677	TTGGATTAAAT CTGTAAATCAG A[AT]GAAATTT ACTACAATTGCT TGTTA	A	T				SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.pcds:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)
2654	cg43306254	120	GCGGCTGCGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCAGC CGCGGTAAAC	G	gap				SILENT- NONCODING	prostaglandin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa	1.40E-211	1 (1p31.2)
2655	cg43306254	171	GCCGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCTCTCCCG CTGCGGCTC	G	gap				SILENT- NONCODING	prostaglandin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa	1.40E-211	1 (1p31.2)
2656	cg43306254	53	TGGCTCCCTCCC GGGCCAGTGAG CC[C/gap]TGGCG CCGCCGCCGCC GCGGTCCCA	C	gap				SILENT- NONCODING	prostaglandin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa	1.40E-211	1 (1p31.2)

2657	cg43306254	73	GAGCCCTGGCG CCGCCCGCGCC GCG[G/gap]TCCC AGCAGCGGAGT AGGCGGCGG	G	gap				SILENT- NONCODI NG	prostagla ndin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
2658	cg42913398	319	TACAACATAAAA AATAAAATAAGC A[A/G]ACTGTCTG AGGGGTTTATAT AAGGT	A	G				SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:O00199 INTEGRAL MEMBRANE SERINE PROTEASE SEPRASE - HOMO SAPIENS (HUMAN), 760 aa.	0.00E+00	2
2659	cg43916732	1438	GCTGCGTCCCA GGACTGAGACG CAG[G/gap]CCAG CCCCGGCCCCCT AGCCCTCAGG	G	gap				SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2660	cg43916732	1448	AGGACTGAGAC GCAGGCCAGCC CCG[G/gap]CCCC TAGCCCTCAGGC CTTCCTTCT	G	gap				SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2661	cg43916732	1500	ATCCAAATAAAT GTTTCTTAATGA G[A/G]AAAAAAA AAAAAAA AAAAA	A	G				SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2662	cg43967594	641	TTGCTAGGTATA ATTTTATTTTATA T[gap]AAAAAGTG TTTCTGTGATTCT TCAG	T	gap				SILENT- NONCODI NG	protease	Human Gene TREMBLNEW- ID:G2738915 SERINE PROTEASE - HOMO SAPIENS (HUMAN), 529 aa.	6.10E-239	2
2663	cg43922779	2882	TTTTTAAACTAA CCAAAAAAGGCC [G/gap]GGTGCTG GGATTACAGGCA TGAGCC	G	gap				SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:O00232 PROTEASOME SUBUNIT P55 - HOMO SAPIENS (HUMAN), 456 aa.	4.40E-236	17

2664	cg43986296	540	CATCTGCTCTGC AGTCCTGCCGCA G[G/gap]ATTCCC TAGTGAAGCAGC TCAGGCC	G	gap			SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
2665	cg43986296	833	CTTCTCAACTTAT ATGTGGGAAGG G[G/gap]TCCCCC ATGCTTGGGGGA CCTAGGC	G	gap			SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE-RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
2666	cg44932353	143	TTCAGCCACACT GACGGCTCTGA GC[C/gap]AGAGC CACCTCCTGGCC CCACTGGT	C	gap			SILENT- NONCODI NG	protease	Human Gene TREMBLNEW- ID:G2880036 SIMILAR TO FURIN-LIKE PROTEASES - HOMO SAPIENS (HUMAN), 286 aa.	1.10E-155	3
2667	cg43306871	108	GTGTTAAGCCTT ACATGACAATCA G[C/gap]ATGAAG ATTACATACAC ATGTTAT	C	gap			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.[pcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2668	cg43306871	230	AGGTTCAGAGAG GGCACTTGGCTT G[C/gap]CCAAAG TCACACAGCAGG GAGTGCC	C	gap			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.[pcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19

2669	cg43306871	232	GTTCAGAGAGG C GCACCTTGCGCTTG CC[C/gap]AAAGT CACACAGCAGG GAGTGGCAG	gap			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. pcIs:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2670	cg43306871	246	CTTGGCTTGCCC A AAAGTCACACAG C[A/G]GGGAGTG GCAGAGGGAAGT CAGGTTG	G			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. pcIs:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2671	cg43306871	313	GCTCTCAGAGGC G TGGGTGATGACC G[G/A]CTTCCTG GCTTCTCTGGAA TAAACC	A			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. pcIs:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19

2672	cg43923853	133	ACACTTTAAGAT ACCATACATGC T[AG]TGTGTATT TACAAAAGTTAC AGGTC	A	G				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa. pcds:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4
2673	cg43923853	190	GAAAAAGAAAC TGTCATTGACAA A[T/C]GCGAGCT CATTTTTGAGC AACAAG	T	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa. pcds:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

2674	cg43923853	295	CTCCGCACCTGC TGAGGCCTGGA GC[C/gap]TGCCT CCCGGGCTGAG GGCTCAGCT	gap				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.[pcds:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4
2675	cg43923853	312	CCTGGAGCCTG CCTCCCGGGCT GAG[G/T]GCTCA GCTCTGGCCTCC GGCTGGAT	T				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.[pcds:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

2676	cg42918089	1136	TTTGAATGTCCTT TCACTCCTTTTAT ATTGGATAAACT CCTTATGGTGT GACT	A	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2677	cg42918089	1139	TGAATGTCCTTTC ACTCCTTTTAAG GTA/TTAAACTCC TTTATGGTGTGA CTGTG	A	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2678	cg42918089	1172	TTTATGGTGTGA CTGTGCTCTTATT C[gap/C]ATCTATA CTTGCAGTGGGT AGATGT	gap	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2679	cg42918089	1178	GTGTGACTGTGT CTTATTTCATCTAT [gap/G]ACTTGCA GTGGGTAGATGT CAATAA	gap	G				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2680	cg42918089	1179	TGTGACTGTGTC TTATTCATCTATA [gap/G]CTTGCAG TGGGTAGATGTC AATAAA	gap	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)
2681	cg42918089	1182	GACTGTGTCCTTA TTCATCTATACTT [gap/T]GCAGTGG GTAGATGTCAAT AAATGT	gap	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)

2682	cg42918089	1183	ACTGTGTCCTTAT TCATCTATACTT G[<i>gap</i>]/T]CAGTGG GTAGATGTCAAT AAATGTT	gap	T				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2683	cg42918089	1188	GTCTTATTTCATCT ATACTTGCAGTG[gap/C]GGTAGAT GTCAATAAATGT TACATA	gap	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2684	cg42918089	1189	TCTTATTCATCTA TACTTGCAGTGG [gap/C]GTAGATG TCAATAAATGTTA CATAC	gap	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2685	cg42918089	1230	TGTTACATACAC AAATAAATAAAAT [G/A]TTTATTCCA TGGTAAATTTTAA AAAA	G	A				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2686	cg42918089	1235	CATACACAAATA AATAAATGTTTA [T/G]TCCATGGTA AATTAAAAA CCG	T	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)
2687	cg42918089	1236	ATACACAAATAA ATAAATGTTTAT [T/G]CCATGGTAA ATTAAAAA CGC	T	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)

2688	cg42918089	1251	AAATGTTTATTCCA ATGGTAAATTTAA A/CJAAAAAACCG CCGATACTGACG GGC	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN) 267 aa.	2.40E-146	11 (11q21)
2689	cg42918089	1252	AATGTTTATTCCA TGGTAAATTTAA A/CJAAAAAACCG CGATACTGACG GC	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN) 267 aa.	2.40E-146	11 (11q21)
2690	cg43074055	1055	CTCTTCCCCGAA CACTGTGGCGTC C[G/gap]GGACGG CCCCACCCGTCC CCCCACA	gap				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.70E-138 (19p13.3)	19 (19p13.3)

2691	cg43990989	110	ATTCCATGTATG TCATAGGTGTGA A[A/gap]CCTTAAA TCCTTCCAACAG CCACTG	A	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:Q92876 PROTEASE M PRECURSOR (EC 3.4.21.-) (NEUROSIN) (ZYME) (SP59) - HOMO SAPIENS (HUMAN), 244 aa.lpcis:SP TREMBL-ID:Q92876 PROTEASE M PRECURSOR - HOMO SAPIENS (HUMAN), 244 aa.	7.50E-136	19
2692	cg43990989	235	GGGGACACCGA CAGTAAGCAGCG GA[G/gap]CTGGG ATTCCAGACACG TGGCTGGG	G	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:Q92876 PROTEASE M PRECURSOR (EC 3.4.21.-) (NEUROSIN) (ZYME) (SP59) - HOMO SAPIENS (HUMAN), 244 aa.lpcis:SP TREMBL-ID:Q92876 PROTEASE M PRECURSOR - HOMO SAPIENS (HUMAN), 244 aa.	7.50E-136	19
2693	cg43967243	1072	GCTGGAACCCAC GGGACATGTTGG TA[G/C]AAGCACT ACTTTAAACACA ATCCCT	G	C			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.lpcis:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130	

2694	cg43987243	209	ATATAGAGTCCT AACCACCTTCGGT G[G/gap]TAGGAG GAGTGGGAGAG GCTCCTTT	G	gap		SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa. pcis:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa	6.40E-130	
2695	cg43974374	496	GGTCACTGTGTC CGTATTACCAAT G[A/G]CAGTCAC CCCAAGAAACAC AAGCAG	A	G		SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q16242 PROTEASOME SUBUNIT MB1 - HOMO SAPIENS (HUMAN), 215 aa (fragment)	7.40E-113 (14q11.2)	14
2696	cg2510140	22	CAAGCAGATAGG ACACTGGAA[A/G] AAGGAATGCCCA TTAAACCCAGAA G	A	G		SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P03356 POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - AKV MURINE LEUKEMIA VIRUS, 1196 aa. pcis:SWISSPROT-ID:P03356 POL POLYPROTEIN (PROTEASE (EC 3.4.23.); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) - AKV MURINE LEUKEMIA VIRUS, 1196 aa.	1.90E-105	

2697	cg43917011	186	AACCTCTCAATGC TTAACCAATTTTCA [G/A]TTGCCAGG AAAGAGGTAGAA ATATC	G	A				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P49662 CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX PROTEASE) (ICE(REL)-I) - HOMO SAPIENS (HUMAN), 377 aa. pcls:SWISSPROT- ID:P49662 CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX PROTEASE) (ICEREL- II) - HOMO SAPIENS (HUMAN), 377 aa.	1.50E-103	11
2698	cg43930253	1288	ATATTGGATGGC GAGGACAGCGT GGT/CJACTGGC TGCGAGTGTTC TGAGAGT	T	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2699	cg43930253	1349	ATGACTTATGAC ACTTGCACAGCA T[G/gap]GCTCTG CCTCACAATGAT GCAGTCA	G	gap				SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2700	cg43930253	1350	TGACTTATGACA CTTGCACAGCAT G[G/gap]CTCTGC CTCACAATGATG CAGTCAG	G	gap				SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2701	cg43930253	1400	GCCACCTGGTGA AGAAAGTGACCTG C[G/A]ACACAGG AAACGATGGGAC CTCAGT	G	A				SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20

2702	cg43947922	934	TAGATTTGAGAC AACTAGCCTGTT A[C/T]TCAGCCCA ATATCCCCCCAT GGTTT	C	T			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P28070 PROTEASOME BETA CHAIN PRECURSOR (EC 3.4.99.46) (MACROPAIN BETA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX BETA CHAIN) (PROTEASOME CHAIN 3) (HSN3) (HSBPROS26) - HOMO SAPIENS (HUMAN), 264 aa.	1.10E-97	
2703	cg43104740	2154	ACATGGATGAGC ACACACACACCA A[ap/G]TGCGCA CACACACCGATG TACACAC	gap	G			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	5.00E-94	13
2704	cg43297588	23	GGCACAGCATG CGGGCGGTGTG[C/G]GCCCCCCC GGTGTCGGCCCT GCIGT	C	G			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2705	cg43297588	24	GGCACAGCATG CGGGCGGTGTG C[G/C]CCCCCCC GGTGTCGGCCCT GCIGTC	G	C			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2706	cg43297588	26	GGCACAGCATG CGGGCGGTGTG CGC[C/G]CCCCC GGTGTCGGCCCT GCIGTCGG	C	G			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2707	cg43297610	153	CAGCTGAGCAG GGTGGCTGTTCC TC[G/T]GCTGGAT TAGGGCTGAATC TGTGGG	G	T			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)

2708	cg43297610	2707	GCCGGACATCC CAGGCACACGT GTG[C/gap]GCCA CCTTCAGCAGGC ATTCGGGTG	C	gap				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)
2709	cg43297610	2760	GGGCTGGTGGC TCATCAGGCCTG GG[C/gap]CCCAC ACTGACAAGCGC CAGATACG	C	gap				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)
2710	cg43917924	315	ATTTGTCTCACTT CGATTCAGACAC [T/G]TAAATGGGA GTTTTCAGTTTAT CCT	T	G				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	1.80E-81	3 (3q21)
2711	cg43921680	347	GCCAAGTCATTT AAAAAGGATTTA G[G/gap]CCACTG CCTTTTCTCTGAG GGAGGAG	G	gap				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2712	cg43921680	612	CATGTTGTAA CAGTAGAGGAG CC[A/G]GGGACT CTGTCTCCATTC TCTCATC	A	G				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2713	cg43921680	689	AAAAAAAACAA AAAAACACAACA A[C/gap]AAAAAA ACTGTCCTCTGA GGAGGCA	C	gap				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2714	cg42033569	513	GCTGTCCATTAG TAGAAGAGCAAG A[G/A]AGCCTTG GATGTCAACGCC TCGCTC	G	A				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-72	

2715	cg44031287	300	TTCACAGGTGCC AGAGCTTAGAGG TIG/TTCACAGGC ACCGGGGTGGC TCCTGC	G	T			SILENT- NONCODI NG	protease	Human Gene Similar to TREMBLNEW- ID:G2736064 UBIQUITIN SPECIFIC PROTEASE 41 - GALLUS GALLUS (CHICKEN), 357 aa.	8.10E-67	1
2716	cg43276961	1111	GATGACAAATAC TGGTTAATTAGC A[AG]TTTAAGAC CAGAGCCAAATT ATCCC	A	G			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59 (11q22.2)	11
2717	cg43276961	1343	GGCCTAAATTC ATGCAGTCTTCT A[C/T]CTAAAAA CAAATACTACTA TTTCT	C	T			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59 (11q22.2)	11

2718	cg43276961	1686	AGTTTGAAATA GTTACCTTCAAA G[G/gap]CCAAGA GAATTCTATTG AAGCATG	G	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)
2719	cg43276961	1693	AAATAGTTACCT TCAAAGGCCAAG A[G/T]AATTCTAT TTGAAGCATGCT CTGTA	G	T			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)
2720	cg43069905	417	TCAGCGCCCTCC ACAGTGGCAGTG C[C/gap]AGCTTG GAATCCCGCTTC CGGTTGT	C	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	1.30E-57	13
2721	cg43316919	1645	AAGGAAAGGAGT ATTGGAAATTCA A[A/gap]CAACCA GATACTCAAGT AGAACCT	A	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT- ID:P22757 HATCHING ENZYME PRECURSOR (EC 3.4.24.12) (HE) (HEZ) (ENVELYSIN) (SEA-URCHIN- HATCHING PROTEINASE) - PARACENTROTUS LIVIDUS (COMMON SEA URCHIN), 587 aa.	8.10E-56	

2722	cg44028327	3348	TGGATGCAATTTG AACCTCTGAGTT TIG/CJTCTTTTCAT TTTAAATATTGTC TGTT	G	C				SILENT- NONCODI NG	protease nhib	Human Gene SWISSPROT-ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)
2723	cg44028327	3540	CAAGGGTCGAC CCCCAAAGGCA GGG[gap/G]CAGA GCCAGCATCTGA GAGGGAGGT	gap	G				SILENT- NONCODI NG	protease nhib	Human Gene SWISSPROT-ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)
2724	cg43979831	1589	GTTGGGGACAA GGATGACACCGA AG[gap]TCCAG GAGTCCAGGACA GCAGGTGC	G	gap				SILENT- NONCODI NG	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
2725	cg43979831	1628	GACAGCAGGTG CTGGCCGGTGG GGA[G/A]CGGG AGGGGCACTGA GATGGGCAG	G	A				SILENT- NONCODI NG	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
2726	cg43920929	320	GGAAAAGAAATTT AAAAGGCAATA A[gap/T]TTTTTT TTCATAAAAGT AAAAGC	gap	T				SILENT- NONCODI NG	protease nhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
2727	cg43268468	1394	TGCTGTCGGGGT CTGGGGAGCCC TC[C/gap]TCCGG GGGCTGGCAG GGTCTGCG	C	gap				SILENT- NONCODI NG	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188 (17p13.3)	17
2728	cg43268468	1560	CTGAGGGGGCT CCAGCCAGCACA GA[G/T]CTTTTT TGCTGCCTTCTA ATCCAG	G	T				SILENT- NONCODI NG	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188 (17p13.3)	17

2729	cg43932980	93	GAGTTATAGCTA CCCCGGCCGCG GA[G/gap]CCGGC TCACTGCACTAC CCCCGCCC	G	gap			SILENT- NONCODI NG	proteasei nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20
2730	cg43932980	3021	GAGAAACACAGT CATTGTCTTAGG T[G/A]TTCTATGG GAGGAAGTGAAT AGAGC	G	A			SILENT- NONCODI NG	proteasei nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20
2731	cg43932980	67	GCAAGAACCAGC GCAAGAGGGAA GC[G/A]GAGTTAT AGCTACCCCGG CCGCGGA	G	A			SILENT- NONCODI NG	proteasei nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20

2732	cg43980892	159	AAAATAATTGATG CAAAATTTCAA GATCATCACTGC TGATGATATTCC TCCA	A				SILENT- NONCODING	reductase	Human Gene SWISSNEW-ID:P54886 DELTA 1-PYRROLINE-5- CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5- SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)] - HOMO SAPIENS (HUMAN), 795 aa.[pcis:SWISSPROT- ID:P54886 DELTA 1-PYRROLINE-5- CARBOXYLATE SYNTHETASE (P5CS) (CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) / GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5- SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)) - HOMO SAPIENS (HUMAN), 795 aa.	0.00E+00	10 (10q24.3)
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2733	cg43990892	446	AAATCTTTCCTTT TTGAAGATGACTT A/G]CATGTGAAA GAAATAAAATGT GAAA	A	G				SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P54886 DELTA 1-PYRROLINE-5- CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5- SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)] - HOMO SAPIENS (HUMAN), 795 aa. pcds:SWISSPROT- ID:P54886 DELTA 1-PYRROLINE-5- CARBOXYLATE SYNTHETASE (P5CS) (CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) / GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5- SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)) - HOMO SAPIENS (HUMAN), 795 aa.	0.00E+00	10 (10q24.3)
2734	cg44002608	282	ATTCAAATTAATTA TTATTTTTTTTTTg ap/T]ACAAAGAAA TAAACCTGTAAA GGAT	gap	T				SILENT- NONCODING	reductase	Human Gene SPTREMBL-ID:Q94511 75KDA SUBUNIT NADH:BIQUINONE REDUCTASE PRECURSOR - DROSOPHILA MELANOGASTER (FRUIT FLY), 653 aa (fragment).	4.60E-223	2
2735	cg43969711	722	CAAAATAAATCAA GCTATTATCGCC T/T]C]GTGAGTAC AAACAATGTTTAT TTGT	T	C				SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)

2736	cg43969711	733	GCTATTATCGCC TTGTGAGTACAA A[<u>gap</u>]/A]CAATGTT TATTGTTTGTA AGTGC	gap	A				SILENT- NONCODING	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)
2737	cg43941472	1139	GGGACAAAGC AGCGTCTGGCTC GA[G <u>gap</u>]/TGGAA GCGTCCAAACCT GCTTTTCC	G	gap				SILENT- NONCODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2738	cg43941472	1208	TTCCGTCAGAGC TTCTGGCTGCTC C[T/A]GAATGGTG GAATGCTGTGTC CTCTC	T	A				SILENT- NONCODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2739	cg43941472	1222	TGGCTGCTCCTG AATGGTGGAATG C[<u>gap</u>]/C]TGTGTC CTCTCTCTGTC TCCIGCT	gap	C				SILENT- NONCODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2740	cg43941472	1247	CTGTGTCCTCTC TTCTGTCTCCTG C[T/C]GCCTGGA GGCTTCGGGGC TCTCCCG	T	C				SILENT- NONCODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2741	cg43941472	1281	GCTTCGGGGCT CTCCCGCCTGCG TT[G/C]TCGGGG CCCAGACGCAA GGCACCGA	G	C				SILENT- NONCODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2742	cg43941472	1440	TCTTTTTAAAG AAGATGGTTTCA[gap/G]CTTTAATA TAATGCTATTATC TTAA	gap	G				SILENT- NONCODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)

2743	cg43941472	1474	TAATGCTATTATCA TTAAGACTTAA A/GJAAGTTGCTG GAGTTTGTA CCAG	A	G				SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2744	cg43941472	1475	AATGCTATTATCT TAAGACTTAA A/GJAGTTGCTGG AGTTTGTA CAGG	A	G				SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2745	cg43987538	115	ACTTTATTACACA TTATTATGTTAC G/AJAGACAAATG CAGATAATTCTT AATT	G	A				SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
2746	cg43987538	86	TTTTTTTTTT TTTAAATTTCTA /GJTAGACTTTATT ACACATTATTAT GT	A	G				SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
2747	cg40312187	2424	AGGATGATGTAG ATTACTGAAAA T/A/GJCAAATTGC AATCATATAAATA AGTG	A	G				SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P31213 3-OXO-5- ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA- REDUCTASE 2) (SR TYPE 2) - HOMO SAPIENS (HUMAN), 254 aa.	5.70E-138	2 (2p23)
2748	cg43918176	50	TTTTTTTTTT TTTTTTTTTTT CJTGTGAGAAAA GAGACTTTATTA GG	T	C				SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2.00E-133	X

2749	cg43927549	1010	TGGGCATCACGT AAGCAGCACACT A[G/C]GAGGCC AGGCGCAGGCA AAGAGAA	G	C				SILENT- NONCODING	reductas. e	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
2750	cg43995873	386	GGGGCGGGGCC TCGCCTGCACAA ATTAGJGGGACG AGGGGGCGGG GCGGCCAC	A	G				SILENT- NONCODING	reductas e	Human Gene Similar to SWISSNEW- ID:P00374 DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) - HOMO SAPIENS (HUMAN), 186 aa.[pcIs:SWISSPROT-ID:P00374 DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) - HOMO SAPIENS (HUMAN), 186 aa.	1.90E-98	5 (5q11.2)
2751	cg43936109	399	TCCAATAAGCAA ATGACATTGGT C[C/gap]ATTGG CATGTGTAATTC TCCTTT	C	gap				SILENT- NONCODING	ribosomal prot	Human Gene SWISSPROT-ID:P49406 PUTATIVE 60S RIBOSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	2.50E-151	2
2752	cg43982087	1708	TTAGTGGCTTCA AAGGCCCAGCT GAIC/AJACCCTCC ACAGCCTAAGGG GTGTCC	C	A				SILENT- NONCODING	ribosomal prot	Human Gene Similar to SWISSPROT- ID:P17103 HYPOTHETICAL 40 KD GTP- BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION - HALOBACTERIUM CUTIRUBRUM, 370 aa.	2.70E-67	17
2753	cg43982087	1759	TAAAGTGCCTCC CCCTGTATTCCC C[C/T]TCCCAGG GCAGCCCCCTGC CCAGCAC	C	T				SILENT- NONCODING	ribosomal prot	Human Gene Similar to SWISSPROT- ID:P17103 HYPOTHETICAL 40 KD GTP- BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION - HALOBACTERIUM CUTIRUBRUM, 370 aa.	2.70E-67	17

2754	cg44923577	838	TCCCAAGAAGAA GGTCAAATAAGG TTT/GGTCTTTC CTTGAAGGGCAG CCTCC	T	G				SILENT- NONCODI NG	ribosomal prot	Human Gene Similar to SPTREMBL- ID:Q95260 UBIQUITIN/RIBOSOMAL FUSION PROTEIN - SUS SCROFA (PIG), 128 aa.	1.10E-65	19 (19p13.1)
2755	cg42845774	566	TAAATGAAGAC ATTTGGGTGTTT C/A/GTGTGAGTG AATTATCTTTTCT CTTG	A	G				SILENT- NONCODI NG	ribosomal prot	Human Gene Similar to TREMBLNEW- ID:E1284377 DJ262D12.2 (MITOCHONDRIAL/CHLOROPLAST 30S RIBOSOMAL PROTEIN S14)-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 128 aa.	1.70E-65	1
2756	cg43255045	5967	ATATCTTGACAC CTGCCAAAGCTT C/G/CJAGCACGG GAAATGAGAAA CACTGG	G	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0.00E+00	1
2757	cg43255051	624	AGGAAGTTTTTA TGCAGAGGTGAC TTC/AJCCCCCTGCA CTATTCAAGGGT TATAA	C	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0.00E+00	1
2758	cg43966202	19	TTTTTCGTCGTTT TTTTT[G/T]TAATA AAGACACTGCTT TTATTTAG	G	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14118 DYSTROGLYCAN PRECURSOR (DYSTROPHIN-ASSOCIATED GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 895 aa.	0.00E+00	3
2759	cg43973080	1686	GGCAAAGGCTC CCAGCTGTAAGG CT[G/A]GTGTGCA ACATCTACTTTAA CAGAC	G	A				SILENT- NONCODI NG	struct	Human Gene TREMBLNEW- ID:G2304981 MYOSIN VI - HOMO SAPIENS (HUMAN), 1262 aa.	0.00E+00	6
2760	cg43957646	1766	AGAAAAGTGAAA CAAAACCATAAA C/A/GJAAGCAGC GGGGTTCACGA CGCTAA	A	G				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:O00185 BETA CATENIN - HOMO SAPIENS (HUMAN), 596 aa.	0.00E+00	10

2761	cg43957640	2076	AAAGGAATGAAG AGGGTGTGAGG CC[C/gap]AATGG GGCTGGGTGGG AGGCGGTGC	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P13796 L- PLASTIN (LYMPHOCYTE CYTOSOLIC PROTEIN 1) (LCP-1) (LC64P) - HOMO SAPIENS (HUMAN), 627 aa.	0.00E+00	13 (13q14.1)
2762	cg44033566	6709	TGACGTTATTAG TTTTGTTTTACCT [gap/G]AATGTAA TAAATTTTATTGT ATAAA	gap	G				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.[pcis:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0.00E+00	14 (14q22)
2763	cg43957486	3192	AAACAAAGGTTG AGATGTAAAGG T[A/G]TTAAATTG ATGTTGCTGGAC TGICA	A	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
2764	cg43957486	3400	ATGTTCAGAAGG TTGCTCTAGATT G[A/C]GAGAAGA GACAAACACCTC CCAGGA	A	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
2765	cg43249606	20	TTTTTTTTTTTT TTTTTG[T/A]GAG AAGCTGAGCTGT TTAATCACCT	T	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.[pcis:SWISSPROT-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.	0.00E+00	
2766	cg44918439	2202	TTTTTTTCTTT TCTTTTTTTTTT[g ap/]CTGTGAAG ATTAACACTAATT ATC	gap	T				SILENT- NONCODI NG 552	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)

2767	cg44918439	2375	TCACATTTTCTCA GTGTGCCCTTCT C/GJTATCTGCC ATGTCCATAGCC ATAA	C	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
2768	cg43967978	1187	AGTTCAGAAATTC TAGGCCCAAAAG G[G/gap]TGCAAC ACCCCTTCAACCA GTTTCAG	G	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2769	cg43967978	1522	TAGAGAAGTAA AGCAACTCAGGC G[gap/G]ATATGA ATTCAAACCTCA GTGTAGA	gap	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2770	cg43967978	1582	AAGTCGGTACAG TGTCACAGGCAG C[C/gap]GTCCCG GAGACGGAGGA AGTGACTA	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2771	cg43967978	1688	GGAGGGCGGG TCTAAAAGGCAG GG[G/gap]CAGTC GCCAGGCCTAG GGCACTGGA	G	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2772	cg43967978	1716	GTCGCCAGGCC TAGGGCACTGGA AG[G/A]GTAGGA GGAGCACAGAG AACCTTCC	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2773	cg43967978	693	AGACCCAGCAC ACTCGGCTTCTG C[C/gap]AGGAGG CCAGTGGAGTG GTTTGGAC	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	

2774	cg43967978	814	CTTGGTAAAGAG CTCTGGGGGTT T[C/gap]CCCCAGA GGAGCCTGTCC CTCTGCCC	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2775	cg44034221	1989	TGCTGTACCTCG ATCTGAATCTGC C[G/gap]GGGCCC CAGCCCACTCCA CCCTGCC	G	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2776	cg44034221	1991	CTGTACCTCGAT CTGAATCTGCCG G[G/gap]GCCCCA GCCCACTCCACC CTGCCAG	G	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2777	cg44034221	1992	TGTACCTCGATC TGAATCTGCCGG G[G/gap]CCCCAG CCCACTCCACCC TGCCAGC	G	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2778	cg44034221	2020	CCAGCCCACTCC ACCCTGCCAGCA G[C/gap]TTCCAG CCAGTCCCCACA GCCTCAT	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2779	cg44034221	2098	CTATCTTCCCC ACCCCAAGCTAC C[C/gap]ATAGGG GCTGCAGAGTTA TAAGCCC	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	

2780	cg43980812	238	TAAACTCGAGGG ATTATTATTCTT G/AJATTGGAGAA AGAGAAGACAGC ATTT	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:Q15654 THYROID RECEPTOR INTERACTING PROTEIN 6 (TRIP6) (OPA- INTERACTING PROTEIN 1) (ZYXIN RELATED PROTEIN 1) (ZRP-1) - HOMO SAPIENS (HUMAN), 476 aa.	2.90E-272	7
2781	cg43931165	218	CGGCTCCCGAG TCTTGGAGAAGA GC/A/GJCGAGAA CCTAGACCGCCC CCGAAAGT	A	G				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q14704 MRNA (KIAA0092) FOR ORF (SMOOTH MUSCLE MYOSIN-RELATED) - HOMO SAPIENS (HUMAN), 474 aa.	3.00E-242	11
2782	cg43987609	996	GCACTCCATAAT AACTGGAATCCC A/C/TJGAGTGTGT ATGCCAAAGTCTC ATGAG	C	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.10E-226	2
2783	cg42491601	1485	TGGAAGAAAATA TCTAAATAGCTA C/C/gapJAGAAAG AGATGCTGCTGA GGTTTIG	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.40E-215	17
2784	cg42491601	1694	AAATGCCTGCA AAATGAAATCC A/G/AJTGAGCACT AGAAATATTAAAA CATC	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.40E-215	17
2785	cg43947066	119	TTTAGCTTTCCA CTGATATCTCAA G/A/CJTACTTTCC AGATATTAAACAG TACTC	A	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2786	cg43947066	1685	CTTAAGCTCTTT AAATCTGTAATT T/CJGAATTACCC AAAGGATTTTA AATG	T	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2

2787	cg43947066	2228	ATACCACCTAGT GTGCTAAAGACT A/C/T/GACTAGCA GCATTAGAGCAG TAAAG	C	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2788	cg43947066	378	TTTTTAAACAGAT ATTTTTTTTTTT /gap]CCTGAGGG ACTCATACTTGA CAACT	T	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2789	cg43947066	74	TTATTTTCTCAAT CAAAATGAAGTA T/C]TTCATGTTAA TTAGACTGTTTA GC	T	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2790	cg43947066	843	CCCAAGATCTAG TACGGGCTATTC A/T/GJGGTTCTGA GGCATGTCCAGC ATGCA	T	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2791	cg43963568	140	CAGATGCTTTCT GAAGAGCCCTG GG[G/gap]CAGGG GGCAGCCCTTGC CCCTCACAT	G	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207 (1q32.1)	1
2792	cg43963568	230	GGATTCAGGTC TGGAGCCAAGAA C/G/C]TAGTCCAA AGATCCCCCTCTT CCCTT	G	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207 (1q32.1)	1
2793	cg43963568	2870	CAGGAGGAGG TCCACTGCATT TG[T/gap]CTCTC AAGTTGAACCTT TCAGAGAA	T	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207 (1q32.1)	1

2794	cg43963568	2872	GGAGGGAGGTC CACTGCATTG TC[T/gap]CTCAA GTTGAACCTTTC AGAGAAAGT	T	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2795	cg43963568	317	GGATGTGATGGC ATCTGGGCAGAG C[C/gap]TATACTT GGGCTAACTCTC CTCCAA	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2796	cg43983086	139	AGCCTAGGATGG TCAGCAGCAAGG T[C/G]TCCCGGG GGATGGGCTTACC TCCCTC	C	G			SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.lpcis:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.lpcis:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10

2797	cg43983086	304	TAGTGGTCAACC CCAGGCCCTCAG GC[gap/A]CATCA CCACTGCAGGTA GTTCATCG	gap	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.lpcis:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.lpcis:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10
2798	cg43983086	432	ACACAGGCAGTT CCTCGCAAACAC T[C/A]CGACTCAA GAAAGCGAGTTT TAAAG	C	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.lpcis:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.lpcis:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10

2799	cg43983086	433	CACAGGCAGTTC CTCGCAAACT C[C/A]GACTCAAG AAAGCGAGTTT AAAGT	C	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.[pcis:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.[pcis:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10
2800	cg43923264	1291	CTGTTCAAGTCC GACCTGCGCCAA T[C/G]CCGCCAT GCTCAGGAGCC ACCAGCA	C	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2801	cg43923264	1364	GGCCGGAAGGC TAGATGGGCAC CC[T/A]GGACAA GAAATTCCCCAA GCACCT	T	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2802	cg43923264	1381	GGGCACCCTGG ACAAAGAAATTC CC[C/T]AAGCACC TTCCCTCCATT CCCCAC	C	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2803	cg43923264	1693	TCAGGGAGGGA AGGGAGCAGG CTG[gap/G]CCCC CAAGCCCTCCCA CGCAGAGGA	gap	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3

2804	cg43923264	304	AGGCGGGGCTA CTACGGGGCGG TGC[C/gap]TGCT GTGGAAATGCCT GCCCGCGCG	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2805	cg43916919	104	CTTTATTGAACAT CTGCAGGGGGC A[C/gap]CTCTGC ACTGACCAGGCA GCCAGAG	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa. pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.30E-188	2 (2cen)
2806	cg43949677	1733	CCTTTGTCTGA TATGCAGAAATG A[T/C]AGGAAAA AACCAATGGTGA AATT	T	C			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
2807	cg42894986	1436	ATTCCAGCTCCT GGCCCTCCTGG AA[C/G]CCAGGC TCTAAACAAGCA GGGAGAG	C	G			SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q28686 50- KDA DYSTROPHIN-ASSOCIATED GLYCOPROTEIN PRECURSOR - ORYCTOLAGUS CUNICULUS (RABBIT), 387 aa.	1.40E-180	17
2808	cg43971282	606	ATGCTGGGACAC CTACAGGCACAC A[G/C]AGGAATA GCAGGGCCACC CTCAGAG	G	C			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P97490 ADENYLATE CYCLASE, TYPE VIII (EC 4.6.1.1) (ATP PYRÓPHOSPHATE- LYASE) (CA(2+))/CALMODULIN ACTIVATED ADENYLYL CYCLASE) - MUS MUSCULUS (MOUSE), 1249 aa.	8.90E-180	2

2809	cg43962437	1425	AGGAGGACCTG GGGGGGGCAAG AGC[gap/C]TCAG GAGAAAGCGTG CCGCCCTTCC	gap	C				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P08247 SYNAPTAPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcis:SWISSPROT-ID:P08247 SYNAPTAPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcis:TREMBLNEW-ID:G2707601 SYNAPTAPHYSIN - HOMO SAPIENS (HUMAN), 313 aa.	4.80E-173	X (Xp11.2 3)
2810	cg43956325	17	TCGTCCTTTTTT TTT[AT]CTTTTAA CAAAAGCAACAA TTTTTA	A	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2811	cg43956325	239	TTATAGAACAAAT GAAATTCTCTGT TIA/CJGGAACACA AGTTGCTGTTTA TATTT	A	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2812	cg43956325	312	AGAAGAAGTAAG GTGGAGCTGTTG G[G/A]AAAGCCC ATCGTGGACCTT TGGAGA	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)

2813	cg43956325	67	ATTATCTTGCTTT ATATTTAATGGA T/GTAGAACTAT AAAGATTCTTAA CTTT	T	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2814	cg43985529	126	ATGCAGGGGG TGCAATTGGCTGC TG[C/gap]CGCTT TTGTAATTGAATT GTTTTAA	C	gap				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
2815	cg43985529	127	TGCAGGGGGCT GCATTGGCTGCT GC[C/gap]GCTTT TGTAATTGAATT GTTTTAA	C	gap				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
2816	cg43305278	336	GGGGGAGCTTC TGGTCCTGGGG GTA[C/gap]CCAC TTGTGAGGGAGT GGGGGGACA	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P51911 CALPONIN H1, SMOOTH MUSCLE (BASIC CALPONIN) - HOMO SAPIENS (HUMAN), 297 aa. pcis:SPTREMBL- ID:Q15416 BASIC CALPONIN - HOMO SAPIENS (HUMAN), 297 aa.	3.10E-162	19
2817	cg44017869	323	AAATGGGAACAA ATATAGATAATC GT/GITTCCTGG GTCAAAGGCATT TAGAAA	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:Q63537 SYNAPSIN 2A - RATTUS NORVEGICUS (RAT), 586 aa.	5.20E-148	
2818	cg42814441	116	CCAGACCGTTCC CGGGCCGGCCA GC[G/C]GCCACC ATGGTGGCCCTG AGGCCTG	G	C				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P26044 RADIXIN (MOESIN B) - SUS SCROFA (PIG), 583 aa.	5.40E-133	22 (22q12.2)

2819	cg43929931	1325	GCACCGCGTTTC CATAGCAGCATG T[C/gap]CTACGG AAACCCAGCACG TGTGTAG	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SP TREMBL-ID:Q64572 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) (PHOSPHORYLASE B KINASE KINASE) (GLYCOGEN SYNTHASE A KINASE) (HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE) - RATTUS NORVEGICUS (RAT), 505 aa.	7.60E-132	12
2820	cg43929931	1326	CACCGCGTTTCC ATAGCAGCATGT C[C/gap]TACGGA AACCAGCACGT GTGTAGA	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SP TREMBL-ID:Q64572 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) (PHOSPHORYLASE B KINASE KINASE) (GLYCOGEN SYNTHASE A KINASE) (HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE) - RATTUS NORVEGICUS (RAT), 505 aa.	7.60E-132	12
2821	cg43918346	913	TTCTGAGTGCAT GAAGTTATAAAG G[A/T]CCTACATG TAATGCATATGT GATGC	A	T			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2822	cg43918346	797	CAGCTTCTTTGT TAATACACCCAT G[G/C]TAAATTTC AACAGTGCCACA TCTGC	G	C			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	

2823	cg43918346	848	ATTCTCTGTTCT CAAGGCACCTG GAATJGGTGAC CCGGGGCCGTC CTCTCCTC	A	T				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15781 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2824	cg43918346	857	TCTCAAGGCACC TGGAAGGTGACC CIGTJGGCCGT CCTCTCCTCCTC TTCATG	G	T				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2825	cg43942332	1232	GTGTTCCGGTGG GAAGGTGGGATT TTT/GJGGTTCTC TGGAATTGAATG TTTAGT	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2826	cg43942332	1542	AATAAGAAATTTT AATGCACGAGTA [A/G]AGGGGGTG GTGGGTTGTGCA CTTTT	A	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2827	cg43942332	398	GCTATATAATTTT AATCTAAAGATT T/GJGGGCATACA GAAAGCATTTCA CAIA	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2828	cg43942340	44	TTTTTTTTTTTT TTTTTTTTTTTTTC TAAAGGAAAT CCCAATCTTTTA TT	C	T				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	1.20E-123	11

2829	cg43942338	1072	GTGTTCCGGTGG GAAGGTGGGATT TTT/GJGGTTCTC TGGAATTGAATG TTTAGT	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2830	cg43942338	1194	ACCCACCGAGA AAAAAGAGCACC A[G/A]GAAAAGA GCAGAAGAGGA CAAGAGA	G	A				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2831	cg43942338	1382	AATAAGAAATTT AATGCACGAGTA [A/G]AGGGGGTG GTGGGTTGTGCA CITTT	A	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2832	cg43961212	882	TACCACGGGTCA TTTAGAAAAACA G[A/gap]AAAAAA ATATACACCTAG TCITTC	A	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	7
2833	cg43961212	889	GGTCATTAGAA AAACAGAAAAAA A[A/gap]TATACAC CTAGTCTTTGCA ATTAAA	A	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	7
2834	cg43981852	150	CAGAGGTCGAG GAGCTCGCCTG GGC[G/gap]TAGA CATCCTCCACAG GAAQAGTGA	G	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	
2835	cg43981852	344	AGATGAAGGTGG CGTGTGGCTGTG G[C/gap]CCTACG CATCCCCGTTCT CCATGCG	C	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	

2836	cg43981852	346	ATGAAGGTGGC GTGTGGCTGTG GCC[C/gap]TACG CATCCCCGTTCT CCATGCGGC	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	
2837	cg43051163	952	GGATCTTTGGC AGAGGAGTGATC TIA/GIAGAAGAA CCGAGAGACGT GGCGTC	A	G			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2838	cg43051163	292	TTAACTCACCCCT GGTATGGCTAAA G[C/gap]CAAGGG CCAGGCACCTG GAAGACTC	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2839	cg43051163	293	TAACTCACCCCTG GTATGGCTAAAG C[C/gap]AAGGGC CAGGCACCTGG AAGACTCT	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2840	cg42887734	977	GCTTCTATCCAC CCATGAGGCACC T[G/gap]GGGCTT CTCAGCCACCCG GTGGTGT	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94 (1q31.3)	1
2841	cg42887734	980	TCTATCCACCCA TGAGGCACCTG GG[G/gap]CTTCT CAGCCACCCCGT GGTGTAAC	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94 (1q31.3)	1
2842	cg42887734	866	CCCCACTTCTTC CCTCCAGCCTGC A[gap]ATGCCCT CCTCTGGAACTG GGATTAA	gap	A			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94 (1q31.3)	1

2843	cg42893961	565	GAGAAAGAGGAA TGAGGGGCAGG GC[C/gap]AGGCC ACGGGGGGGCA CCTCAATAA	C	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q01449 MYOSIN REGULATORY LIGHT CHAIN, CARDIAC MUSCLE ISOFORM - HOMO SAPIENS (HUMAN), 175 aa.	2.50E-89	
2844	cg42896604	269	CCCTTCATTTTTT TTTTTTTTTTTTT /TJAGAAACAAAG ATCAGTTAAATTT TA	A	T				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q14843 MYOSIN LIGHT CHAIN 2 - HOMO SAPIENS (HUMAN), 170 aa.	8.60E-87	12 (12q23)
2845	cg43282400	2067	TAATGAAATAAT TTGTAAATGTCI C/gap]TTTAAAG TTTAATGATACTT CTGA	C	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P45591 COFILIN, MUSCLE ISOFORM - MUS MUSCULUS (MOUSE), 166 aa.	8.00E-84	14
2846	cg43336710	150	CTTCTGTGCTGC ATGCAGAGGGG TG[C/T]AAGGCCA GGCAGCTGAC CTGGTCA	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P13928 ANNEXIN VIII (VASCULAR ANTICOAGULANT-BETA) (VAC-BETA) - HOMO SAPIENS (HUMAN), 327 aa.	1.70E-83	10 (10q11.2)
2847	cg43336710	336	TCTCGGTTGGGA TGGATTTCGTGT C[G/A]TTTCTCAG CTGCTGAAGGAT GTGTG	G	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P13928 ANNEXIN VIII (VASCULAR ANTICOAGULANT-BETA) (VAC-BETA) - HOMO SAPIENS (HUMAN), 327 aa.	1.70E-83	10 (10q11.2)
2848	cg43135652	598	TCCTGGGTTGG GGAGGGGGTCG GG[G/gap]TCCCA GGACCTGAGCCT GGCCATGT	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P02591 TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES (TN-C) - ORYCTOLAGUS CUNICULUS (RABBIT), 161 aa.	1.20E-82	3 (3p21.3)
2849	cg43976895	433	AGGGACGAGAG CCGTGGGTCCC AAC[G/gap]GGGG CCCTGGACACC ACTGGCAAT	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P40145 ADENYLATE CYCLASE, TYPE VIII (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)/CALMODULIN ACTIVATED ADENYLYL CYCLASE) - HOMO SAPIENS (HUMAN), 1251 aa.	9.40E-82	5

2850	cg43916621	564	AGCATTCTGCT CCCCTCCGTGG GA[G/gap]CAGCG TCTCCTTTTCAAT TCAITGTG	G					SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P35749 MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) -HOMO SAPIENS (HUMAN), 1086 aa (fragment).	2.80E-81	16 (16p13.1 3)
2851	cg42898003	312	CTTCCAGACAAA GACCGACAAGG GGT[G]CGCGCC TCCCTGGTGGG GACCCGGC	T	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
2852	cg42898003	318	GACAAAGACCCA CAAGGGGTCCG GC[C/gap]TCCGT GGTGGGGACCC GGCAGGGCG	C	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
2853	cg43919386	1505	ATACATATGGAT GTACTCTCTTG C[A/C]CCAAATTA TCTTGATACATT CAAAAT	A	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	9.80E-79	12 (12q21.3)
2854	cg43919386	1554	ATTGTCTGGTT AAAAATAGGTG G[T/A]AGATATTG AGGCCAAGAATA TTGCA	T	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	9.80E-79	12 (12q21.3)
2855	cg42731508	1868	ACACCGGGTGA CCCCTTAGGGCA CC[C/gap]AGGCA AGATCCCCTAAGA GGCACCCA	C	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2
2856	cg42731508	1986	CTCCCTCCGG GTCGGATTCTGG AG[G/T]GTGGGA GGCATCTTGCC TGCAGTA	G	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2

2857	cg44014373	205	GTGAGACTGTTA CAGAAAAA A[T/gap]AAAAGTT TCTGAGTCTGAT AATTCC	T	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.10E-70	17
2858	cg43977049	133	CTGGGGCCCGA GGAGCTCAGGA AA[C/T]GGAAGC GGAGTCTTTGCA TAGTTCT	C	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:Q01995 SMOOTH MUSCLE PROTEIN 22-ALPHA (SM22-ALPHA) (TRANSGELIN) (WS3-10) (22 KD ACTIN- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 200 aa.	1.80E-69	
2859	cg42379998	254	ATCAAAACAAAG TAAAAGATGTT A[T/C]AAAAGCCA TTTCCTTTTCTTT CCCC	T	C			SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q63811 CALMODULIN-DEPENDENT PROTEIN PHOSPHATASE REGULATORY SUBUNIT BETA 2 ISOFORM - MUS MUSCULUS (MOUSE), 179 aa (fragment).	2.70E-67	
2860	cg43929049	1046	AGAAAGTAAACCT CTAAAACTGAAG A[C/A]GACCCCTCT AAAGGAGAAAAC TATAG	C	A			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa. lpcds:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2861	cg43929049	253	GGTTCTATATA CCTTCTGGATTT T[A/gap]AAAAAAC CCAAAAATTAAT GGCTCA	A	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2862	cg43929049	259	ATATACCTTCTG GATTTTAAAAAAA [gap/A]CCCAAAA ATTAATGGCTCA AGATAC	gap	A			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2863	cg43929049	29	TTTTTTTTTTTTT TTTTTTTTTTTTT/ GTTTAAATCAA TAAACATGTAGA TT	T	G			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2864	cg43929049	34	TTTTTTTTTTT TTTTTTTTTTT /TATTCAATAAAC ATGTAGATTATT T	A	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2865	cg43929049	35	TTTTTTTTTTT TTTTTTTTTTT /TJTCAATAAACA TGTAAGATTATT T	A	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2866	cg43929049	429	AAAATTACAGAA GCTTCAAATTGT T/A/GTGTGTTTCA CAAAATTGCTA CATAT	A	G			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2867	cg43929049	737	AGGCACTTGAA ACATTAAGTATAT [G/C]TACAAATGT GCAAGTAAACA AACA	G	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa. pcds:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2868	cg43929049	853	ATGCAGAGTTTG TTTATGAAATGA A[C/A]CAAAGCAG TTTGTCATTTCTT ACTA	C	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa. pcds:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2869	cg43936426	358	GGGAGGAGAG AGAAGGGGACA CCA[T/A]TTCTTT AGACACATCTGT GTTCIG	T	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67 1 (1q32)	
2870	cg43936426	430	GGCCAGGAGTTT GGGTGTGCACT GG[G/T]TGCTTT CAACTGGGTGGA ACCAA	G	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67 1 (1q32)	
2871	cg43936426	450	ACTGGGTGCTTT TCAACTGGGTGG A[A/gap]CCAAAC TGAGTGCTTGAA GTCTCGC	A	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67 1 (1q32)	

2872	cg43936426	480	ACTGAGTCCTTG AAGCTCGCTCC TIGTJAGGCTGCA GAAGAATAGATG GCTTT	G	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2873	cg43936426	493	AGTCTCGCTCCT GAGGCTGCAGA AGATJATAGATG GCTTTCCCTGC CTCGAG	A	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2874	cg43936426	520	TAGATGGCTTT CCCTGCCCTCGAG G[G/gap]TGGGAT AAGGGAGGCAA AGCTGGGA	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2875	cg43936426	524	TGGCTTTTCCCT GCCTCGAGGGT GG[G/C]ATAAGG GAGGCAAAGCT GGGAGAA	G	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2876	cg43936426	531	TCCCTGCCCTCGA GGGTGGGATAA GG[G/gap]AGGCA AAGCTGGGAGAA AGAAAGGG	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2877	cg43936426	553	AGGGAGGCAAA GCTGGGAGAAA GAA[G/G]GGGAG AGAGAGAAAACG AATGGCCG	A	G				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2878	cg43936426	587	GAGAAAACGAAT GGCCGGGCACAG GT[G/gap]CCTGG GCCCCAGCCTTC AAGTGCGG	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)

2879	cg43933305	418	ACAGTTAAGATA CATTAAAAAAA A[<i>gap</i>]GGAAAG ATACCCACAATT CCATTCT	A	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2880	cg43933305	696	CACCTGTACAAC CTCCCCTGACAG ATTCTAGTGAGAG CCCGGCGGGG CCAGGG	T	C			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2881	cg43933305	740	GCCAGGGGCTC TGTTGTGCTTTGG AG[G <i>gap</i>]CTACT GCCTCTGGAATG TTTCGCAT	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2882	cg43986028	43	GGAGGCGCGAG TGAAGGAAGACG AA[G <i>gap</i>]TGGT GACCCGACCGG CTGTGGTGT	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:P91837 RIC (RAS WHICH INTERACTS WITH CALMODULIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 264 aa.	5.00E-59	1
2883	cg43986623	2964	CCATCGGTCCGT CCATCCATGTCC C[C <i>gap</i>]AGTTGA CCGCCCGGCAC CACTAGCT	C	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P15941 MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT) (EPISIALIN) (TUMOR- ASSOCIATED MUCIN) (CARCINOMA- ASSOCIATED MUCIN) (TUMOR- ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANUT- REACTIVE URINARY MUCIN) (PUM) - HOMO SAPIENS (HUMAN), 1255 aa.	6.60E-57 (7q11.23)	7
2884	cg43919048	1279	GAGGTGAGAGA ATTCCAAAGTTT GA[G <i>gap</i>]GGGAGT GGTCCAAAGAGT AACAACT	G	A			SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q07569 MYOSIN HEAVY CHAIN - ENTAMOEBA HISTOLYTICA, 2139 aa.	1.70E-56	3

2885	cg43919048	186	GAGAGGCTAGG CAGTGAACACAT CA[C/T]GTATGCA ATGAGAAATAA CCAACT	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q07569 MYOSIN HEAVY CHAIN - ENTAMOEBA HISTOLYTICA, 2139 aa.	1.70E-56	3
2886	cg43927885	2154	ATGCTGGAGGTG GGGGTGCTGTG TT[C/T]TAGACCC CCCATATTATCC CAGTGT	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2887	cg43927885	641	CTCTCAGCCATA TCTTTCAGCCCC C[C/A]CTCCCTG GATCCGTGTGTG TGTGT	C	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2888	cg43927885	782	AGATGATTTTC CGGTTGTCTTA A[C/A]ACCCCTTC CTGAGGTTCCCT TCACC	C	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2889	cg43958532	254	TCCTGACTCCAG GCTAGGTCCCA A[G/gap]GGGAGG TCAGGCTCAGAC TTGGACC	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20
2890	cg43958532	281	GGAGGTCAGGC TCAGACTTGGAC CT[G/A]GGCGCT GGAAGTGTGAGT AATGGTT	G	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20

2891	cg43958532	69	TTTCTTTTCAAG ATGCTACATAGT C/GJAAACAGAAC TGGGTTGGTCTT TTAT	C	G				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20
2892	cg43977322	25	TTTTTTTTTTT TTTTTTCAGA[C/ TTCAGCCACC AGGTTATTTTCA TG	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2893	cg43977322	431	ATGGAAGTTGG TTTAAAGCCAGA A[G]ATCTGGAGA GATGTCATGCCA GGCAG	G	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2894	cg43977322	62	GGTTATTTCAT GCTATAAATAAA T/GJTCCCTATTA GTTCCCATTTTC TTA	T	G				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2895	cg43961860	215	AGTTTAGCAGTC TGCTTAAATGT T[A/gap]AAAAAAA AAATCATAAAAA GCCATT	A	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.50E-51	
2896	cg43961860	225	TCTGCTTAAAT GTAAAAA A[A/gap]TCATAAA AAGCCATTGTTT TGTTAC	A	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.50E-51	
2897	cg43918310	535	ATGCTGAATCCC CTATCCCATTTCT GTT/CJGTATGAGT CCCATTTGCCTT GCAAT	T	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50 1 (1q21)	

2898	cg42673122	249	ACCAGGAGGGG GCTGGGGCGG CCA[G/gap]CACC AGCGCGTCCT GCTCAGCCCC	G	gap				SILENT- NONCODING	sulfotransferase	Human Gene SPTREMBL-ID:Q99999 CEREBROSIDE SULFOTRANSFERASE HOMO SAPIENS (HUMAN), 423 aa.	1.50E-209	22
2899	cg43974392	1785	CCAGAGGGTGG TGTTGGTGCCAG GG[G/A]TCCATCT TTCCAGAAATCCA TGCCTG	G	A				SILENT- NONCODING	sulfotransferase	Human Gene TREMBLNEW-ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2900	cg43974392	2178	GATTCCTTTCAT CTCAGCAAAATG G[G/gap]CACTGC CAGAGCCATTTC TGATCAC	G	gap				SILENT- NONCODING	sulfotransferase	Human Gene TREMBLNEW-ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2901	cg43974392	2311	AGTCCGGCTTCC TGGCAACAAGGT A[G/gap]GCCCTG GTGCAGGGCAA GCCGCAGC	G	gap				SILENT- NONCODING	sulfotransferase	Human Gene TREMBLNEW-ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2902	cg43999676	1452	AAAATTAGCCAG GAGCATTGGCTC A[G/gap]TGTCTG TAATCCCAGCAC TTTGGA	G	gap				SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2903	cg43999676	1592	AAATTAGCCGGG CATGGTGGTGCA C[A/G]CCTATAGT CCCAGCTACTCG GGAGG	A	G				SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)

2904	cg43999876	1815	ACACCTATAGTC CCAGCTACTCGG G[A/G]GGCTGAG GTAGGAGAATCG TTTGAA	A	G				SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2905	cg43999876	1738	TCTCAAAAGAA AGAAGTGACTAG G[G/gap]TTCAGA GAACGAGGTTTC AAAGCCC	G	gap				SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2906	cg43317375	751	CACTAGGTCTTC AGAATGGACGTC C[T/C]TCTGCCAG AGACTTCCAGCG GGCGG	T	C				SILENT- NONCODING	sulfotransferase	Human Gene Homologous to TREMBLNEW-ID:E1253895 DJ388M5.3 (SULFOTRANSFERASE (SULFOKINASE, EC 2.8.2.1) LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 284 aa.	8.50E-133	22
2907	cg43972499	141	AATGAAGATGGG GCAGACTGGGC CC[C/gap]AGCAT CTGAGGCCCCCA CCCCCATGC	C	gap				SILENT- NONCODING	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0.00E+00	2

2908	cg43972499	50	TTTTTTTTTTTT TTTTTTTTTTTTTT/ A]TCAAGGGACA GCTCGGCTGTTT ATT	T	A				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0.00E+00	2
2909	cg43986130	186	CGCACACAATAA GCTGGGCTGA GC[C/gap]AGGAG GCAGCGGGGT GTTGGGGA	C	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2910	cg43986130	279	GGAGCCCCCTC TGCTATCTCAGC CA[A/G]GAGGAA GGAGAGACCAA GGCACAGA	A	G				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2911	cg43986130	47	AAACAAAGGCT TTAATTCACCTCC A[G/A]CCACCCTC TGTCGCCGAGTG TCCCA	G	A				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2912	cg43986130	83	TCCCGCAGTGTC CCAGGCAGAGG CC[C/gap]TCTCC CTTCCCAGAGG CACTGGGA	C	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9

2913	cg43054994	2317	CATGGTGAATAT AAGAACTGAATT GTT/gapJACATGT GCTGCATGAAGA GCTAATT	T	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSNEW-ID:P54840 GLYCOGEN [STARCH] SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa. pcis:SWISSPROT- ID:P54840 GLYCOGEN (STARCH) SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa. pcis:TREMBLNEW-ID:E1228798 LIVER GLYCOGEN SYNTHASE - HOMO SAPIENS (HUMAN), 703 aa.	0.00E+00	12
2914	cg43054994	2820	AGAACCATGATT TAGATGTAGTTT T[A/G]CAGAGACA AAAATCCATGAG TGAAT	A	G			SILENT- NONCODI NG	synthase	Human Gene SWISSNEW-ID:P54840 GLYCOGEN [STARCH] SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa. pcis:SWISSPROT- ID:P54840 GLYCOGEN (STARCH) SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa. pcis:TREMBLNEW-ID:E1228798 LIVER GLYCOGEN SYNTHASE - HOMO SAPIENS (HUMAN), 703 aa.	0.00E+00	12
2915	cg40388639	5040	GCCGGCTGCAA GTTTGTAAGCG GG[G/gap]ACAGA CACTGCTGAACC TTTCCTCT	G	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0.00E+00 (12q24.2)	12
2916	cg43987111	680	TTGAGAAACAAG GTGACCGATGG GG[C/gap]ACTCT GCAGCCCCACC CACCATCGG	C	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP-- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00 (1p34.1)	18
2917	cg43981333	18	TTTTTTTTTAGCT ATCC[G/A]ATAAT TATTTATTGAAAG AAATGAC	G	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P18858 DNA LIGASE I (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) - HOMO SAPIENS (HUMAN), 919 aa.	0.00E+00 (19q13.2)	19

2918	cg43971304	2483	CCCCGATCCAGAT TCTGCACGGGGT G[T/C]GGCCCCG CAGTGCCCCCAC CCAGTC	T	C				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2919	cg43971304	2559	TCCAGTTTCCAA GTTCCTGCACTC C[A/T]GAATCCAC AAAGCCGTGCCT TTCCTC	A	T				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2920	cg43971304	2654	TGGACCGCTTCC CAGAGGCCAGG AA[gap/A]TCTGC CATTACTCTGCG GTGGIGCC	gap	A				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2921	cg43971304	2953	GAGGGATGTTCT AGCCCTCCCTGG C[A/gap]TGTCAG AGCCAGGCTCTG CCTGGAG	A	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2922	cg43971304	68	GAGCGTCTTGCA AGCTTCCCGTCG G[G/gap]CACCAG CTACTCGGCCCC GCACCCCT	G	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2923	cg43918681	33	TTTTTTTTTACC ATTTTTTTTTTTT /A]TTTATTTCCAG GACTATGTTTTTA C	T	A				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	0.00E+00	3 (3p21.1)

2924	cg43983214	484	GACCCAAGTGAA GCGCAGGTGG GT[G/T]TGAATCC TAGGCAGCTGG CTTCTCA	G	T				SILENT- NONCODI NG	synthase	Human Gene SPTREMBL-ID:Q13735 5-AMINOLEVULINATE SYNTHASE PRECURSOR - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	X (Xp11.2 1)
2925	cg43949316	211	TTATTTAAACAG GGATCCATCAGA [G/C]GTGGTGAA CTATCAAGGTCA AGGTT	G	C				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2926	cg43949316	348	GAACAAACCCGA TGTAAGGCAC CTTAAJAGCTGG GAGAAGCTGTG GTGTTCA	T	A				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2927	cg43949316	591	TTCTGCTCTAGA AGGAAGGGGAA CC[C/gap]TTCCC CCAGTATCAATT TCAGCAGC	C	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2928	cg43967343	384	CCCCGCCGTGCA GAACCCCTGCTTG CA[G/gap]CTCAG GTTTCGGGGTGC TTGAGGAG	G	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q92903 PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP- DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) - HOMO SAPIENS (HUMAN), 461 aa. cds: SPTREMBL- ID:000163 CDP-DIACYLGLYCEROL SYNTHASE - HOMO SAPIENS (HUMAN), 461 aa.	8.50E-254	4

2929	cg43976335	108	AAGGCAGAAATTA C GGGAAAGGCTAT G[C/gap]CCCTCC ACTCCCCCTCCT CCTACCA	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2930	cg43976335	111	GCAGAAATTAGGG C AAAGGCTATGCC C[C/gap]TCCACT CCCCCTCCTCCT ACCACTC	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2931	cg43976335	182	ACTGGAACCTGC G TGAAAGGCTGA T[G/A]AGGGGCT GACAGGAGTGG GGCAGGG	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2932	cg43959826	522	GCCGATGCCTG C GCTCCATCCAGA GC[C/gap]AGCCC AGCCCCAGGGAG GCTGCATGG	gap			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN-III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa.	7.00E-140	10 (10q25.2)
2933	cg43953338	2968	TTTGTGTTTTTCAT T CTCCTAAAGTG[T/G]TTTTTATTTC CTTGTATCTGTA GTC	G			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P44708 GLUCOSAMINE-FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE- 6- PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L- GLUTAMINE-D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa.	3.10E-107	2 (2p13)

2934	cg43982623	106	TCCTGCCTCCTC TCTCAGACAGGG A[G/A]GCGGGAA CCAGACTTACTG ATCCAA	G	A			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N- ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGLUCOSAMINE (BETA 1- >4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS TAURUS (BOVINE), 402 aa.	8.20E-105	1
2935	cg43982623	200	GCAGCGACACA GCATCCCCTCTG GT[C/gap]CCCTC CTGGGGCTGCT CCTCAGCAG	C	gap			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N- ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGLUCOSAMINE (BETA 1- >4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS TAURUS (BOVINE), 402 aa.	8.20E-105	1
2936	cg43982623	211	GCATCCCCTCTG GTCCCCTCCTGG G[G/gap]CTGCTC CTCAGCAGGGG GCGCACCA	G	gap			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N- ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGLUCOSAMINE (BETA 1- >4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS TAURUS (BOVINE), 402 aa.	8.20E-105	1
2937	cg43987048	35	TTTTTTTTTTT TTTTTTTTTTTAA /GJCATTAAAAAT CAGTATTTAATTA C	A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:G2984031 3-OXOACYL-[ACYL- CARRIER-PROTEIN] SYNTHASE II - AQUIFEX AEOLICUS, 415 aa.	1.20E-86	

2938	cg43124627	1928	TTTCATTAATTAC CATATCTATAAA A/gap]CAAACATA GTATCTGTCAAT CTCTA	A	gap				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. pcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.70E-79	16
2939	cg43933068	289	AGCCAGGGTCG GTGAAGGATCCC AA[A/G]ATGGCTG GGCGAAAACTTG CTCTAA	A	G				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.90E-75	12
2940	cg43275028	3001	ACACCTAAGCCA AGACACTGGTTC TTC/gap]CTTCCG GAATGAGGCCCT GGGAGGA	C	gap				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa. pcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2941	cg43275028	3213	ATGAAGACACAG CTGTTAACAATT G[G/gap]CTGATC AGCCCCCAGAAT GCCTCAG	G	gap				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa. pcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)

2942	cg43275028	705	CTTACCTTGACC ACACATTCCTG C[G/A]GAGAAGA TGGACGACGCT GTGGCTC	G	A				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2943	cg43275028	7134	ATTTTATACAAGA AGATAAAAAAAT[A/G]TAACTCCTT GCTACCAGTAAG TAAG	A	G				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2944	cg43275028	852	AAAATCTGATCG AGGATTTCAACT C[G/T]GGGCTGA TTGGGCCCCCTGC TTATCT	G	T				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.2E-65	1 (1q23)
2945	cg42521802	1609	AGTCTCCAGAAC CCATGATGAACT G[T/gap]GATCTG CCGTGGTCCTGC CGTGGTC	T	gap				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P15535 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGLUCOSAMINE (BETA 1- >4) GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - MUS MUSCULUS (MOUSE), 389 aa.	3.7E-65	

2946	cg43064068	1672	TCGGGAAAGCC CGTGCGCAGTG AGAGCATCTAA GAGACATTCATT TGGATT	A	G				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572.aa	7.4E-65	
2947	cg43064068	1674	CGGAAAGCCC GTGCGCAGTGA GACIAGITCTAAG AGACATTCATTT GGATTCC	A	G				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572.aa	7.4E-65	
2948	cg43064068	1679	AAGCCCGTGCG CAGTGAGACATC TAIAGGAGACAT TCATTGGATTG CCCTCT	A	G				SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572.aa	7.4E-65	

2949	cg43064068	1741	CTTTCCCTTTG GGCCCTTGGCCT T[C/A]CTATGATG ATATGAGATTCT TTATG	C	A			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572.aa	7.4E-65	
2950	cg43064068	1767	CTATGATGATAT GAGATTCTTTAT G[G/A]AAGAACAT GAATATAAGTTTT GTCT	G	A			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572.aa	7.4E-65	
2951	cg43064068	1780	AGATTCTTTATG GAAGAACATGAA T[A/G]TAAGTTTT GTCTTGGCCCTGG TTTTG	A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572.aa	7.4E-65	

2952	cg42875572	162	GCAGTTTTTTAC TATTACAAAATG [T/C]CATTTAGAG TGGAGGTGGCC ACCTT	T	C				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2953	cg42875572	168	TTTTACTATTAC AAATGTCATTTI A/G]GAGTGGAG GTGGCCACCTTC AGTAG	A	G				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2954	cg42875572	174	TATTACAAAATG TCATTAGAGTG[G/AJAGGTGGCCA CCTTCAGTAGCT GAGG	G	A				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2955	cg42875572	213	CAGTAGCTGAGG CAATGTCITTTCA C[G/A]TGAGATG GCCACAGAAAGTG TGGTTC	G	A				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2956	cg42875572	226	AATGTCITTTAC GTGAGATGGCCA C[A/T]GAAGTGTG GTTCCCTGGAAC GGCTC	A	T				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2957	cg42875572	245	GGCCACAGAAAGT GTGGTTCCTGGA A[C/T]TGGCTCAC AAAGGCCACAG GCTGTC	C	T				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2958	cg42875572	253	AAGTGTGGTTCC TGGAAGTGGCTC A[C/G]AAAGGCC ACAGGCTGTCCT GGGTGA	C	G				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14

2959	cg42875572	324	GCACCAAAAAGG CTCAGTCTTCTG TTTCTCTTCATA CGTCGTCTCGTC AAAGG	T	C				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.80E-53	14
2960	cg42875572	333	AGGCTCAGTCTT CTGTTTCTTCATA [C/G]GTCGTCTC GTCAAAGGGCCT GTCCA	C	G				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.80E-53	14
2961	cg43931248	2107	CATGGGGGCTG TATTTAAGGACA CC[C/gap]GTGCC CCAAGCCCACT GGGGCCCC	C	gap				SILENT- NONCODI NG	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
2962	cg43931248	713	ACCACTGCGCCC TTCTCCCTGAGG A[gap/G]GCTCAG CTTCCCTCGAG GCCCTCC	gap	G				SILENT- NONCODI NG	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
2963	cg43274187	57	TGAGTATCTACA TTCAATTGCTTTA [G/gap]CTAAATTA ACAAAAACATG CAAAAT	G	gap				SILENT- NONCODI NG	tgf	Human Gene SWISSPROT-ID:O00292 TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING- ASSOCIATED FACTOR) - HOMO SAPIENS (HUMAN), 370 aa.	1.4E-186	
2964	cg43980446	1401	GTCCATCAATG AAAGCACATTCC C[A/G]TACGTTTG CTGGAAGGATG GCAIGT	A	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1)	15
2965	cg43980446	1658	TGATGATTCTGA TTGGGGGAAAT A[T/C]AGTTCTAC CTATCTATATTG TTTT	T	C				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1)	15

2966	cg43980446	1701	TTTGTTTCTTT TAATTATTGGT C/TCTGGATGG TGAATTAATGAA GCAA	C	T				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2967	cg43980446	795	ATCCATGCAAGA ACACAAAGCCTA TTT/GJTAACT AAAAAAAGAAG AGATT	T	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2968	cg43980446	796	TCCATGCAAGAA CACAAAGCCTAT TTT/GJTAACTA AAAAAAAGAAGA GATTG	T	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2969	cg43980446	797	CCATGCAAGAAC ACAAAGCCTATT TTT/GJTAACTAA AAAAAAGAAGAG ATTGT	T	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2970	cg4332146	777	TCAAACTCTGT CAAGAACTCCGT CTT/GTGCTTGGG GTTATTCAGTGT GACCTA	T	G				SILENT- NONCODI NG	tgf	Human Gene Similar to SWISSPROT- ID:P01135 TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF- ALPHA) (EGF-LIKE TGF) (ETGF) (TGF TYPE 1) - HOMO SAPIENS (HUMAN), 160 aa.	5.2E-84	2 (2p13)
2971	cg43047272	1700	GGCGGCTAGG GGAAGATCGGG GAG[ap/G]CTGG TTTTGATGAAAG TATGTTAAC	gap	G				SILENT- NONCODI NG	tgf	Human Gene Similar to SPTREMBL- ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	5.2E-74	
2972	cg43047272	1740	GTATGTTAACTTT TCTTTCCACTT gap/GJGGACCC TGTTCAAGTATCT TTTGTA	gap	G				SILENT- NONCODI NG	tgf	Human Gene Similar to SPTREMBL- ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	5.2E-74	

2973	cg43272560	3230	CCCAGCCCAGCT CAGCTCAGCTAC T[gap]CCAAGG GCAGGACCAATG GCTGAGC	G	gap			SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2974	cg43272560	3459	GCCCCCTCACAG GCTTGGGGTTT TC[A]ATGTGAA ACACATGCCAGT TTTAA	A	T			SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2975	cg43272560	3700	AATTGCACCTT TGCTGGATGCA C[A]CTTCTGAC CTTGCTGCCACA ACCTG	A	T			SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2976	cg43272560	3744	CAACCTGTGGG GTCTGATGTGTC CC[T]ATGATGGG TGCTGCCCTCAG GGACTG	T	A			SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2977	cg43272560	3745	AACCTGTGGGT CTGATGTGTCCT TT[A]GATGGGT CTGCCCTCAGG GACTGC	T	A			SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2978	cg43272560	4243	TAGGCCCTTTCA TAAACCAACAAAC T[C/G]TAGCAAGA TGCAAATGCATG GCAAA	C	G			SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2979	cg43272560	4338	ACCAAGACAGTG CTGAGATTGGAA A[gap]GGGCAC TCATTGGATTG CCTTACT	A	gap			SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)

2980	cg43261247	3334	CCCTAAACACTA CCAAATAGCTCT TTA/CJTGGGCA GGCTGGGCATG TCCAAAG	A	C			SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:P37173 TGF-BETA RECEPTOR TYPE II PRECURSOR (TGFR-2) - HOMO SAPIENS (HUMAN), 567 aa.	2.0e-316	3 (3p22)
2981	cg43982633	458	CAGATACTATAT TTGGATGTGACA G[G/T]TGTITTTT CTTTGTACAAG AGTGC	G	T			SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2982	cg43982633	459	AGATACTATAATT GGATGTGACAG G[T/G]GTTTTTTC TTTTGTACAAGA GTGCA	T	G			SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2983	cg43982633	742	GAAGTAAACTG TTAAATCATCAT [C/gap]ATGATCA TGATGATCATCA TCATGA	C	gap			SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2984	cg43982633	943	GCTTTCCTTAAA GGAAAAA A[A/gap]TGTTC AGTTGAATGGAA CTGTTTC	A	gap			SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2985	cg43921327	1385	CCATGGACTCTT GCCTCGGTGCA GT[C/T]TCCACTC TTGACCCCCACC TCCTAC	C	T			SILENT- NONCODI NG	thioester ase	Human Gene Homologous to TREMBLNEW-ID:G2501961 PALMITOYL-PROTEIN THIOESTERASE 2 - HOMO SAPIENS (HUMAN), 302 aa.	1.1E-141	

2986	cg43918322	1109	CACAGCCCTGCC CATCTTCTGGG C[C/gap]TGCGG GACGACATCTAG TTCAATG	C	gap				SILENT- NONCODI NG	thioester ase	Human Gene Similar to SPTREMBL- ID:Q19781 SIMILAR TO ACYL-COA THIOESTERASE. NCBI GI: 1213545 - CAENORHABDITIS ELEGANS, 343 aa.	1.1E-53	20
2987	cg36988276	172	TGGAGGTTTTC TCTGCAATGCA G[G/A]AAGAAATC AGGTGGATGGAT GCATA	G	A				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0 2 (2p21)	
2988	cg44030467	1747	TTCTCAACGGT ACACAGACTATT G[A/G]CATCAGC ATCACCTAGAA CTTGTT	A	G				SILENT- NONCODI NG	tm7	Human Gene TREMBLNEW- ID:E1248507 C3A ANAPHYLATOXIN RECEPTOR - HOMO SAPIENS (HUMAN), 482 aa.	3.9E-265	12
2989	cg4338230	264	GGCTGCGGCA AGGAGGGTGA TGC[A/T]ATGTGG TCTGAAGCCCTG GAAGGGC	A	T				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P11229 MUSCARINIC ACETYLCHOLINE RECEPTOR M1 - HOMO SAPIENS (HUMAN), 460 aa.	7.7E-253	
2990	cg43946035	1974	GGGACTCTGATA TAAAGGAAGAAT A[A/gap]GTCAC GTAAACACAGAAC TTTAA	A	gap				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P24530 ENDOTHELIN B RECEPTOR PRECURSOR (ET-B) (ENDOTHELIN RECEPTOR NON-SELECTIVE TYPE) - HOMO SAPIENS (HUMAN), 442 aa.	1.1E-242 (13q22)	13
2991	cg41084824	1896	GGCATGGTACCA GCCCTGGGGCT GG[G/gap]CCCCC CAGCTCAGGGG CAGCTCATA	G	gap				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.7E-241	11
2992	cg43985000	1935	AGAAATGCTTTC CAAAACCGCAAG G[G/gap]TAGACT GGTTATCCACC CACAAACA	G	gap				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4

2993	cg43985000	2222	TTCTACTTTTTT AAGTGATTTTTT T/gap]GTCCCTTCA GCCAAACACAAAT ATGGG	T	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2994	cg43985000	2252	TTCAGCCCAAACA CAATATGGGCTC A[A/G]GTCACATTT TATTTGAAATGT CATT	A	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2995	cg43985000	2787	AAAGATCGAATT TTTCAGATGATT C[G/A]GAAATTTT CATTGAGGTATT TGTA	G	A			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2996	cg43985000	2863	ATCACCTCCTAT TCTCTTAATTTT [G/C]TTAAATGT TAACTGGCAGTA AGTC	G	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2997	cg43985000	2988	AATAATTACCCA CAAATGCCACCA G[gap/]TAACTTA CGATTCTTCACT TCTTGGG	gap	T			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2998	cg43985000	2994	TACCCACAAATG CCACCAGAACTT A[gap/]A]CGATTG TTCACCTCTTGG GGTTTC	gap	A			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
2999	cg43985000	3324	GTTGTGCCAAAG TGCATAGTCTGA G[gap/C]TAAAT CTAGGTGATTGT TCATCAT	gap	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4

3000	cg43985000	4080	AGCCAGAAGCCA AGGCCCTGAGTT G[G/gap]CAGTGG CCCATAAAGTGTA AAATAAA	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
3001	cg39565524	1715	CTAGCCTCAGCC GCTCCTGGTGG GG[gap/G]AATGG CTGGGGCTGGG CAGGACCCCT	gap	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P51575 P2X PURINOCEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
3002	cg39565524	1727	CGCTCCTGGTG GGGAATGGCTG GGG[C/G]TGGGC AGGACCCCTCCCA CACACCTG	C	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P51575 P2X PURINOCEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
3003	cg36847035	217	GTGCTCCTGGCT ACCTCGCACAGC G[G/gap]TGCCCG CCCGGCCGTCA GTACCATG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P35372 MU-TYPE OPIOID RECEPTOR (MOR-1) HOMO SAPIENS (HUMAN), 400 aa.	1.40E-219	6 (6q24)
3004	cg42704619	120	GCGGCTGCGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCAGC CGCGGTAAAC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3005	cg42704619	171	GCCGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCCCTCCCG CTGCGGCTC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

3006	cg42704619	53	TGGCTCCCTCCC GGCCAGTGAG CC[C/gap]TGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3007	cg42704619	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G/gap]TCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3008	cg43306266	120	GCGGCTGCGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCAGC CGCGGTAAAC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3009	cg43306266	171	GCCGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCTCTCCCG CTGCGGCTC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3010	cg43306266	53	TGGCTCCCTCCC GGCCAGTGAG CC[C/gap]TGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3011	cg43306266	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G/gap]TCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

3012	cg44031327	952	CTCCTAAAGCAC GGACCAGCCGTT G[G/gap]AGCCCC CAAATCCAGTAG GGGGTGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P35414 PROBABLE G PROTEIN-COUPLED RECEPTOR APJ - HOMO SAPIENS (HUMAN), 380 aa.	5.70E-209	11
3013	cg43283108	1724	CCAAGCCACTCC AAGAGCCAGCC CC[gap/C]TTTCT GCTCCACAAAA CCACAGTT	gap	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43119 PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR) - HOMO SAPIENS (HUMAN), 386 aa.	8.30E-208	19 (19q13.3)
3014	cg43282263	1976	CTGGAGGCTCC CATGGGCTAGGA GC[C/gap]AGTGT GAGGCTGTAAC TATACTAA	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P41231 P2U PURINOCEPTOR 1 (ATP RECEPTOR) (P2U1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 377 aa.	9.80E-205	
3015	cg43329467	2631	CCAGGACAATGA AATACTCCAGCA C[G/C]TGTGGCT GACGAATTGTT TCTACA	G	C			SILENT- NONCODI NG	tm7	Human Gene SWISSNEW-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8- RELATED RECEPTOR DRY12) (FLOW- INDUCED ENDOTHELIAL G PROTEIN- COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPCR30) (GPCR-BR) - HOMO SAPIENS (HUMAN), 375 aa. pcis:SWISSPROT- ID:Q99527 CHEMOKINE RECEPTOR- LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN- COUPLED RECEPTOR GPCR30) - HOMO SAPIENS (HUMAN), 375 aa. pcis:TREMBLNEW-ID:G2656121 G- PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 375 aa.	8.20E-201	7

3016	cg43329467	680	CTTTCGGCAAT CTTGAAAGCTGC AIG/CJGGCGCAG AGACATGGATGT GACTTC	G	C				SILENT- NONCODI NG	tm7	Human Gene SWISSNEW-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8- RELATED RECEPTOR DRY12) (FLOW- INDUCED ENDOTHELIAL G PROTEIN- COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPCR30) (GPCR-BR) - HOMO SAPIENS (HUMAN), 375 aa.lpcis:SWISSPROT- ID:Q99527 CHEMOKINE RECEPTOR LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN- COUPLED RECEPTOR GPCR30) - HOMO SAPIENS (HUMAN), 375 aa.lpcis:TREMBLNEW-ID:G2656121 G- PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 375 aa.	8.20E-201	7
3017	cg38277960	1396	AGCTACCTCAAC CAATGCCGAAA A[gap]/AJGACAGG GCTGATAAGCTA ACACCAG	gap	A				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32248 C- C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CC-CKR-7) (CCR-7) (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1) (EBI1) (BLR2) - HOMO SAPIENS (HUMAN), 378 aa.	4.10E-199	17 (17q12)
3018	cg2751286	1554	TTTGTGTCCTTAA CGTGAGAGCAAA [gap]/AJTGCATGT AATCCAACATGG CTACTT	gap	A				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3019	cg2751286	1566	AACGTGAGAGCA AATGCATGTAAT C[C/gap]AACATG GCTACTTGCTTT GAAGGCT	C	gap				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X

3020	cg2751286	1587	AATCGAACATGG CTACTTGCTTTG A[A/gap]GGCTCA CCAGAAATTATTT TAAGTG	A	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3021	cg2751286	1601	ACTTGCTTTGAA GGCTCACCAGAA TTT/gap]ATTTTAA AGTGGTTTAAAT AAAATA	T	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3022	cg2751286	1607	TTTGAAGGCTCA CCAGAATTATTT TTT/gap]AAGTGGT TTTAATAAAATAA CAAAAT	T	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3023	cg2751286	1616	TCACCAGAAATTA TTTTTAAGTGGTT TTT/gap]TAATAAAAT AACAAATTTTGA CCIA	T	A			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3024	cg2751286	414	TAAGAGTTCTAT GTTTCTCTCACA G[gap/G]AAGGCA TAAGAACTAGGA GCIGCTG	gap	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3025	cg43031008	540	CTTCTAGCCAT TTGTTGGCAAGA A[A/gap]TAATAAT TAAATTTTATT AAAC	A	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195 (17q12)	17
3026	cg43031008	551	TTTGTGGCAAG AAATAATAATTAA [A/gap]TTTTTTAT TAAACACAAACT TTTTA	A	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195 (17q12)	17

3027	cg43031008	635	TATTCGTTTACAA ATAAAATGAAAI gap/AJTATTTATTT GCATTTTATTGT GCT	gap	A				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)
3028	cg43031008	720	TACTTCGAGTT GGAGATGGAA AGTCJGCCCAAT GAAAGAAATATA AAAGAA	T	C				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)
3029	cg42704646	117	GCGGCTGCGCC CCGCACCATGG GGG[gap/G]CAGC CCAGCCCCCAGC CGCGGTAAAC	gap	G				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3030	cg42704646	167	GCGGACCTCCG CCGCCGCCCGC GCC[gap/G]CGTC TGCCCCCTCCCG CTGCGGCTC	gap	G				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3031	cg42704646	52	TGGCTCCCTCCC GGGCCAGTGAG CC[gap/C]TGGCG CCGCCCGCGGC GCGTCCCAG	gap	C				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3032	cg42704646	71	TGAGCCTGCGG CCGCCCGCGGC GCC[gap/G]TCCC AGCAGCGGAGT AGGGCGGCGG	gap	G				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)

3033	cg43308845	1524	AGTGAGGGGAA ACCAGGGCCTG AGC[C/gap]AAGC TAGAATTCCTC TCTCTGACT	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P49238 PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMK BRL-1) (CMKBLR1) - HOMO SAPIENS (HUMAN), 355 aa.	2.00E-190	3 (14q11.2)
3034	cg43308845	2647	CCCCCCTAGAAA CGTTTGGAACAA T[C/G]TAAACTT TAAAGCTCGAAA ACAAT	C	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P49238 PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMK BRL-1) (CMKBLR1) - HOMO SAPIENS (HUMAN), 355 aa.	2.00E-190	3 (14q11.2)
3035	cg43047341	671	GAAGGCAGGCC CAGGCTGTGACA GC[C/gap]GCCAG TATCCAGCAGCA CGCCCAGG	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P21731 THROMBOXANE A2 RECEPTOR (TXA2- R) (PROSTANOID TP RECEPTOR) - HOMO SAPIENS (HUMAN), 369 aa.	2.80E-190	
3036	cg43328050	1796	GCGGACGTCAG CACTCAGGCCT GC[A/G]GGGACT CAGCACAGCTCT GGATTCT	A	G			SILENT- NONCODI NG	tm7	Human Gene TREMBLNEW-ID:E322207 P2Y-LIKE G-PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 367 aa.	3.30E-188	2
3037	cg42268169	7500	CACTTGAGCCCA GGAGTTGAGAC T[A/G]CAGTGAAC TATGATTGCACC ACTGC	A	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P56486 THROMBOXANE A2 RECEPTOR (TXA2- R) (PROSTANOID TP RECEPTOR) - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 343 aa.	4.90E-177	
3038	cg42268169	7533	CTATGATTGCAC CACTGCACTCCA G[A/C]CTAGGTG ACAGAGTAAGAC CCTGAC	A	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P56486 THROMBOXANE A2 RECEPTOR (TXA2- R) (PROSTANOID TP RECEPTOR) - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 343 aa.	4.90E-177	

3039	cg44011188	1412	AGCTGAGCTGAC CCCAAGCCGAA GG[ap/G]TCCCG ACTCCTCTCGGG AGCCTGGA	gap	G			SILENT- NONCODI NG	tm7	Human Gene Homologous to SWISSPROT-ID:P35626 BETA- ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (BETA-ARK-2) (G- PROTEIN COUPLED RECEPTOR KINASE 3) - HOMO SAPIENS (HUMAN), 688 aa.	3.10E-119	22
3040	cg43993798	131	ATCCACATAAGA GCTCTGAGGGG AA[G/A]GAATGAT TATTATCCTTATT TTAA	G	A			SILENT- NONCODI NG	tm7	Human Gene Homologous to SWISSPROT-ID:P31421 METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR - RATTUS NORVEGICUS (RAT), 872 aa.	6.90E-109	3 (3q21)
3041	cg42891000	1295	TGAGTCCAAGCC CTTCTCTGTAC A[C/gap]TTAGTC CCAGTCTCTGGA ATATTG	C	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3042	cg42891000	1606	TGGAGGGAGAT GTGGAGCTGAC CCT[G/C]TCCAG CCTGTCCACGGA GAGGAAGG	G	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3043	cg42891000	530	AGCAGGCCTTAT TATTATTATTATT T/A]TTTTTTTTTG CTGACAAGTCCA AGA	T	A			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3044	cg42891000	649	CCTGCTTCCTTT TGCCTGTTATTA ATT/C]CGCTGCAA TAAAGCCATTAG AATGT	T	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3045	cg42891000	973	CCCCAGGATTCC AAGAGCCCAAT C[C/gap]TGCGGT GGGAGTGAAGG GGAGGCAG	C	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)

3046	cg43285474	2177	TGGTTGAATGAT TTCCCACTCAGG G[C/gap]CTGGGG CCAAGAGGAAAA ACAGGGA	C	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P30083 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP- R-2) - RATTUS NORVEGICUS (RAT); 459 aa.	4.40E-85	3 (3p22)
3047	cg42284367	1202	TTTTCAGCAAG AGGCTCCCGAG CG[A/G]GCAAGC TCAGTTTACACC CGATCCA	A	G			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.80E-83	3 (3q21)
3048	cg42284367	1218	GCTCCCGAGCG AGCAAGCTCAGT TTTATTCACCCGA TCCACTGGGGA GCAGGAA	A	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.80E-83	3 (3q21)
3049	cg11687629	323	TCAGCTTCCAGT CTTATCTGAAGA CIC/TJCCGGCAC CAAAGTGACCAG GAGGCA	C	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	8.90E-83	
3050	cg43970708	258	TCAGCTCACTGC AGCCTCCACCTC CIC/TJGGGTTCAA GCGATTCTCCTG CCICA	C	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3051	cg43970708	282	CTCACTGCAGCC TCCACCTCCCGG GTT/CJTCAAAGCGA TTCTCCTGCCTC AGCCT	T	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3052	cg43970708	277	ACCTCCCGGTT CAAGCGATTCTC CTT/CJGCTCAG CCTCCCAAGTAG CTGGGA	T	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	

3053	cg43970708	324	GGGACTACAGG CGCATGCCACCA TG[C/T]CTGGCTA ATTTTGTATTTT TAGTA	C	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3054	cg43089531	408	TTTAAAAGCTTT GATTAGAAGCCA A[C/T]TTGATTTA GGAGTTCCCACT GGCAA	C	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3055	cg43089531	435	TGATTAGGAGT TCCCACTGGCAA A[A/T]TAGGGAAC AATATGAGCATC AAGGA	A	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3056	cg43089531	803	AGCATTTTCACG TTTGACATGATA G[T/C]AACTCAA CTAACTCTTTAC CACAT	T	C				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3057	cg21411454	1822	AATGTGCTCTCC TAGGCCACAGG GC[C/gap]TTTGG CAGGTGCAGCC CCCACTGCC	C	gap				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3058	cg21411454	466	CAGCTTTCAAAA AGAGTGCTGCC A[G/T]AAAAAGCC TTCCACCCTCCT GTCTG	G	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3059	cg21411454	492	AAAAGCCTTCC ACCCTCCTGTCT G[G/gap]CTTTAG AAGGACCCCTGAG CCCCAGG	G	gap				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2

3060	cg21411454	523	GAAGGACCCTGA GCCCAAGGCG CA[G/gap]CCACA GGACTCTGCTGC AGAGGGGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3061	cg21411454	563	GCAGAGGGGG TTGTGTACAGAT AG[gap/G]TAGGG CTTTACGCCTAG CTTCGAAA	gap	G			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3062	cg21411454	568	AGGGGGTTGT GTACAGATAGTA GG[G/gap]CTTTA CGCCTAGCTTCG AAATGGAT	G	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3063	cg21411454	574	TTGTGTACAGAT AGTAGGGCTTTA C[gap/C]GCCTAG CTTCGAAATGGA TAACGTC	gap	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3064	cg43040271	2038	CGTTTAAGGAAGA TCATTAAGTGTA A[G/C]TTCTGCCG CCAGTGATGACG GAGGA	G	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPRÖT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. pcis: SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.90E-74	
3065	cg40359282	1381	TTTAAAGTGAC AAGTTGACTTGC C[G/A]TTTGACAGT GGGTGCGCCTA AGCGAC	G	A			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q93127 G PROTEIN-COUPLED RECEPTOR - BALANUS AMPHITRITE, 379 aa.	2.10E-67	

3066	cg43040273	2989	TTTCTACTTTTAA AGACCCCCCCC C[G/C]CCCCAACA GAACACTAAACA GACTAT	G	C				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
3067	cg43040273	3473	GCTTCAGTTGTT TTCCCGAGCAAA G[gap/G]TCTAAA GTTTACAGTAAA TAAATTG	gap	G				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
3068	cg41554459	1566	ATGATGAATGAG ATGTAAATGTGC C[A/C]AGAATATA TTATATAAAGAAT TTTA	A	C				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P53453 D(2)-LIKE DOPAMINE RECEPTOR - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 463 aa.	9.10E-50	2
3069	cg43028527	2928	AAAATACAGCTG GATTGGGTTATG A[G/A]TATTTACG TTTTTGTAATAA ATCT	G	A				SILENT- NONCODI NG	tnf	Human Gene SPTREMBL-ID:P78536 TNF-ALPHA CONVERTING ENZYME - HOMO SAPIENS (HUMAN), 824 aa.	0.00E+00	2
3070	cg43028527	3214	AAATATATATCTA AATTAGAAATC A/GITTTGGGTTA ATATGGCTCTTC ATAA	A	G				SILENT- NONCODI NG	tnf	Human Gene SPTREMBL-ID:P78536 TNF-ALPHA CONVERTING ENZYME - HOMO SAPIENS (HUMAN), 824 aa.	0.00E+00	2
3071	cg43336100	1661	GGTATGTACCTT ATTACAAAAAA A[T/gap]GATGAA AACATATTTATAC TACAAG	T	gap				SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
3072	cg43336100	35	AATTCGGGCTCA AACTCAGCTCAC TTT[gap]GAGAGT CTCCTCCCGCCA GCTGTGG	T	gap				SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)

3073	cg43336100	45	CAAACTCAGCTC ACTTGAGAGTCT C[C/gap]TCCCGC CAGCTGTGGAAA GAACTTT	C	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
3074	cg44131329	1022	CCTGTGTTCTCT CCAAAGAGCAGA A[A/gap]GTGGGT ACTATACGTGGC TACGTTG	A	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	2.90E-166	17
3075	cg44131329	2372	GACCCAGGCAG CAGCAGCATGG GGT[T/gap]GGCC AATGGGCGGG TTCCACAGGA	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	2.90E-166	17
3076	cg43303573	272	TACATATATACAT ATACCACAAATA G/CJAAAAATGAC TGAAAGAAAAA ATAT	G	C			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	
3077	cg43303573	515	GTTTGTGATCATC CTTTTCTTTTTT T/gap]TATAAGTG GCTAAATCTTCC AGCTA	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	
3078	cg43303573	516	TTTGTGATCATCCT TTTTTTTTTTTTTT gap]ATAAGTGGC TAAATCTTCCAG CTAA	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	

3079	cg43965652	1131	TTTTTAAAAAAA GAAATTCTGTTCT A/GJAAAGTATTT CAGACCAAAAAGG AGGT	A	G				SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3080	cg43965652	56	ATTAAACTTGAC AAGCTATGGCTT G[C/gap]CGCCAT CAATGACGCCTA TTGGGTT	C	gap				SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3081	cg43965652	57	TTAAACTTGAA AGCTATGGCTTG C[C/gap]GCCATC AATGACGCCTAT TGGGTT	C	gap				SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3082	cg43965652	677	GTCTCTGAAAC TAAATCAGACT TT[C]AGATTCT CTGAAACAGTTC TGGT	T	C				SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3083	cg43962131	136	AGAGCGGGCGT GGGACCAGACC CTC[gap]TCCAC AGCCAGCCTGG CCAAGGTGGC	gap	T				SILENT- NONCODI NG	tnfrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3084	cg43962131	210	AAGCACCAGG GGTCTAGGAATG CT[C/gap]CCCCCT TCTCTCCAGGGG CCAGAGGG	C	gap				SILENT- NONCODI NG	tnfrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3085	cg43962131	213	CACCAGGGGT CTAGGAATGCTC CC[C/gap]CTTCT CTCCAGGGGCC AGAGGGGAG	C	gap				SILENT- NONCODI NG	tnfrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9

3086	cg43962131	214	ACCCAGGGGTCT AGGAATGCTCCC C[C/gap]TTCTCT CCAGGGGCCAG AGGGGAGA	C	gap			SILENT- NONCODING	tnfrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3087	cg43962131	89	CACTTTACCCGC AGCTGTGCTGTG C[A/gap]CCTCCC ACACAGTGGTCT GAGCAGA	A	gap			SILENT- NONCODING	tnfrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3088	cg43985041	1779	GGCCAAAGAGCA GAGGCAGCGAG TTG[G/T]GGAAAG CCTCTGCTGCCA TGGTGTG	G	T			SILENT- NONCODING	tnfrecept or	Human Gene SWISSNEW-ID:P20333 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) - HOMO SAPIENS (HUMAN), 461 aa. pcds:SWISSPROT- ID:P20333 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) - HOMO SAPIENS (HUMAN), 461 aa.	1.30E-255	1 (1p36.3)
3089	cg43984024	113	TAGGTCCCATTC TTTTATTGTCAT [G/A]TGGTTACAA TATAAATACACTT GCC	G	A			SILENT- NONCODING	tnfrecept or	Human Gene SWISSPROT-ID:P36941 LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR) - HOMO SAPIENS (HUMAN), 435 aa.	2.40E-242	12
3090	cg43335558	1176	AGACTCTGAGAC AGTGCTTCGACA A[G/C]TTTGCAA CATGGTGCCCTT TGACT	G	C			SILENT- NONCODING	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8

3091	cg43335558	1183	GAGACAGTGCTT A CGACAAAGTTTGC A/GJACATGGTG CCCTTTGACTCC TGGGA	A	G				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
3092	cg43335558	1186	ACAGTGCTTCGA A CAAGTTTGCAAA C/A/TJTGCTGCC TTTGACTCCTGG GAGCA	A	T				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
3093	cg43335562	1386	TCTGCCATGTCC C TAAGTGTGATTC T/C/TJTCAGGAA GTGAGACCTTCC CTGGT	C	T				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
3094	cg43335562	1397	CTAAGTGTGATT G CTCTTCAGGAAG T/G/CJAGACCTTC CCTGGTTTACCT TTTT	G	C				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
3095	cg43943896	372	AACAGCATGGAA G GAGAACCAGTTT C/G/CJTTCAGCT ACCTGGGAAGAC GGTTG	G	C				SILENT- NONCODI NG	traffic	Human Gene SPTREMBL-ID:P97412 LYSOSOMAL TRAFFICKING REGULATOR - MUS MUSCULUS (MOUSE), 3788 aa.	0.00E+00 (1q42.1)	1
3096	cg43988937	73	TTTTTTTGTAGTT A ATTAAAAAAA A/gap]CAAAAAC ACAACCAAAAGA ACTGA	A	gap				SILENT- NONCODI NG	traffic	Human Gene SPTREMBL-ID:Q99408 PUTATIVE NUCLEOLAR TRAFFICKING PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 1410 aa.	0.00E+00 5 (5q32)	5 (5q32)
3097	cg43994751	532	CAGATTTAGGTC gap CATAAAAGAAAG G[gap/A]AAAAA ATTATTCTAGTTA TATAA	gap	A				SILENT- NONCODI NG	traffic	Human Gene Similar to SPTREMBL- ID:O08547 VESICLE TRAFFICKING PROTEIN SEC22B - MUS MUSCULUS (MOUSE), 215 aa.	1.70E-88	

3098	cg43934751	1050	GGCTGCCTGATC CAGGTGCACAG GC[C/gap]TCCGG TCACGGTTAAAG CCAAGCTG	C	gap			SILENT- NONCODI NG	traffic	Human Gene Similar to SWISSPROT- ID:Q02792 RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' EXORIBONUCLEASE) (EC 3.1.11.-) (P116) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1006 aa.	6.50E-55	
3099	cg43934751	709	CTCCCTCCACGA TCATCTCGTCTG G[G/gap]TGGATA CCCACCAAGGCC CAGCTAGC	G	gap			SILENT- NONCODI NG	traffic	Human Gene Similar to SWISSPROT- ID:Q02792 RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' EXORIBONUCLEASE) (EC 3.1.11.-) (P116) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1006 aa.	6.50E-55	
3100	cg43995002	124	TTCAATGGAACA TCCCGCGCTTAG C[G/gap]CAGTGT TGAATCTAACAC CGAAAAA	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3101	cg43995002	575	AAAACCCACGC TTTAAACAAACAT [A/C]TTTGGGGT GGCTATGGCACC TTTGA	A	C			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3102	cg43995002	77	TTTTTTTTTTTT TTTTTTTTTTTTT A]GAAAACACCA CTGCTCTTTATT CA	T	A			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3103	cg43995002	79	TTTTTTTTTTTT TTTTTTTTTTTGA TTAAACCAACACT GGCTCTTTATTCA AT	A	T			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3104	cg43995002	80	TTTTTTTTTTTT TTTTTTTTTTGA TTAAACCAACACT CTCTTTATTCAA TG	A	T			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11

3105	cg43995002	791	AGATAAAGAAAGT AACAAAGGAAAA A[G/A]AAAAAAT TAATAAAAAATTC ACGA	G	A			SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3106	cg43948839	329	GGTGCCTGCAG AGCAAGGAGGG GGG[C/gap]CCCC CAAAATGGCTCG GCCCCCTGCA	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.lpcis:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0.00E+00	17
3107	cg43949599	376	CACCCACCTTG GATTGGCCGC AG[G/gap]TGTGG AGGGCCTCATCA AACTCTTT	G	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P17480 NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90) - HOMO SAPIENS (HUMAN), 764 aa.	0.00E+00	17
3108	cg44027791	185	ATACCTCAAGCA GTTACAACATAA A[A/T]TAAAGTTG GATTTTGTGTTAA TTTA	A	T			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
3109	cg44027791	572	ACAGTGTTTCATC ATCTGAAGTAGA G[A/gap]GTATAA GGCAACGTTCTC CATAGAA	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
3110	cg44027791	60	GTTATTTTGAAG ATTTGCGCTCAG G[gap/C]AACTAA ATTATTAGCAA GAAAAA	gap	C			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17

3111	cg43328754	22	GGAATTCCTTT TTTTTTTTT[T/G]T GGCTCAAAACT CATCTTTATTGG	T	G				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (- REL) - HOMO SAPIENS (HUMAN), 579 aa.	0.00E+00	19
3112	cg43933098	417	CAGCCTGAGGAT GAGGCACAGGG AG[G/gap]CAGGG CCCATCACTCAG GAGGCCAT	G	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa. pcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3113	cg43933098	425	GGATGAGGCAC AGGGAGGCAGG GCC[C/gap]ATCA CTCAGGAGGCC ATGGGAGAAA	C	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa. pcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22

3114	cg43933098	458	AGGAGGCCATG GGAGAAACAGTC TC[C/T]GGGAGG TGCTGCACCTGG GGACCCA	C	T				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3115	cg43933098	57	TTTTTTTTTTTT TTTTTTTTTTTTTT GJTGGGTGGTA CCAATCTGTGTT TAT	T	G				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3116	cg43933098	58	TTTTTTTTTTTT TTTTTTTTTTTTTT CJTGGGTGGTAC CAATCTGTGTT ATT	T	C				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22

3117	cg43933098	582	CCCTCTGCCAC TCTGAAAGAGG G[G/gap]CTTGCC GCTGGGGAGGG ATTAGGGG	G	gap			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.pcds:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3118	cg43933098	704	CCTCAACTTACC ATGGGGTTACTT C[C/T]TGATAAAC CCATCATAAATG AAAAT	C	T			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.pcds:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3119	cg43934374	5008	AGTGAACATATG CCACTGCCCTGGC C[T/C]TTTTCCTT CAGAGCTTGTTG TCCT	T	C			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.pcds:SWISSPROT-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	15 (15q21)

3120	cg43921342	2083	GGTTTGTGTTTAC TGGAAAAA A[A/gap]ATGCTC CTGTCAGCCCAG GCAACAG	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.[pcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0.00E+00	
3121	cg43921342	2084	GTTTGTGTTTACT GGAAAAA A[A/gap]TGCTCC TGTCAGCCCAGG CAACAGG	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.[pcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0.00E+00	
3122	cg43936136	1135	ATGCCAGTGTGA CTCTTAAACCT T[C/T]CCATCTGG AGTCCTGTATTT TCTCT	C	T			SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q99840 TRANSCRIPTION FACTOR NFATX2 - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	
3123	cg44028034	254	CAGAACACAGCC AGTTACGCAACA G[C/gap]GCAAGG CCTGCTCCAGGC CCCACCT	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P42230 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 5A (MAMMARY GLAND FACTOR) - MUS MUSCULUS (MOUSE), 793 aa.	0.00E+00	

3124	cg44130900	1668	TTAGTACACAGA AATTCTGCAGAT G[C/G]TATTGTAC ACATGTGACAAC CTATG	C	G				SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
3125	cg44130900	2140	TTGTATCCAGAA ATGTATACTCAT C[G/A]TATTTTAA AGCTAAATTTATT TTTT	G	A				SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
3126	cg43968711	277	TTAGGAGAAACA TCCTTTAATTTCTT C[G/T]AAAGAGGT GAAAATAAGATT TTTT	C	G				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3127	cg43968711	286	ACATCTTTTATTT CTTCTAAAGAGG T[G/G]GAAAATAAG ATTTTTTTAATAT TTC	T	G				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3128	cg43968711	303	TAAAGAGGTGAA AATAAGATTTT [T/gap]AATATTTT TCACTCATAAGA TTTT	T	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3129	cg43968711	351	TTTAAACTCTTAA AAATGCAATATC T/CJTCTTTTCAAA GCACATGCCATC TTA	T	C				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3130	cg43968711	467	AATTCTGCATTA AAAAACCCCTATG C[G/A]ACTTTCTG CAAATATATTCC GTCCT	G	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11

3131	cg43968711	473	GCATTA AAAAAC CCTATGCGACTT TTC/TTGCAAATA TATCCCTCTTTA TTAT	C	T				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.3E-292	11
3132	cg43968711	486	CTATGCGACTTT CTGCAAATATAT TTC/GJCCTCTTTA TTATTCAGGGAC TCCAA	C	G				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3133	cg43968711	557	TATTTATCGTTTC TTATTTCCGTAG G/gap]AAACACAG AACCAATGATGT CTTCT	G	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3134	cg43968711	566	TTTCTTATTTCCGA TAGGAAACACAG [A/G]ACCAATGAT GTCTTCTGACAA CIGT	A	G				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3135	cg43947662	2433	GGCCCCCTCCCT CCCAGGTCTCGC T[G/gap]CTCTCTT TCCCCTCCAGGC CTCGCT	G	gap				SILENT- NONCODING	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa.	3.70E-276	12
3136	cg43947662	2462	TCITTCCCTCC AGGCCTCGCTTC CTT/gap]GGTCAG TCCCACGATCAC TTCCGGT	T	gap				SILENT- NONCODING	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa.	3.70E-276	12
3137	cg43011561	1783	AGGCTTGGTCCA ATACATGGCTCT G[C/gap]CCCCCA GAACCTAAGGCT CTCACTG	C	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P35269 TRANSCRIPTION INITIATION FACTOR IIF, ALPHA SUBUNIT (TIF-ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa.	4.30E-275	19 (19p13.3)

3138	cg44024015	1729	CCGGGATGGGC CGACCAAACCTT TA[G/C]CAGCCC AGCAATTTCCCGA AGCCCCGA	G	C			SILENT- NONCODING NG	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3139	cg44024015	2456	TGTGTCCCTTT ACTGAGCGCACA G[C/gap]CACAGC CTGTCCTTGTCAG GTGGACC	C	gap			SILENT- NONCODING NG	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3140	cg44024015	2457	GTGTCCCCTTTA CTGAGCGCACA GC[C/gap]ACAGC CTGTCCTTGTCAG GTGGACCC	C	gap			SILENT- NONCODING NG	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3141	cg43917801	175	ATACATTTATTCA TGCCAGTCTGTT G[A]CATGCAGGC TTTTTGGCTTCC TACC	G	A			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa. [pcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249 (6p22.3)	6
3142	cg43917801	2344	AGAAAGAAAAG TAAGCAGGGCTG G[C/gap]TTCGCC CGCGTTCTCGTC GTCGGAT	C	gap			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa. [pcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249 (6p22.3)	6
3143	cg43917801	3091	GGGAGCTGGCG GCGCGGCTGC TGG[G/gap]CCTC CGCCTTCTTTTC TACGTGAA	G	gap			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa. [pcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249 (6p22.3)	6

3144	cg43917801	377	GGAATCAACTGC TTCAGGGAAAA G[A/gap]AAAAA AAAAA CTTGCCT	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3145	cg43917801	393	GGGAAAAAGAAA AAAAA A[A/gap]GACTTG CCTGGGAGGCC GCGAGAA	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3146	cg43917801	635	GGACTTTTCTCT CTTTACCCACCT C[C/gap]GCCCC GCGAGGAGTTG AGGGGCA	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3147	cg43917801	654	CACCTCCGCCCC TGCGAGGAGTTG A[G/gap]GGGCCA GTTCCGCCGCC GCGCGCGT	G	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3148	cg43917801	657	CTCCGCCCCCTGC GAGGAGTTGAG GG[G/gap]CCAGT TCGGCCGCCGC GCGCGTCTT	G	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3149	cg42906458	22	TTTTTTTTTTT TTTTTTTTT/GTT AGCTATCATAAC TTTATTAAACA	T	G			SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q92759 TRANSCRIPTION FACTOR TFIH - HOMO SAPIENS (HUMAN), 462 aa.	4.20E-245	

3150	cg43920700	1897	GCCTTCCTCCCG CTGACCCCGCC CC[G/C]GCCCTTCT GGGGAAGGAAC AAAGTCC	G	C				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NFI-X) (NF-IX) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa.	2.10E-243	19 (19p13.3)
3151	cg43918762	1031	AAGATCAGATAA ATAAAAAA A[A/gap]GGCTTA AAACAGACTCAC CATATT	A	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3152	cg43918762	1452	TTTGTGTTTGT TTAAAAA gap/AJGGGTTTCTAC AAACTTGGCAGA AGTTT	gap	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3153	cg43918762	699	GTGGAATAAAAT AAACTTTTTTTT T/gap]CTCCCTAC AATACATAGAAG GGTTA	T	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3154	cg43998635	277	TGCTGAGAAAGA GGAAGGAGTCTC C[T/A]TGAGCTCC AGCATCAGGGG CAGAAA	T	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P43694 TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4) - HOMO SAPIENS (HUMAN), 442 aa.	1.60E-236	8 (8p23.1)
3155	cg43129605	1480	CTTGGAGGAC CAGGGTTCCAG AG[A/T]AGCTCAC CTTGTCTCTGCA GCCCTG	A	T				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20

3156	cg43129605	1481	TTGGAGGGACCA GGGTTTCCAGAG A[AT]GCTCACCT TGCTCTCTGCAGC CCTGG	A	T			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3157	cg43129605	1811	TCCACATGTGTG TGCATGAGTCCA T[G/C]TGTGCGC GTGGGGGGCT CTAACTG	G	C			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3158	cg43129605	1813	CACATGTGTGTG CATGAGTCCATG T[G/C]TGGCGT GGGGGGGGCTCT AACTGCA	G	C			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3159	cg43129605	1857	AACTGCACITTC GGCCCTTTTGCT CTT/GGGGGGTC CCACAAGGCCCA GGGCAG	T	G			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20

3160	cg43128605	1858	ACTGCACCTTTTCG GCCCTTTTGCTC TIG/TJGGGGTCC CACAAAGGCCCA GGGCAGT	G	T			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
3161	cg43128605	2054	TTGGTGAGCCCTG GGGAATCAGCAA A[gap/A]GGGGAG GAGGGGTGTGG GGTTGATA	gap	A			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3162	cg43128605	2265	TCTCCAGGGGG CCAGTTCAGGGC CC[C/gap]AGCTG CCCCCCAGGAT GGATATGAG	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3163	cg43921348	341	GCCCACCCAGA CCTAGGGGCAG GGC[C/gap]AGGA GCAAAACAAGAG GGAGAGGCA	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa. [pcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.	3.80E-228	

3164	cg43984259	363	CCTGCAGGTTCT AGGGCTAAAGG CC[C/gap]AGCAG AAGTGGGCACGT GAGAGGGC	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
3165	cg43984259	457	GCTAGAAAGTGGT GCTGGCATGTGC C[C/gap]AGTTCC ACCCACCCCTTC CCTCCTA	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
3166	cg42345420	223	CTTCACCTATAA TGCAACTAATCA TIG/CJTACTTAGT TGCTATGTTAAT CTATT	G	C			SILENT- NONCODING	transcript factor	Human Gene SPTRÉMBL-ID:Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR - HOMO SAPIENS (HUMAN), 399 aa.	1.50E-210	
3167	cg42479822	235	GTAATATTTTACC AAAAAAA gap/AJGAAAAAAGT GAACAGTCTGCC AGTGT	gap	A			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06547 GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA 2) - HOMO SAPIENS (HUMAN), 383 aa.	2.00E-197	15
3168	cg42479822	433	AAAGCAATTTT TCCGTAAGAATC[A/G]TTTCCTGGG GAGAAATAAGTC CATA	A	G			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06547 GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA 2) - HOMO SAPIENS (HUMAN), 383 aa.	2.00E-197	15
3169	cg21646034	93	TGTGTGTAGCGG GGCCGCGTCAG CC[C/gap]GGCCG GGTACGAGGCG CCTCGGGTC	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GABBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	15

3170	cg21646034	97	TGTAGCGGGGC CGCGTCAGCCC GGC[C/gap]GGGT ACGAGGCGCCT CGGGTCCCCG	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	15
3171	cg43998970	1481	CCACAGACTGAG CTGGCCACAGAG GG[G/gap]TGGAA CTGCTGATGGGA TTTCCTTC	G	gap			SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12
3172	cg43947199	1485	AATATGTTTTGAA ACAGGTACCATA C/AJAATTATTATA TGGTCTCCCTAC TGA	C	A			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.pcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3173	cg43947199	236	AAACATTATTTCAG AAAATGTACTTT G/CJTTTTTGAAT AAAACAAAATCT TCA	G	C			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.pcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8

3174	cg43947199	299	CAAAATAGAGGT GAGTTGGTACCA GTTGJGGGCCAA TTCTTAACACGG ACATTT	T	C				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.lpcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3175	cg43947199	423	CAAAGCATGTAC TGAGGTCCTTTCT AIC/TJGGGTGCC TGACAGAATGCA GATTCA	C	T				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.lpcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3176	cg43947199	550	ACAATTTTGTCT TACTCCAAACAG[A/gap]AAAAAATG GTACACACTTTA ACAAA	A	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.lpcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8

3177	cg43947199	556	TTTGTCTTACTC CAAACAGAAAA A[A/gap]TGGTAC ACACTTTAACAA AAGCAAA	A	gap				SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. [pcds:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3178	cg43948504	483	GAGTTTGGTAAT TTGCACTTGTTTT [gap/T]GTAACT GAACTGCTCCTC TCCICA	gap	T				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P29084 TRANSCRIPTION INITIATION FACTOR IIE, BETA SUBUNIT (TFIIE-BETA) - HOMO SAPIENS (HUMAN), 291 aa.	9.50E-152	8 (8p21)
3179	cg43948504	515	GAACTGCTCCTC TCCTCAGCCGCA A[gap/A]GAAGCA GATAGGAAGACA GTCTTCA	gap	A				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P29084 TRANSCRIPTION INITIATION FACTOR IIE, BETA SUBUNIT (TFIIE-BETA) - HOMO SAPIENS (HUMAN), 291 aa.	9.50E-152	8 (8p21)
3180	cg43992817	137	TGGAAGAATCAG TTCGAAGACATA A[T/A]AGCCTTTA CTTTTCTTTTA TTAT	T	A				SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
3181	cg43992817	499	GGGTTGGGAG TTTAGGAGGAGG GG[T/C]GGCCTG AGCCCCCTCAGT TCCGCCA	T	C				SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3

3182	cg43992817	508	AGTTTAGGAGGA GGGTGGCCTG AG[C/gap]CCCCCT CAGTTCCGCCAC GGCCTCCA	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
3183	cg43935832	3340	AAACTGGTGCAT ACTGGCATTGGC C[C/gap]TTGGTG GGGAGCACAGA CACAGGAT	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:P42224 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) - HOMO SAPIENS (HUMAN), 750 aa. pcis:SWISSPROT-ID:P42224 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1- ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) - HOMO SAPIENS (HUMAN), 750 aa. pcis:TREMBLNEW-ID:G2281071 TRANSCRIPTION FACTOR ISGF-3 - HOMO SAPIENS (HUMAN), 750 aa.	3.20E-144	
3184	cg43289377	1472	TGGTACAAAGAA TAGATGCAGGCA G[C/T]CATAGGTA CAAGGGATTCCC TTAAT	C	T			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138 (5q31.1)	5
3185	cg43299377	1635	TGAGATGACGTT AACAGGACCCCT G[G/gap]CCAGTT TCCATGAGATCT GGGTCTC	G	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138 (5q31.1)	5

3186	cg43299377	1666	TTCCATGAGATC TGGGTCTCTGTC A/C/T/TTCAGGG GGTAGGCTCCTG GAGGC	C	T				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3187	cg43299377	1840	GAGAGACCTGG GGATGTAGGTGC CG[G/gap]CTCCG CAGGGCTAGTAA GCAGTTCT	G	gap				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3188	cg43299377	524	CAAAGTGCTGGG ATTACAGGCGTG A[G/gap]CCACCG CGCCTGGCCCG GCAGCCCT	G	gap				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3189	cg43283688	1091	GAGTTTATAAAT TAAAGGTCAAAT A/C]CTGAAGCTT TTTATTTAGGCTT TTC	A	C				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:P18846 CYCLIC-AMP- DEPENDENT TRANSCRIPTION FACTOR ATF-1 (TREB36 PROTEIN) - HOMO SAPIENS (HUMAN), 271 aa.	1.90E-137	12
3190	cg43283688	1092	AGTTTATAAAT AAAAGGTCAAAT C/AJTGAAGCTTT TTATTTAGGCTTT TCC	C	A				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:P18846 CYCLIC-AMP- DEPENDENT TRANSCRIPTION FACTOR ATF-1 (TREB36 PROTEIN) - HOMO SAPIENS (HUMAN), 271 aa.	1.90E-137	12
3191	cg44012692	2080	CTCTTGACCTG AGAGTGGGAGTT T[C/T]GTAGGAAC ACAGGAAGGAG ACCAAC	C	T				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9

3192	cg44012692	4499	ATCACCCCGACG CGGGTGGCGAG GGTTCJCCCGCC GAGCGCCAGGT CTAAGAGA	T	C				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9
3193	cg44012692	4581	AACCCCTGCTCC GGCCGGTCCGC AC[C/gap]GTTCC GGCATTCTCTTG CTCAGTAA	C	gap				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9
3194	cg43982109	1886	AGTGACCCGACG CCAATCTCGGAG A[G/gap]CCTCCT GGCAATACACAA CTCCAGC	G	gap				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa.	5.60E-131	10 (7p)
3195	cg43310921	98	TGTTCCCTTCAA TTAAAAA [gap/A]TACAAA GCTACGTAGAA ACGTCA	gap	A				SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:O00112 LIVER- SPECIFIC BHLH-ZIP TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 429 aa (fragment).	7.20E-124	19
3196	cg43263063	174	GCGCAGGCCCC GCAGCCGGGCC AGC[G/C]CGCCG CCCCGGCCGC GGCTGCCTC	G	C				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13887 TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2) - HOMO SAPIENS (HUMAN), 219 aa.	3.50E-122	
3197	cg43263063	491	CACCAGAGTGAA ACGACTGCCCT C[C/gap]TCCGGC CCCGACCCAGG CCCTCCCT	C	gap				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13887 TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2) - HOMO SAPIENS (HUMAN), 219 aa.	3.50E-122	

3198	cg43918209	934	CGATGGCTCCCC GGGACAGAGT CC[C/gap]TCTCC GGCCTCTCAG CAGCCCCGG	C	gap				SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3199	cg43918209	105	TCTAACAACG CCAGGTAGACG GA[G/gap]TTAAA AAGATCCACCG CACGAAAG	G	gap				SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3200	cg43918209	1841	CAGGTGCACTCC GGACAACGGC TC[G/T]CTCACGC CTCTCTACACAA ACCAAC	G	T				SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3201	cg43918209	346	CGCTGGAACCTG GGAACCTACTGG G[C/G]ACCTCTAA TGCAGATGAGAA AAACT	C	G				SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3202	cg43918209	490	GCCACTCTCCTC CCCACTGCCCCAG G[G/gap]CGGGTG CACGCCCCAGG ACCTCCTC	G	gap				SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3203	cg43918209	511	AGGCGGGTGC ACGCCCCAGGA CCT[gap/T]CCTC CCAGGCCCCAC ACCCACGCAA	gap	T				SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3204	cg43918209	517	GGGTGCACGCC CCAGGACCTCCT CC[C/gap]AGGCC CCACACCCACGC AAGCGGAC	C	gap				SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19

3205	cg43918209	524	CGCCCCAGGAC CTCCTCCACGGC CC[C/gap]ACACC CACGCAAGGCG ACAGGAAGC	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3206	cg43918209	532	GACCTCCTCCCA GGCCCCACACC CA[C/g]GCAAGG CGACAGGAAGCT CCCCACG	C	G			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3207	cg43918209	533	ACCTCCTCCAG GCCCCACACCCA C[G/C]CAAGGCG ACAGGAAGCTCC CCACGC	G	C			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3208	cg43918209	869	GTCTCTGCGGAA GGCGCCCGCGC CC[C/gap]CGGCT CAGACTCCTCGG TGCCGTCC	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3209	cg43918209	870	TCTCTGCGGAAG GGCCCCCGCGC CC[C/gap]GGCTC AGACTCCTCGGT GCCGTCCC	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3210	cg43918942	203	CATGGGAGGA TGAGGCCCCCTG GGG[G/gap]TCAG TGAGGCACGGC TCTGCCTCAA	G	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

3211	cg43918942	290	TCGGCCACATCC GGGGCAGCCAT GC[C/gap]AGAGC TGAGACCTCCTA CGAGTGGT	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3212	cg43918942	476	GCCAGGACACTA TGCAGGCTATGC C[C/gap]GCACTG CCTACAGAGCTA TGCTCAG	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3213	cg43918942	544	CTCAGCTGTCGG GCACTCAGTTCA C[C/gap]TGCCGG CAGCCGCAGGC GCTCCTGG	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3214	cg43918942	93	AAGCCCTCGAGA AGCCCTGGCAG GA[A/C]CCAGGC TGGCTACTGAGC TCTGGGC	A	C			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTRMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3215	cg43983354	1336	CCACCCCGCCC CCAGTGGCTGG GCG[G/gap]CCCC GGCTCCGGCCC CTGGGGGAGC	G	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.[pcis:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103 (19q13.2)	19

3216	cg43993354	1377	CTGGGGGAGCG CCAGCGGGTGG TGA[T/C]CAGAGC AGGGCCACAC CCCGGCAG	T	C				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.pcds:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103	19 (19q13.2)
3217	cg43993354	1508	GGTGATTGGATC TGGCCAGAAAG GC[gap/C]AGCCA TGCCGAGGTCC CAGGGGACG	gap	C				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.pcds:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103	19 (19q13.2)
3218	cg43995484	3358	TGGAAGAAAGAA GCATTGAAAAACA A[A/C]GACATTCT TCCCACTTCTTG GATT	A	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q62318 TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1) - MUS MUSCULUS (MOUSE), 834 aa.	1.80E-96	
3219	cg42930883	1095	GGAAGGAGACA CATTCACAAAGA AA[C/A]GTTGCGA AAATTGCGAAAT CTGTTG	C	A				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)
3220	cg42930883	1125	CGAAATTCGCA AATCTGTTGTGC AT[C/G]CTCAAT GAAACGCCTTT CGGCT	T	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)

3221	cg42930883	1348	TTAATGTATTTT GTAAATAGTTTA AGTACATTTCTTT TTTTACGTAAAC CTG	A	G				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTRMBL- ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)
3222	cg43051067	1933	TGCTGTACTTT ACAATTCAACTA CATTGTCTCTAC CCAGCATTTAAC GGCAA	A	T				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcis:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.30E-91	
3223	cg43297584	222	ACTTGCGACAAG TTGCCGGAGCC GC[G/gap]GGGC GCGGGCGGCGG ACAGATTGAC	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.60E-90	
3224	cg43917302	1743	CATTACGGCGA AGCCGCCACGC GG[C/gap]CCCGG ACGCCGCCCTTG CGGCCCCAG	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7
3225	cg43917302	1802	GCTCCCCCGA GGTGGCGCCGC CCC[C/gap]GCTC TTCTTCTGAGCC TAGTTCTCA	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7

3226	cg43917302	1949	GCCGCGGGACA CCTGTTTCTTC CC[G/gap]CAGTG TCTGCGTCCGCA CAGCATAC	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. cds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7
3227	cg43917396	497	GACTTGCCAGAC GAGGCTCTATT C[G/gap]GGCTGC TGCAGCCCCACTT TTCTCGT	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3228	cg43917396	660	TCCCGGCGCTG GGAGAGGGCTC GCT[G/gap]GCTC TCCAGCCCACTC ACCACTCTC	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3229	cg43917396	677	GCTCGCTGGCTC TCCAGCCCCACTC A[gap/C]CCAGTC TCTGGATGCTCT GCAGTTC	gap	C				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3230	cg43917396	679	CTCGCTGGCTCT CCAGCCCCACTCA C[C/gap]AGTCTC TGGATGCTCTGC AGTTCAT	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3231	cg43917396	76	CCCCCTGGGAC TCAAGGCAGAAG TG[C/gap]CACTC CCTCCGTTGACC ACGGCTGG	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	

3232	cg42702130	675	GAGGGGCACAC AGACTGTGGCAG AG[C/gap]TGCGC CCATCCCGCAGA GGCCCCCTG	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3233	cg42702130	706	CCATCCCGCAGA GGCCCCCTGTCCA C[C/A]TGGAGAC CCGGAGACAGA GGCCTGG	C	A				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3234	cg42702130	899	AGTCCCATGGCA CAGAGCAAGGC GG[G/gap]CAGGG AACGGTTATTTT CTAAATA	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3235	cg43317047	1468	GAAGCTACTGTT TTCTCTTTTGTTC [A/G]TTTTACCTC TTTCTTACTCTTA CTA	A	G				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	3.80E-61	6
3236	cg43944978	227	TTGTGGTAAATT TTTTATCCTAAA [A/gap]CAACTCA CCTTGGCCGAAA AATGGG	A	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3237	cg43944978	284	CCCAAGGTCCCG TACTAGGCCGGA G[G/gap]AGAAAA GGACCTACCTCC TACAGGG	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3238	cg43944978	339	AAACAAGGAGAG CTAGGACTCAAT G[G/gap]TCGCCC AAGGCCCAAGG GTCTCCAG	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17

3239	cg43944978	591	ACTGAGCCTCTG GATCAGCACCT CTT[C]GATAGGAA GCAAGGAAGCA CACTAC	T	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3240	cg43922509	38	TGCTTTTTTTT TTTTTTTTTTT GTTGCTTTTCATA GAGTTTATTGA AA	T	G				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:P14741 TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT (EIF- 2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCN3) (GCD COMPLEX SUBUNIT GCN3) (TRANSCRIPTIONAL ACTIVATOR GCN3) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 305 aa.	1.20E-55	12
3241	cg42746806	143	GGAATTGCCCCA CGCAGGAGGCA GG[G/C]CGCTGC GGAGACCCCGAG GGCTACGA	G	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:O00343 BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 113 aa (fragment). pcis:TREMBLNEW- ID:G1732371 NEUROGENIC BHLH TRANSCRIPTION FACTOR - RATTUS NORVEGICUS (RAT), 113 aa (fragment).	2.00E-55	
3242	cg42746806	145	AATTCGCCACG CAGGAGGCAGG GC[G/T]CTGCGG AGACCCCGAGG CTACGAGA	G	T				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:O00343 BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 113 aa (fragment). pcis:TREMBLNEW- ID:G1732371 NEUROGENIC BHLH TRANSCRIPTION FACTOR - RATTUS NORVEGICUS (RAT), 113 aa (fragment).	2.00E-55	
3243	cg44928765	237	CTGCAGAGACTT AAGTTCTCTTTG C[C/T]CCAGTGC CCAGACCTGCCT TCTCTT	C	T				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	2.10E-53	16

3244	cg44928765	421	GTAAGGGGGAG GAGAAACACAAA CA[C/T]CTTCCGT GTGAATCTAAAG CATGGA	C	T				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	2.10E-53	16
3245	cg43979598	1031	CACCTAAAGG TTAGGTCAGGCT C[C/A]TCCCAGTG GCCTTCAAAAA TAAAT	C	A				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3246	cg43979598	134	AAACAGTGGAGA CGAGTGTAGCAC T[G/A]TCCCCAA ATCACCAACCCC CAGGT	G	A				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3247	cg43979598	178	CCCAGGTCCCAA GGCCTGGGCTG GG[C/gap]CAGCG CTAACAGGTGAG CCCAGGAG	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3248	cg43979598	179	CCAGGTCCCAAG GCCTGGGCTGG GC[C/gap]AGCGC TAACAGGTGAGC CCAGGAGT	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3249	cg43979598	563	TGGAGTACTGGC TGGAGGGGCCC CC[gap/C]AGACG GGGACCACCCC CCAAAAAA	gap	C				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3250	cg43979598	703	CCCTGGCCAAA AGTTGGTTGAAA A[gap/A]GGATAA GCTGTCTGAGAG AAAGGTT	gap	A				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)

3251	cg43978598	732	AAGCTGTCTGAG AGAAAGGTTGGG G[ap/G]AGGTGG AAATTTCTATTCC AAGGGT	gap	G				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3252	cg41074975	149	GGAAAAGCCAG CGAGAGGCAGG TGT[G/C]TAAAGG GAGCCTCTCAGC ATGCAGG	G	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q13263 TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1) - HOMO SAPIENS (HUMAN), 835 aa.	5.70E-51	11
3253	cg43946772	1795	ACTACTGATGTG CAAGCAAACCAT A[A/G]AAGGTACA GTTCTCCAGAAA GCATA	A	G				SILENT- NONCODING	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGLACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3254	cg43946772	895	TCITTTGGCTAAG TCATTTAAATAAT [T/C]TTTTTAAAC ATTTTCAGTCAA ATTT	T	C				SILENT- NONCODING	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGLACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3255	cg43946772	896	CTTTGGCTAAGT CATTTAAATAAT [T/C]TTTTTAAACA TTTTCAGTCAAAT TTT	T	C				SILENT- NONCODING	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGLACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3256	cg42166807	1619	AGAAGAATCCTT TGACTGAAGCAT G[A/T]ATGTAGAC TCGAAAGTACAG CATGG	A	T				SILENT- NONCODING	transferase	Human Gene SWISSPROT-ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA-1,6- N-ACETYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA- 1,6-N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-ACETYLGLUCOSAMINYL- TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)

3257	cg42166807	1672	TAGTCTAGTATA AGGGATCGGATC A[G/T]TGCTCAGC CTCTCCCTTGAG TGACA	G	T				SILENT- NONCODING	transferrase	Human Gene SWISSPROT-ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA-1,6- N-ACETYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA- 1,6-N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-ACETYLGLUCOSAMINYLT TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)
3258	cg43916882	141	CTCAGCTCACTG CAAGCTCTGCCT CTTCTGGATTCA TGCCTTTCTCCT GCCTC	T	C				SILENT- NONCODING	transferrase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1
3259	cg43916882	533	TCCACGGCTTT AAACAAAGCAAA A[C/A]AAACCAC CAATCCTAATAA CCCCC	C	A				SILENT- NONCODING	transferrase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1

3260	cg43916882	563	CCACCAATCCTA ATAACCCCTC C[C/T]TGCCCGT CTCCACGCTGTG CGGAG	C	T				SILENT- NONCODING	transferase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1
3261	cg43948635	1630	TTTGGAGCAGCT CATCCATCTCTC A[G/A]GTGGGG TCCTCCGGCAG GCAGCTT	G	A				SILENT- NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3262	cg43948635	816	CAATGCCAAACA CATAGTATGAGA A[T/G]TTTACTTT TTAAGAAATTAAT TTAT	T	G				SILENT- NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3263	cg43948635	818	ATGCCAAACACA TAGTATGAGAA TTT[G/T]ACTTTT AAGAAATTAATTT ATTT	T	G				SILENT- NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3264	cg43948635	985	TGCAC TTCAGCT ACGTGAAAATAA A[A/G]TTTCTTTG GGAAGGTGACAT TTGGC	A	G				SILENT- NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3265	cg43311354	1596	GAGAACACAGTG GCTGGTTTAA A[A/gap]TTCTTTC CACACCTGTCAA ACCAA	A	gap				SILENT- NONCODING	transferase	Human Gene TREMBLNEW-ID:G385673 FARNESYL-PROTEIN TRANSFERASE BETA SUBUNIT, FTPASE BETA SUBUNIT=PRENYL-PROTEIN TRANSFERASE DPR1/RAM1 HOMOLOG - BOS TAURUS, 437 aa.	8.50E-238	14 (14q23)

3266	cg44017777	229	ACATCATTCCTTT TGATCTCCTGTG[G/TATCCCTATA GTTATTTCAAGT AAAG	G	T				SILENT- NONCODING	transfere se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)(+)- ARGININE ADP- RIBOSYLTRANSFERASE) (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9.00E-195	
3267	cg43995237	239	GTATACACAAAG A AACTGTAGTCAG A[A/T]TAACAGGA CTTCAGAAATAA AAGCA	A	T				SILENT- NONCODING	transfere se	Human Gene SWISSPROT-ID:P53611 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL- GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1
3268	cg43258046	495	ATGTGGTGAAC T C GGATGTGCTACC G[C/gap]AAGACA GAGGACTTCTTC ACCATCT	C	gap				SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2673964 LECITHIN:CHOLESTEROL ACYL TRANSFERASE - AKODON TORQUES, 294 aa (fragment).	3.20E-146	16 (16q22.1)
3269	cg44000740	274	TGCTCTGGGACT A TGGGCAAGTCTT A[A/G]GCAAGCC ATTCTGCTTTC TGGGCC	A	G				SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S-TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS-THETA) - HOMO SAPIENS (HUMAN), 239 aa.	1.60E-117	16
3270	cg43949162	109	TTACAGCTCAGA C GGAGAGTCATT A[C/T]TAGACATT CGGTTGTTATTA AACAC	C	T				SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6

3271	cg43949162	18	TTTTTTTTTTT TTTTT/AJTCAAT GACTCATAAATT CTTTATTT	T	A				SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
3272	cg43949162	51	CTCATAAAATTCCTT TATTTGGCTAA[C/T]ACTGATTGC ATTCATTACTAC CATT	C	T				SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
3273	cg43920566	1312	ATGCTAGCAGC AGATTTTTTTTTT gap/T]ATTGGTAC ATATTATCCTTCA AATC	gap	T				SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3274	cg43920566	1845	ACAGGATGTTGC TTACCAGGACGG A[G/gap]TTTTGG TATCTTAGTACT GAAGTTA	G	gap				SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3275	cg43920566	2268	GGTTTTCTGTC CACAGGATATAA C[T/gap]TTTTTTT ATATAACAAGCA TAACAC	T	gap				SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3276	cg43920566	2275	CCTGCCACAGGA TATAACTTTTTTT T[gap]ATATAACA AGCATAACACAC CACTG	T	gap				SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3277	cg43928442	40	TTTTTTTTTTT TTTTTTTTTTT[G /T]TTTGCCTGAT GGCATTAGGTTT AT	G	T				SILENT- NONCODING	transfere se	Human Gene Similar to SPTREMBL- ID:O09034 GLUTATHIONE S- TRANSFERASE SUBUNIT 13 - RATTUS NORVEGICUS (RAT), 226 aa.	2.60E-87	7

3278	cg43954704	359	GTTGCTCCTGTC CTGGGGGGCTC TG[C/gap]CTCCA CCTCCAGTCCA GGATGTCT	C	gap				SILENT- NONCODING	transferrase	Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1,0 N- ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	1.10E-68	2
3279	cg43954704	360	TGCTCCTGTC TGCGGGGGCTCT GC[C/gap]TCCAC CTCCAGTCCAG GATGTCTG	C	gap				SILENT- NONCODING	transferrase	Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1,0 N- ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	1.10E-68	2
3280	cg43266642	220	GAGGGGAGGG CCTCCGAGTTCC CA[AG]ACAAAAC ACAGGTACCTAA GGGCTT	A	G				SILENT- NONCODING	transferrase	Human Gene Similar to TREMBLNEW- ID:G2688966 CARNITINE ACETYL TRANSFERASE - MAGNAPORTHE GRISEA (RICE BLAST FUNGUS), 608 aa.	3.20E-64	22
3281	cg43917654	360	AAAAATCTACT CTTAATGTATATT [A/gap]TTTCATAT TTGTTTAACAAAA GCAG	A	gap				SILENT- NONCODING	transferrase	Human Gene Similar to SWISSPROT- ID:P41819 DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S- ADENOSYLMETHIONINE-6-N', N'- ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 318 aa.	3.00E-52	5
3282	cg43917654	898	CTCCCTAAGAAC CATAAAAAAAGA T[A/C]ATTTTATT GTTAATTTCATTG CAGT	A	C				SILENT- NONCODING	transferrase	Human Gene Similar to SWISSPROT- ID:P41819 DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S- ADENOSYLMETHIONINE-6-N', N'- ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 318 aa.	3.00E-52	5

3283	cg43936623	112	CATCAACAGAGT TGGGTTTAGGGT T[C/gap]CCCAGG AGAGCAAGGGA GATGGATG	C	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3284	cg43936623	292	TTAAACAGTCAC CACCTGGTACAG T[G/T]TTACAAAA TGGGAGAGTG ACCACA	G	T				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3285	cg43936623	977	ACTGTGGGAGG CAGGGTTGTGTG TG[C/gap]ATCCG CTGAAATTACCC TTGGCTTA	C	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3286	cg43919796	4264	CACTGTATTG GCGCATGTTGGT G[G/gap]CCCTCT GTGCCCTAGATA TATGCAC	G	gap				SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) (MIP) - HOMO SAPIENS (HUMAN), 890 aa. pcls:SWISSPROT-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	5
3287	cg43998978	5306	TCCTTGGGGCTG CAGTTTGTGGT T[gap/A]GAGGGG CCTGGAGAAAT CATTTC	gap	A				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3288	cg43998978	5412	CCAGGCACTCAA AAGCTGGGAACC A[G/C]GATCTCAG CGCCAGGTCTAC CAGTT	G	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16

3289	cg43998978	5413	CAGGCACTCAAA AGCTGGGAACCA G[G/C]ATCTCAG CGCCAGGCTCTAC CAGTTC	G	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3290	cg43998978	5426	GCTGGGAACCA GGATCTCAGCGC CA[G/C]GTCTACC AGTTCTCGTTT GGGCCA	G	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3291	cg43998978	5427	CTGGGAACCA GATCTCAGCGCC AG[G/C]TCTACCA GTTCTCGTTTTG GGCCAG	G	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3292	cg43998978	5794	AGTCCTAGCAGA AAATGTGTTAG G[G/gap]GCCTGG CCCAAAGCAGTG TGGTTG	G	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3293	cg43998978	5795	GTCTAGCAGAA AAATGTGTTAGG G[G/gap]CCTGGC CCAAAGCAGTGT TGGTTGC	G	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3294	cg43998978	5953	CTCCCAAGTATT ACCAGTGGGTAC C[A/gap]AAAAAA ATGTCCCTTTGA GTCCTT	A	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3295	cg43998978	5960	GTATTACCAAGTG GGTACCACAAAA A[A/gap]TGTCCTC CTTGAGTCTTTT CCTTGTT	A	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16

3296	cg43998978	6126	TTGAATATCAAT GATTTTTTTTTTTT[T/gap]TAAGTACT GTTCCGGGGGAG AAAAAC	T	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3297	cg43998978	6127	TGAATATCAATG ATTTTTTTTTTTT[T/gap]AAGTACTG TTCCGGGGGAGAA AAACA	T	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3298	cg43998978	6306	AGCAGCATCTTT TAAAGCCTGTTC T[T/C]TAAGGTGT CTCGTTAGAGCC CAAAG	T	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3299	cg42684254	2485	CCATATATTTTCT GAGTAGCATATA[T/G]AATTTTATTG CTGGAATCTACT AGA	T	G				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P31645 SODIUM-DEPENDENT SEROTONIN TRANSPORTER (5HT TRANSPORTER) (5HTT) - HOMO SAPIENS (HUMAN), 630 aa.	0	17 (17q11.1)
3300	cg40351913	3767	TTCTGGGGAGG GACACAGAGGA CAG[T/C]TTCCCC ATCGCCTTCTGG TTGTTGA	T	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
3301	cg40351913	3786	GGACAGTTTCCC CATCGCCTTCTG G[T/C]TGTGAAG ACAGCACAGAGA GCGGC	T	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
3302	cg40351913	3789	CAGTTTCCCAT CGCCTTCTGGTT G[T/C]TGAAGACA GCACAGAGAGC GGCTTC	T	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)

3303	cg43935986	2512	GCCAGATAGCTG TTCCTGAGTTGC A/A/GIGCACGAT GGAGATTTGGAC ACTGTG	A	G				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3304	cg43935986	2553	GGACACTGTGTG CTTTGGTGGG T[G/A]GAGAGGT GGGTGGGGTG GGGTGTG	G	A				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3305	cg43935986	2697	TATTTTAAATAT TTTCCTTCTTAC G/A/TGAACTGTA TACATTCATATA GAAA	G	A				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3306	cg43934544	221	GGCCACAGGC CCCTGCTCCGG CCG[C/T]CGCTT GCAGACCCGGG GCGCCGATG	C	T				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P48029 SODIUM- AND CHLORIDE- DEPENDENT CREATINE TRANSPORTER 1 (CT1) - HOMO SAPIENS (HUMAN), 635 aa.	0	X
3307	cg43935086	2211	TACTTTTAAATGA CTCTGGAATCTG gap/C/JGTAGGCT CGAGCGGTTCC CAAGGCG	gap	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0	X
3308	cg43935086	29	TTTTTTTTTTTT TTTTTTTTTTTTG T]GGAATGTATG ATTTTTTTAATAA AA	G	T				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0.00E+00	X
3309	cg43935086	30	TTTTTTTTTTTT TTTTTTTTTTTTG G/T]GAATGTATG ATTTTTTTAATAA AAC	G	T				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0.00E+00	X

3310	cg43934534	1405	GTCCCCGCAGG CCCACCACCCTC AC[G/C]CAGCCC CAGCCCTCCAGC CTCTGTC	G	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P48029 SODIUM- AND CHLORIDE- DEPENDENT CREATINE TRANSPORTER 1 (CT1) - HOMO SAPIENS (HUMAN), 635 aa.	7.50E-294	
3311	cg43964039	1018	CTCTTCTCATGG TAATAGTGTGGC C[C/A]TCAGTGCA AAGGAGACTAGA ACCCG	C	A				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3312	cg43964039	494	ATTACTTCACAT TCAAAATAATGCI gap/GJATTTCAAG CCTGAGCATCAC GGCTG	gap	G				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3313	cg43964039	778	CCCTCAATCCAC AAGCATTTCAAA A[T/C]CTTTTTTC TAAAACCAGCC ATTGA	T	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3314	cg43964039	864	TATTTACAAGTT GGCTTGTCAGAG T[A/T]TACTATAA CTTAGTGCTGT ATTGA	A	T				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3315	cg43992017	206	CCTGAGCTTCCT GCTTAGGGGCC GG[C/gap]CCCCA CCCACAGGGTCT CCCTGGAC	C	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q14728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN MRNA - HOMO SAPIENS (HUMAN), 455 aa.	4.40E-241	
3316	cg44026704	172	CCTTCTGCTGGC CAGTCTGGGCAC CT[A/GCAGGGCC CCTGAGGGAGG GAGCTGT	T	A				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q99808 EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 456 aa.	1.50E-240	6

3317	cg43920728	85	CCATTTTCCACT AACAAAATAATTT [A/gap]GGATGAA GAATTCTGACTC AGTGTC	A	gap				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa.	2.90E-237	1 (1p31)
3318	cg43317499	220	CTGCCTCAGCCA CCTGAGTAGCTG G[C/G]AAGACAG AGCATAACCTTC GGTGGC	C	G				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q90406 TRANSMEMBRANE TRANSPORTER - DISCOPYGE OMMATA (ELECTRIC RAY), 724 aa.	1.20E-231	15
3319	cg39377146	4180	TGTCAAGTCCGT TCCGAAGGCATT T[G/T]CCACTAGT TTTTGGACTATG TAAAC	G	T				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	1.60E-225	
3320	cg44003311	766	TCACGTCCGAGC TGCCAGGCAGT C[C/T]TTCTGCGC CCTCTGCTGGCC AGATG	C	T				SILENT- NONCODI NG	transport	Human Gene TREMBLNEW- ID:G2921449 ORGANIC CATION TRANSPORTER-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 424 aa.	1.50E-217	
3321	cg44011204	229	CACACACACACA CACACACACACA C[A/gap]CACACG TGCACACACACA TCCCCC	A	gap				SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. pcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	

3322	cg44011204	234	CACACACACACA CACACACACACA C[<i>gap</i> /A]GTGCAC ACACACATCCCC CCACAAC	gap	A			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pc s:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. pc s:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3323	cg44011204	234	CACACACACACA CACACACACACA C[<i>gap</i> /A]GTGCAC ACACACATCCCC CCACAAC	gap	A			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pc s:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. pc s:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3324	cg44011204	59	ATAGTTGACACT CAATTTTATTGCT [A/ <i>gap</i>]AAAAAAA TGCTCTCTGGAG TGACA	A gap	gap			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pc s:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. pc s:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	

3325	cg44011204	531	ATCTCCTGTCCT GGAGGGTGCTG GG[G/gap]CCCCT GGCTCCCCAGA GTGTGCAGG	G	gap				SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. pcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3326	cg44011204	67	CACTCAATTTTAT TGCTAAAAAA A/gap]TGTCCTCT GGAGTGACAGC AGGTAT	A	gap				SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3327	cg43988801	1574	CAAAAGTTTGGC CACTTCCCTCTC A[A/G]AGACTAAC CCAGAAGGGAAT AAGAT	A	G				SILENT- NONCODI NG	transport	Human Gene TREMBLNEW- ID:E1283177 ABC TRANSPORTER - RATTUS NORVEGICUS (RAT), 565 aa.	9.80E-195	
3328	cg44025532	1782	CCTGCTGGCCA GGCAAGGGCC AGA[C/gap]CCCC CCCCAACCCCCA GCTGCCATC	C	gap				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.80E-174	
3329	cg44025532	1790	CCAGGCAAGGG GCCAGACCCCC CCC[C/gap]AACC CCCAGCTGCCAT CGCTCTCCC	C	gap				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.80E-174	

3330	cg43924839	176	TGAAGAAATGTG TATCATCTAACA G[C/A]AAAGAAAT ATGAACCAGATA ATGAA	C	A				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
3331	cg43924839	526	CCTTGTTACTTG AGTATTGTAGCC T[C/T]ACCATGAT TTTTTTTAAACACC GTAT	C	T				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
3332	cg42328251	238	ACACACACACAC ACACACACACAC A[gap/C]GACAAA ACCACAGGGCTA AGACACA	gap	C				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P97511 ZINC TRANSPORTER - MUS MUSCULUS (MOUSE), 341 aa.	6.40E-146	2
3333	cg43928832	363	TTTTTTTTTTTT TTTTTTTTTTTT[A T]AGTATTAAAG AGATTTATTAAAT C	A	T				SILENT- NONCODI NG	transport	Human Gene Homologous to SWISSPROT-ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa.	2.00E-126	2
3334	cg44930322	977	CTTTTGTTTATTA GCACCAATTTCTI C[T]GCCACTAAG CTATTTGTTTAT TAT	C	T				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	4.80E-113	
3335	cg43924433	226	TCAATACCTTCA TTACATTTATAAA T/A]ACAAGATT ACACAGCACCCC ATCA	T	A				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3336	cg43924433	251	TACAAGATTTAC ACAGCACCCCAT C[A/gap]AAAAA AAAATTAAACCC CTTTACA	A	gap				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9

3337	cg43924433	261	ACACAGCACCCC ATCAAAAAAAA A[gap]TTAAAC CCTTTACAAATAT CTACA	A	gap				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3338	cg43924433	261	CACAGCACCCCA TCAAAAAAAA A[gap]TTAAAC CCTTTACAAATAT CTACA	gap	A				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3339	cg43924433	261	CACAGCACCCCA TCAAAAAAAA A[gap]TTAAAC CCTTTACAAATAT CTACA	gap	A				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3340	cg43924433	334	TTCAAAGGGTG CTCTGTTAAAG T[G/C]GGCCCTA GTTAATGGTCCA TTTACT	G	C				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3341	cg43924433	339	AGGGGTGCTCT GTTAAAGGTGG CC[C/ gap]TAGTT AATGGTCCATT ACIGGTGC	C	gap				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3342	cg43924433	569	TGCATACTCAGA GCAGTTAAGGCA G[G/T]AGTGTGAT GGATGAGAAAA CTTIG	G	T				SILENT- NONCODI NG	transport	Human Gene Homologous to SPREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3343	cg43961977	149	AACATTCACCA AAATCATGACT A[T/C]GCATCTAA CAGCTTCAAAAT ATAGA	T	C				SILENT- NONCODI NG	transport	Human Gene Similar to SPREMBL- ID:Q07837 NA+-INDEPENDENT NEUTRAL AND BASIC AMINO ACID TRANSPORT PROTEIN - HOMO SAPIENS (HUMAN), 685 aa.	5.90E-75	2

3344	cg2986272	1143	ACCTCAGCGAG GGCAACGCGAG CTGT[G]CCGGA GCCCCCGCCC CGGAGCCCG	T	G				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:O08726 GALANIN RECEPTOR TYPE 2 (GAL2-R) (GALR2) - RATTUS NORVEGICUS (RAT), 372 aa.	3.60E-62	
3345	cg43319894	250	TGCTTCAGAGAT CCCTGCTGGCTC C[A/T]CGAGCAC CCTGGCCCGCA AAGAAGC	A	T				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3346	cg43319894	273	CCACGAGCACC CTGGCCCGCAAA GA[A/G]GCTGGG GGACGTCGGA GCGAGTCG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3347	cg43319894	297	AAGCTGGGGA CGTCGGAAGCG AGT[C/A]GAATTT GTGACATTTGCA CCAGCAC	C	A				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3348	cg43319894	315	AGCGAGTCGAAT TTGTGACATTTG C[A/G]CCAGCAC CCCCAGCCCGAG GAGCCTG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3349	cg43319894	366	AGGAGCCTGTAG GGCCCCCGGCT GT[A/G]CAGTCCA TCCTGGTAGCAG GTGAGG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3350	cg43319894	378	GGCCCCCGGCT GTACAGTCCATC CT[G/T]GTAGCAG GTGAGGAGGAC ATCCGCT	G	T				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11

3351	cg43319894	381	CCCCGGCTGTACA AGTCCATCCTGG T[A/G]GCAGGTG AGGAGGACATCC GCTGGG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3352	cg43319894	387	CTGTACAGTCCA TCCTGGTAGCAG G[T/C]GAGGAGG ACATCCGCTGGG TGTGGG	T	C				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3353	cg43319894	411	GTGAGGAGGAC ATCCGCTGGTG TG[C/T]GAGGAC ATGGGGCTGAA GGACCCAG	C	T				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3354	cg43319894	834	TGAAACGGCTGT GGGAGGCTGGG CC[C/gap]TGGA CGCCCTCTCATA GCGTCCAG	C	gap				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3355	cg43941204	1662	CACATTTCATTT CTGCGCCTTTTC TTC/GITCACCCG GGTGGCGCTGG AAGTTAT	C	G				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P09836 REGULATORY PROTEIN UHPG - ESCHERICHIA COLI, 439 aa.	8.40E-57	11
3356	cg43941204	1866	CCCTGTCCTGCC CGCATCCTACCC C[A/gap]TCCCCA CCTGAAAGTGAGG CTATCCC	A	gap				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P09836 REGULATORY PROTEIN UHPG - ESCHERICHIA COLI, 439 aa.	8.40E-57	11
3357	cg43941204	1955	GGTCCTAAGTCC TCTCAGCAGTGG G[T/C]GACTGCT GTTGCCAATACC TCAGAC	T	C				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P09836 REGULATORY PROTEIN UHPG - ESCHERICHIA COLI, 439 aa.	8.40E-57	11

3358	cg43990999	1607	TATTGAATCTGG GTTCTTTTITGAC [gap/TTTTTTTTT TTCCCAATCCAA CAGCA	gap	T				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P32802 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 667 aa.	7.50E-55	10
3359	cg43269525	1024	TCGTCTCTGGAAC TTCTGACAATCT G[G/C]CATGACA ATGAGGGGTGGG CATGATT	G	C				SILENT- NONCODI NG	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN--PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.50E-163	15
3360	cg43291895	1030	GTTGTTTCGTTT GGCTTTTCTCC[C/TTCCCCATGT CTGTTCTGGGT TTCA	C	T				SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3361	cg43291895	1075	TTTTCACGTGCT TCAGAGAAGAGG G[G/gap]CTGCC CACCGCCACTCA CGTCACT	G	gap				SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	

3362	cg43291895	1182	AGGGAGCTGA GCCCAGCTTCTA CC[G/gap]GGGTC CCCCAGCTTCCG GACTGGCC	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3363	cg43291895	1185	GGAGCTGAGCC CGACTTCTACCG GG[G/gap]TCCCC CAGCTTCCGGAC TGGCCGCA	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3364	cg43291895	1230	GCCGCACCCCG GAGGAGCCACG GGG[G/gap]CGCT GCTGGGAACGT GGCGGGGGG	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3365	cg43291895	1262	TGGGAACGTGG GCGGGGGCCCG TTT[C/T]CTGACA CTACCAGCCTGG GAGGCC	C	T			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	

3366	cg43291895	1304	GGGAGGCCAG GTGTAGCGGTCC GA[G/gap]GGGCC CGGTCCTGCCTG TCAGCTCC	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3367	cg43291895	1354	CAGGTCCTGGA GCCACGTCCAG CAC[A/T]GAGTG GACGGATTACCC GTGGCCGA	A	T			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3368	cg44003015	265	TTTTTTTTTTT TTTTTTTTTTTIG TTCCTTCAGGAG CATGTTTATTGT GTT	G	T			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P52483 UBIQUITIN- CONJUGATING ENZYME E2-23 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - MUS MUSCULUS (MOUSE), 207 aa.	1.10E-109	
3369	cg44003015	318	AGATGATACATC AGGTGCTCTCTG A[G/gap]CTACAA AGGGTAAAAGGA AATCCTC	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P52483 UBIQUITIN- CONJUGATING ENZYME E2-23 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - MUS MUSCULUS (MOUSE), 207 aa.	1.10E-109	
3370	cg44005525	725	CAGCTCTCTTCT GTGACAGACAAA T[C/A]ATGTAAGA ACTGTGAAACCC CAGTT	C	A			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	

3371	cg44005525	735	CTGTGACAGACA AATCATGTAAGA A[CTTTGTGAAAC CCCAGTTTATGT AGCGT	C	T				SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH8 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
3372	cg44923887	1328	GGGCTGGGCTG GCTGCTCTGGAG GA[G/A]GGGTC AGCAGGGGCC AGGCGACC	G	A				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3373	cg44923887	2326	AAGCGAACGCCA GGCGGTGGCAC GT[G/A]TCAATT CCACAGAGTCCT GCTTTG	G	A				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3374	cg44923887	2367	TCCTGCTTTGCG GGGTGTCTGAAT G[C/T]ACTGCAC GGGTCTCTGCT CACACT	C	T				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22

3375	cg44923887	2413	ACACTTGCTGGA ACCAATCGTGGC A[G/C]ATTTTAGT CCACAGGTCGCT TTTCC	G	C				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3376	cg44923887	836	TGAACAATGTTA GGCTGCCGAAC CT[G/A]CCCCATCA CTCCCCACTTCT GCACAG	G	A				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3377	cg43916797	310	AAGGCCAAAGGT TGAAGGGGTAG GG[AT]GATGTAA AAGAGTTGGGAA CAAAGC	A	T				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:P51669 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 147 aa. cds:SWISSPROT-ID:P51669 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 147 aa	5.20E-80	5

3378	cg43939935	1049	CAGTAAATAAA CTGTACAAAGGC ATTATTAGAAT AACAAAAAATATT TTAC	T	A				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.lpcsl:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12
3379	cg43939935	1050	AGTAAATAAAC TGACAAAGGCA TTTATTAGAATA ACAAAAAATATTT TACT	T	A				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.lpcsl:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12
3380	cg43939935	236	CAAGAGACAAGG TTGCAACCCGAA G[G/gap]TTAACA TTTATGTATTAT GACTGG	G	gap				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.lpcsl:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12

3381	cg43094404	4004	TCCACAACCTAAT ATAGACAACCTT A[C/T]GCGTGCG TAAGAGTTTAC ATGGCA	C	T				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SPTRMBL- ID:O08759 E6-AP UBIQUITIN PROTEIN LIGASE - MUS MUSCULUS (MOUSE), 885 aa.	3.20E-73	4
3382	cg43974851	1140	GCGGGCTCCTCTC TCTCATCCATGT C[C/gap]TTTCAG GTCTCAGCGTTT GCTCGCT	C	gap				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1
3383	cg43974851	162	CAGAACACTTTA TGGTTTCAAATC C[T/gap]TTTTTTT TTTTTACCCCAA AGGAAA	T	gap				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1
3384	cg43974851	174	TGGTTTCAAATC CTTTTTTTTTTTT T/gap]ACCCCAAA GGAAATTTGAGA ATTCA	T	gap				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1

3385	cg43947722	336	TACAATTAAAATA AAATAAGCATTTT T/GTTATGATTTT ACAAATATTGTTT AT	T	G			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN- LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa. pcis:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	
3386	cg43947722	769	GAGTGAAGTAAT ACATGCTAGAA C/ATTTCAGGGC CAATTGGAAAGT CATTAT	A	T			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN- LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa. pcis:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	

3387	cg43947722	780	TCACATGCTAGA ACATCAGGGCCA A[T/C]TGGAAAGT CATTATGAACAC TTGCA	T	C				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN- LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa.[pcis:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	
3388	cg43948669	1717	GGAAGCAGCG CCGAGCGGGC GAG[T/gap]TCAC GCTTCGGCCCC GCCGCTCTCC	T	gap				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P55854 UBIQUITIN-LIKE PROTEIN SMT3A - HOMO SAPIENS (HUMAN), .103 aa.	5.10E-50	21
3389	cg43948669	1718	GGAAGCAGCG CCGAGCGGGC AGT[T/gap]CAGG CTTCGGCCCCG CCGCTCTCCC	T	gap				SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P55854 UBIQUITIN-LIKE PROTEIN SMT3A - HOMO SAPIENS (HUMAN), 103 aa.	5.10E-50	21
3390	cg42940644	112	CTTCTTGAAGGT GCAGGCCTTGG AC[C/G]TGCCCA GACTCACAGTCC TGGCTGC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SP TREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1

3391	cg42940844	323	GTGACCCCTCAGA AATCACAAGGGA G[C/T]GGAGAGA GCTGTGTTCAAC ATGAAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1
3392	cg42940844	327	CCCTCAGAAATC ACAAGGGAGCG GA[G/A]AGAGCT GTGTTCAACATG AAACGCT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1
3393	cg43297012	2231	CTACGTTAACTT TGCCCTAGTAGAG G[gap/C]CCTTCT TTGCACCTTGCTT CTCATT	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P48382 DNA BINDING PROTEIN RFX5 - Homo sapiens (Human), 616 aa.	0.00E+00	1
3394	cg43917756	277	TTCCCCAAGCCA CGCAGGCCATG GC[C/gap]TCAGC TCAGCAGGCTCT CCTCAGTG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa.	0.00E+00	1
3395	cg43920218	5887	AGTCCTTAAAC AGCAGGAAAGGT G[G/A]GCCTGTC CCCCCTTTGTGC AGCTAC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3396	cg43920218	5758	CTGGGCCTCATT CCTCCAAGTCCA C[G/T]GGAGGGT CCAGAAGAGGG AGTCAGA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3397	cg43920218	6123	GACACTGCTGGC GGGGGCTCAGT GA[G/gap]CACTA CTCACAGATCCA CACCTGAC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1

3398	cg43920218	6174	CCTGTTGGGTGCG AGTCAGGCTGG GC[C/gap]TTGGT CTGCACTGTAGC ACCTGTGT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3399	cg43920218	6229	TGAGTTCACATC ATGAATGTGGTG A[C/T]TCCCGAGA TACCATCTCAGG CTTAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3400	cg43920218	6523	GTATAATATAT GATATAGATTTAT [A/T]TATGTTGTA ACGCCATATATT GAAG	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3401	cg43920218	6539	TAGATTATATAT GTTGTAACGCCA [T/C]ATATTGAAG GCCAACATAACT GGTG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3402	cg43920218	6592	CAGGGTGGGTG ACAGAAATGAA AG[C/T]CTTTTG GTGATTGTTAA GCAAGA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3403	cg43920218	6609	AATGAAAGCCTT TTTGGTGATTGT T[A/T]AAGCAAGA TGTGTATAAAGA AATAA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3404	cg43920218	6616	GCCTTTTGGTG ATTGTTAAAGCA A[G/A]ATGTGTAT AAAGAAATAAAT AGTTT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1

3405	cg43921252	154	CTCCTCCACGGT GGGTGCCAGCA GG[C/gap]TCTCC CCTTCCAGTGA CCTCCCTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3406	cg43921252	607	ATGTCACAGGGT CCCCGGGGTGG GG[G/gap]CAGCA GCCAGGGCAGA AAAGCAGAA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3407	cg43921266	915	TTATTTTCTTTG GCTTCAAGCCCC [C/gap]TCCCATG ACGTGCAGGGC AGGGGGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3408	cg43921266	924	TTTGCTTCAAG CCCCCTCCCATG A[C/G]GTGCAGG GCAGGGGGTGG GCATGAG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3409	cg43921266	102	GAAATGGGGAG GCAAGGGCTCTT TA[gap/A]GCGTT TGCCAAAACCAC TGCCACAC	gap A	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3410	cg43921266	984	ACGCAGGAAGC CTCCACCCCCAC CC[C/gap]TGCCT GGCAGGTCCCA GATTACATG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3411	cg43921266	118	GGCTCTTAGCG TTTGCCAAAACC A[gap/A]CTGCCA CACCCCTCCACC CCCTCTT	gap A	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

3412	cg43921266	168	TGCCTTCCTCCT CCACGGTGGGT GC[C/gap]AGCAG GCTCTCCCTTT CCAGTGAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3413	cg43921266	482	TAGTGAATCAC AGCAGGCCAAG CC[C/gap]AGGGG CCCGGCTCAAG CTGTCCTCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3414	cg43921266	628	ATGTCACAGGGT CCCCGGGTGG GG[G/gap]CAGCA GCCAGGGCAGA AAAGCAGAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3415	cg43921266	654	CAGCAGCCAGG GCAGAAAGCAG AA[G/gap]CTAGC CTCTATAAAGC ACCCCTTT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3416	cg43921266	805	GAGATAGATGCT TTTTTTTTTTTT gap/T]GCTTGTGT TTTTCTTCAGTA TAA	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3417	cg43921266	866	AAATAACTTCTCT TAGAAAAAAA gap/A]TACAGAA AAAAAACCAAA GGTT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3418	cg43921266	911	AGGGTTATTTT CTTTGGCTTCAA G[C/gap]CCCCTC CCATGACGTGCA GGGCAGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

3419	cg43921289	2069	CCACGTGAGTG GTAGCCGCCGC TGA[G/gap]GCCG AGCCTGCACTGG GGCCACCCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3420	cg43921289	2070	CACGTGAGTGGT AGCCGCCGCTG AG[G/gap]CCGAG CCTGCACTGGG GCCACCCAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3421	cg43921289	2087	CCGCTGAGGCC GAGCCTGCACTG GG[G/gap]CCACC CAGCCAGGCCT GGGGGCAGC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3422	cg43921289	2093	AGGCCGAGCCT GCACTGGGGCC ACC[C/gap]AGCC AGCCTGGGGG CAGCCTCTCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3423	cg43929067	21	CCCCTTTTTTTT TTTTTTTT[A/TGA CTTCTCTACATC AGTTTATT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3424	cg43929067	209	ACAAAAGGGACC TGGAATCTGTAA G[G/C]TGATTCCA AAACGAAATAA GTAGA	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3425	cg43929067	22	CCCCTTTTTTTT TTTTTTTT[T/A/JGA CTTCTCTACATC AGTTTATT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1

3426	cg43929067	23	CCCCTTTTTTTT TTTTTTTTTG/TJA CTTTCCTACATC AGTTTATTAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3427	cg43929067	24	CCCCTTTTTTTT TTTTTTTTTG[AT] CTTTCCTACATC AGTTTATTAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3428	cg43929067	25	CCCCTTTTTTTT TTTTTTTTGAC/ TJTTCCCTACATC AGTTTATTAA A	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3429	cg43929067	54	CCTACATCAGTT TTATTAAACAC [A/T]AACAAAGTAT TTCTCTTTCTGTA AGG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3430	cg43929790	189	AAGTACAGCAGC CAACATCTGGTC T[C/gap]AGAGCT GCTGGGAAAG GGCAGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12839 (H326) - HOMO SAPIENS (HUMAN), 597 aa.	0	1
3431	cg43932517	138	CTTTCCTACTGG CGCCGGCTCCT GC[C/gap]AGAGG TCGGGTGACA GCAGGATCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14746 LDLC PROTEIN - Homo sapiens (Human), 738 aa.	0	1
3432	cg43932517	80	GGTTGTTGTTT TTTTTTTTTTT T/AJGGGAGACA CTTCTTTTATTA GGA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14746 LDLC PROTEIN - Homo sapiens (Human), 738 aa.	0	1

3433	cg43935021	1881	TCCTCTGACTTT TACGGAGGGCTT G[C/gap]CAAAGT AGCCTATTGCAG CCAAAGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43308 KIAA0425 - HOMO SAPIENS (HUMAN), 1224 aa.	0	1
3434	cg43935021	1882	CCTCTGACTTTT ACGGAGGGCTT GC[C/gap]AAAGT AGCCTATTGCAG CCAAAGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43308 KIAA0425 - HOMO SAPIENS (HUMAN), 1224 aa.	0	1
3435	cg43944866	124	GCCCCAGCAG GAGCACCACCAC GG[C/T]TAGCAA AGAATCCGAGAC CCCGCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0	1
3436	cg43947011	127	TAGCTCTTTT TTTTTTTTTTTG TTTGGGATAATC TATTTTAATGAAA CT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3437	cg43947011	265	CTGTGGGCTGG AGGTGGGATAGC CA[C/gap]CCGCA GCACGCCACC CTAATGTGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3438	cg43947011	267	GTGGGCTGGAG GTGGGATACCA CC[C/gap]GCAGC ACGCCACCCCTA ATGTGCCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1

3439	cg43947011	330	GAGAAAGGACA GTGGGAAGGAG ACA[G/gap]TAGG CTCAGCCCAGAG ATGCCCTG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3440	cg43948542	4725	ATTAGTATCTTCT CAGATACAGACC [A/G]TTTATGAT TTTTTAAAGTA AAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
3441	cg43948542	4772	AAAAGTTCTAAA ATGAAGTCACAC A[A/G]GACAAATTA TTCTTATGCCTA AGTTA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
3442	cg43950151	991	CACACAGTCAAC ACCTTGGTGACA G[G/gap]CATCTG CCCCCACTTCAA CCAGTAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
3443	cg43950151	2156	ACACGTGCCCTC GGGGAGCCCA CA[C/T]GGCACTT AGGGCTGGCAG CACCGCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1

3444	cg43950151	273	CGTTTTTTTTTT TTTTTTTATGGI ATTTTCCCAACTA GGTTTTATTTAG TT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
3445	cg43961075	114	CCTTGAAAACCT CTCATCCCTGA A[G/gap]GGTGGG GTGACCACCGCT CTGGGAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49746 THROMBOSPONDIN 3 PRECURSOR - Homo sapiens (Human), 956 aa.	0	1
3446	cg43969426	4957	TATTTTCATCCAAA TCAAGCTAAAT GTTTATTTAAGTT GATTCGAGAGT ACA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0	1
3447	cg43970200	270	AGTAGCTTTTCA GCATTCAGTTT GTA/TGGCTCATG GGAAATGTTACT TAGCA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0	1
3448	cg43970200	319	CATCAAGATGTG GTTTGATGAGTG A/A/GJCAATGTCA GTATCAACTGTA CTTAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0	1
3449	cg43994728	1881	CAGGAATTTAA ACCAAGGATAAG A/G/TATGCCCTT GTCAAAATCTTGG TTCCA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75041 KIAA0453 PROTEIN - HOMO SAPIENS (HUMAN), 1052 aa (fragment).	0	1
3450	cg43994728	2157	AACAGTTCAATG GGACTTTTTTT [gap/T]CCTTCTCA ATCAACAGAGTT TACCA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75041 KIAA0453 PROTEIN - HOMO SAPIENS (HUMAN), 1052 aa (fragment).	0	1

3451	cg44020180	1972	TTGTAGCAGAGA CACAGTGGCCTA G[C/gap]CAATCG GCAGTGCTATAC ACACAGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0	1
3452	cg43925699	2081	TTGTTATAAGGC GCTGGGAGAGG AT[G/gap]GGCAG CTCCCACTGCC CAGAGCGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
3453	cg43925699	2083	GTTATAAGGCGC TGGGAGAGGAT GG[G/gap]CAGCT CCCACTGCCCA GAGCGGAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
3454	cg43926985	4868	CAGCATGTCCCA GTCAGTGCAGCA A[C/T]GCCCTTGTG TTTGTTTCATTTT TTTA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
3455	cg43926985	5521	GTATAAATTAGA AAATGAAAAATG T[G/A]TGAATAAC ATTGTATGAAAT AAACC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
3456	cg43961763	115	TTTTGGTCCAG TACTCCACAAA C[A/G]CTACAGAC AGTAACAAAATA ATTCA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETOGNIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa.	0	2
3457	cg44033553	635	TCATGCCTGAGA CCAGAATGGAAT A[G/A]AACAAATCC ATTGAATACAG CGATG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42331 HYPOTHETICAL PROTEIN KIAA0053 - Homo sapiens (Human), 638 aa.	0	2

3458	cg44911887	144	CCGAGGCCTCCT TGCTTCCCGCTC T[G/C]CGAGGAG CCTTTCATCCGA AGCGCG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3459	cg44911887	165	CTCTGCGAGGA GCCTTTCATCCG AA[G/gap]GCGGG ACGATGCCGGAT AATCGGCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3460	cg44911887	96	GAGCTTGGCCG GTTTCGAGTCGC TG[A/G]CCTGCA GCTTCCCTGTGG TTTCCCG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3461	cg44927137	3131	ATTTGGTGTGC TACAAAAGCCTT T[A/G]CAAAATTAT CAGTAGTAGTTT TTTTT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
3462	cg44927137	3449	TTTGTCTATAAT GGAGCTGTTTAT G[A/G]CAATTTAA TACCATTCTCTTT GTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
3463	cg43301812	1497	ATGGACAATGAG TGCTCCTCTGCA C[C/T]CCCCCATA TCAATGGCAGTG GAACC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0	3
3464	cg43308354	1161	CACCTAGTCCTC TGCTACCAACTC A[T/C]GTCATGAT GGGGATGAGCC AGACAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3

3465	cg43308354	1382	CAATGGTGTGT TAGACTCCCTA TTT/gap]TTTTAAA ATGCTAATTAC ATTCTT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3466	cg43308354	300	GACAGAACAATC AAAGACCAACGT G[C/gap]ACCTTG CTTCCATACCA GGCTGAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3467	cg43308354	436	CTGTGGGAGA GGTAGGCAAT GGC[C/gap]TCCT GCAACGGGCC CAGATCCGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3468	cg43308354	90	ATAATACAGCA GATATTGTTGGG G[G/TTTCTTT TTCTGTCAAGT AAGAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3469	cg43918935	3056	CTGTGTTTATCA TGTTATATCGT C[C/TAAGAAAGTA TTAAGGCTTTAG GTAGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
3470	cg43925942	4379	AAATACCTCCGA AACCAGGAATTC A[G/A]TGTATGTT TGTTTATACTGT TTGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3471	cg43925942	5380	GCTATAGTTGCG GGTGAACAGTC A[A/G]CCTTTCTA GTAGTTTATGAT ATTGC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3

3472	cg43925942	5427	TTGCCCTCTTTG TATCCCATTTTC TTCJACAGTTTTT TCCGCAGACTTC TTTC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3473	cg43925942	5713	ATGGTTTTCTCT CAGTCTCTAAG C/TJGGTCTATG TTATAGCTCTAG CAGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3474	cg43925942	5909	ATTATTGCAACT ATATTTGCCTG A/TJGCTTGATCA AAGGTCATTTGT GTAG	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3475	cg43925942	5984	GTAATTAAAAAT ATTAAATCACA A/TJAAAAATTCTA TTATTGGAGAGC ATC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3476	cg43925942	5967	ATTAAAAAATAT TAAATCACAATA A/TJAATTCTATTA TTGGAGAGCATC TTT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3477	cg43936625	38	TTTTTTTTTTTT TTTTTTTTTTTTA /TJACTAAAGAA TAAAGATTTTAT T	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14688 KIAA0183 PROTEIN - HOMO SAPIENS (HUMAN), 1062 aa (fragment).	0	3
3478	cg43936697	3385	TAAATGTTTTTG GCCGGGCGTGG TG[gap]CTCAT GCCTGTAATCTC AGTACATT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0	3

3479	cg43940975	130	TCCTTTTCTTTT TTTTTTTCTA[G/T]GAGAAATTA GCTGTTCTTTATT GAC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
3480	cg43940975	131	CTTTTCTTTTCT TTTTTTTCTAG[G/T]AGAAATTTAG CTGTTCTTTATTG ACA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
3481	cg43957007	2507	AGTGATCCTTCT GCCTCAGCCTCC C/A/GJAGTAGCT GGGATTACAGGT GAGCAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92611 MYELOBLAST KIAA0212 - HOMO SAPIENS (HUMAN), 657 aa.	0	3
3482	cg43979396	6657	AAAAGGAGAGG GGTTAAGATGCA CC[G/A]AGGCTG TAGCTGGGCTAC TTGATCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31595 KIAA0620 PROTEIN - HOMO SAPIENS (HUMAN), 1985 aa (fragment).	0	3
3483	cg43979396	6750	AGCTTTTATATAT TAAAAAACGTAT[C/T]ATGCACCAA CTGTGAATAGCT GCCG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31595 KIAA0620 PROTEIN - HOMO SAPIENS (HUMAN), 1985 aa (fragment).	0	3
3484	cg44021891	466	TGGTAATACTGA GGGGCTGGACA GA[G/gap]GCTCT TCTGAGCCTCAA GCGCCAGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3
3485	cg44021891	479	GGGCTGGACAG AGGCTCTTCTGA GC[C/gap]TCAAG CGCCAGGGACA GAGACCTAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3

3486	cg43917191	1115	CTATATGGAGTA AAATAAGTTAAA A[C/T]TTTCTCTAA TGAGAAATAGCTG ACAGG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
3487	cg43917191	1120	TGGAGTAAATA AGTTAAACTTTT [C/T]TAATGAGAA TAGCTGACAGGC AGCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
3488	cg43918628	3240	GTGTGTGTGTAT ATATATATATATA [T/gap]AATACATT CTATCTTACCCT AATCA	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3489	cg43918628	3241	TGTGTGTGTATA TATATATATATAT [A/gap]ATACATTC TATCTTACCCTA ATCAT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3490	cg43918628	387	ACAAAATCTAAA AAGAAAACAAAG C[gap/A]AAAAAA AAAAAACCCCTT CATATTC	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3491	cg43926426	5172	TGTACATATCTG GGCCTTTGGAG GC[C/gap]ACGTG TGGCATGGGAG GGGCTACCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75338 RGS12 - HOMO SAPIENS (HUMAN), 1376 aa.	0	4
3492	cg43930981	1381	CAAGCCAGGTCT TCCCGTCTTCTT G[G/gap]TGTGGC CACACCCTGTCC GGCATAT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4

3493	cg43930961	26	TTTTTTTTTTTT TTATAGGCAAGG [C/T]TTTATGTTA TATTTATTTATTT TCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
3494	cg43930961	629	AAAATCCAAGAC CAGCAGTTCCTC A[C/A]ATTGAGT ACTACTCAGATT GGCAG	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
3495	cg43935402	14000	GACCACTCACGA TAAAGCAGATT TT[<i>gap</i>]CTCTGC CTCTGCCACAAG GTTTCAG	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
3496	cg43979400	1082	CACACTTTCATC TCTGTTGCTGAA A[G/ <i>gap</i>]CCTCTG AGCTTCAGCTAC TTAACTA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3497	cg43979400	2010	GCACATACTGCT CCTCCTGGCCTC TT[G/ <i>gap</i>]CCTGTG GCACAATGCCAT GAGAGCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3498	cg43979400	2080	CACAGACGCGA CTCACAAAGATGC GC[C/ <i>gap</i>]GGCTC CCCGGGCTCAC CAAGGAGAA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3499	cg43994452	163	ACTGGCAGGGA CCTCCCCCACAG CC[A/G]CCCCCA CAGGGTTCTCTG TTTCCCA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4

3500	cg43994452	242	ACACATTCACCC ACTACCTGCTGG A[G/C]AGGAGGG TCATGAGGCAGC CTGTGG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3501	cg43994452	50	TTTTTTTTTTT TTTTTTTTTTT[G /T]CAGGTTCCAC CAGAGGCTTTTA TTT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3502	cg43994452	572	TTCCAGACACCG GAACCTCCTAGT C[T/C]AGCCTGG CACACCCCATGTC ACTCAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3503	cg43994452	593	AGTCTAGCCTGG CACACCCCATGTC A[C/T]TCAGAAAG GTCAGGCTCAG GGTGGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3504	cg43994452	697	GCAGCCTTCCCT TTGTCGGGGTCC A[T/C]GCAATCTA CACATGGTCGCA AGGTC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3505	cg43994452	772	GGGCACAGACG GCACTGGTGCAT GC[C/gap]TGTCG GGCTGGGGCCA CACTGGGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3508	cg43260923	908	CACATAATTCCA ATTTTATTGAAT [G/A]TAGAGATT TATGAAAACAAA TCCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15023 KIA0305 - HOMO SAPIENS (HUMAN), 1539 aa.	0	5

3507	cg43916866	104	TGTGTGCCAGGA CAACCGCCGG AG[C/gap]CACCG CAGCTCCCGATA CCGATGTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3508	cg43916866	1412	CCTGTCGAGATC ACAGCAGGTCCA A[A/T]ATAAAGTG ACAACTAGATTT AATAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3509	cg43916866	1413	CTGTCGAGATCA CAGCAGGTCCAA A[A/T]TAAAGTGA CAACTAGATTTA ATAAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3510	cg43916866	176	AATTGCTTACCA CTTAGGGAAAA A[T/C]TGTGAAG TATAAACACAGCC AGAAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3511	cg43933355	236	CTGAGACTTAAT AAATGAGATAAA A[G/A]CAGTTTCT TACACCTAAGAA ACTGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
3512	cg43933355	42	TTTTTTTTTTTT TTTTTTTTTTTTT AJTTCGAACCAAG AGAACATTTTTTA T	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
3513	cg43933355	403	CCAGGGGATGC TGGGCTTGTTAG CA[C/T]TCAAGCT CTGGGACCTGAT TGGCCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5

3514	cg43934069	304	AGTAAAGATTTC TTTTGGTGATATA [C/gap]CAGAGTT AAGGCAGTAGA AGAATA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92585 MYELOBLAST KIAA0200 - HOMO SAPIENS (HUMAN), 1016 aa.	0	5
3515	cg43934068	582	GTCTGAGCACCC TTTTCTTCTGAGT [C/T]GTGGCTCCT GGAAGACGGGG CTGTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92585 MYELOBLAST KIAA0200 - HOMO SAPIENS (HUMAN), 1016 aa.	0	5
3516	cg43942958	1107	CAAGCAAGGGC AGATCTGAGAGC CT[C/G]TAATGCT AGGCAGGTGCA GCTGGTG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3517	cg43942958	1353	GGAGGAAAGG CAGGAGGAGAT GAG[G/gap]CCAG CCCCACTGATGA CACCTTGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3518	cg43942958	1378	GCCAGCCCCACT GATGACACCTTG G[G/gap]CCAGGC CTCACAGCTGCA GGCATCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3519	cg43942958	329	AGTGAGGGTATC CTTGTGGCTCCA G[C/gap]CCTGGG GCCCCCTGCGG TCACCTTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3520	cg43942958	331	TGAGGGTATCCT TGTTGGCTCCAGC C[C/gap]TGGGGC CCCCTGCGGTCA CCTTTGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5

3521	cg43951735	319	ATAAATCTTCTCT TAGGCTAAACAA C/gapJAAGACTCG GTCATAAATTCA GAGGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14776 PUTATIVE TRANSCRIPTION FACTOR CA150 - HOMO SAPIENS (HUMAN), 1098 aa.	0	5
3522	cg43951735	34	TTTTTTTTTTTT TTTTTTTTTTTTA TTTATAAAAAGG GTTGGTTTATTG TAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14776 PUTATIVE TRANSCRIPTION FACTOR CA150 - HOMO SAPIENS (HUMAN), 1098 aa.	0	5
3523	cg43981461	5659	ATTAAGAAGTT CATAGATTTCAC AIC/TGAATGTAA ATGTGTTATATG GAGAC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43314 KIAA0433 - HOMO SAPIENS (HUMAN), 1243 aa.	0	5
3524	cg43985488	443	CACGCCAGGCC CCAAGCAGGGT GAG[G/gap]CCTC CAACCCGGCCA GCTGAGCAGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16643 DREBRIN E - Homo sapiens (Human), 649 aa.	0	5
3525	cg43985488	711	GAATGCAGGCAC GGCGGCCCGTC TG[G/gap]CCAGA GGCTGATGCAG GTGGCGGGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16643 DREBRIN E - Homo sapiens (Human), 649 aa.	0	5
3526	cg44026925	5069	CAATGAATCAAG ACTTCTACCCAA AIG/AJCAACATTT TTTTAAACTATAT TTAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3527	cg44026925	5421	AATCAAATTCAA AGATTTAATTCCT [G/C]CTATGAATT CTAAAGTTCGGC AAAC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5

3528	cg44026925	5450	TGAATTCTAAAG TTCGGCAAACCA A[T/C]TCATCATA AAATCCAAATAA TCTTG	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3529	cg44026925	5504	CCTATTTATCTA GTGATTCATCTC C[A/G]ATTCTGTT GAAAAGGCATAA TATAA	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3530	cg44026925	5525	CTCCAAATTCTGT TGAAAAAGCATA A[T/C]ATAAATGT TGATGAGACTAG ACTCT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3531	cg44026925	5536	TTGAAAAAGCAT AATATAAATGTT G[A/G]TGAGACTA GACTCTAATGGA TATGT	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3532	cg44026925	5541	AAAGCATAAATAT AAATGTTGATGA G[A/T]CTAGACTC TAATGGATATGT TTATA	A	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3533	cg43308181	5595	ATCATTTCCTTT TTTTTTTTTTTTT[gap]CTGTTGTGG AAAAGCGTGAAT TTGT	T	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92514 MYELOBLAST KIAA0240 - HOMO SAPIENS (HUMAN), 983 aa (fragment).	0	6
3534	cg43308181	5912	AAAATGTTTGTGA AAAAAATAAATAA A[gap]CTATAACA AATTGCAGTTTA TTTTG	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92514 MYELOBLAST KIAA0240 - HOMO SAPIENS (HUMAN), 983 aa (fragment).	0	6

3535	cg43924112	351	AAAATCTGAGAC AAGACTAAACAA A[C/gap]AACAAA AAAATCTCTAAC ACAAAAT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
3536	cg43924112	5634	CGCCGCCCGCC CCGGCCCAAAA GTC[C/gap]GCCC GCGCTGTCCACA CAGTGGGCA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
3537	cg43925091	168	TTTTATAATCAA ACTCTTGGGTTT T/AJATTTCTGTAA AAGCTCCAGCTC TAC	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa.	0	6
3538	cg43929503	327	TTTGGTTTATAGT GAGAGATTATT T/AJGAAGAAATA TTACAACATATAA AAA	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
3539	cg43929503	430	TAATAAAAACTTA TTAAAATCCAGAI ATTGACACAAAG TACTGCACAATT TGAT	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
3540	cg43929503	5399	TGTCCTTTCCA AATCTTTGAGCC G[G/C]CTGCGGA CATCGTCGGGCA GCGAGA	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6

3541	cg43947531	101	CAAATTAACAA GTTTGTGAACA G[C/A]TTTCTTT CTAATAATGA CTATG	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14244 MICROTUBULE ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 749 aa.	0	6
3542	cg43998751	2414	GGCTACAGTACC ATGCCTCTCAGC C[C/gap]CGTGTG TATAATATGAAG ACCAAAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3543	cg43998751	346	GCGGGGTGGAG CGGCACGCGCC TTC[G/T]GCAGGA GGCTGAGTGTCC GTCTCGC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3544	cg43998751	352	TGGAGCGGCAC GCGCCTTCGGC AGG[A/C]GGCTG AGTGTCCTGCTC GCGCCCGG	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3545	cg43998667	395	AACTGTTTATAA CAACACAAAAT A/gap]AAAAAAA CAATGTTACTATT TAGG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6
3546	cg43998667	403	TATAACAACAC AAATAAAAAA A[A/gap]CAATGTT ACTATTACGGC AAACAG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6

3547	cg43944072	282	TTAGTGGCGGTAC ATGCAGCCCTCG G[C/gap]ACGGAG GGTCAGTCCCC GCIGTCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60719 CULLIN 1 - HOMO SAPIENS (HUMAN), 776 aa.	0	7
3548	cg44018111	266	ACTCCCAGGACG GGGGCCAGGCC CC[gap/C]TAAA AGGCACAATGGC AGGGCAGG	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O60568 PROCOLLAGEN-LYSINE,2- OXOGLUTARATE 5-DIOXYGENASE 3 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 3) (LH3) - Homo sapiens (Human), 738 aa.	0	7
3549	cg43316178	2924	GTCCACCACTCT ACCCACACAGGA GG[G/gap]CCGCC CGCCACCAAGC CTCACCTGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14163 KIAA0150 PROTEIN - HOMO SAPIENS (HUMAN), 944 aa (fragment).	0	8
3550	cg43274140	3669	GGTGGGAGAGG GGGAGTCTCAC GGG[G/gap]CCCC AGGCTTATTCAG AACTGGTGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75151 KIAA0662 PROTEIN - HOMO SAPIENS (HUMAN), 677 aa (fragment).	0	9
3551	cg43274140	3831	CATGTACATTTC TAACAAAGTTTAT [C/T]GTGGCTATT AAAGTGTTTATT TCC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75151 KIAA0662 PROTEIN - HOMO SAPIENS (HUMAN), 677 aa (fragment).	0	9
3552	cg43916922	172	TTACCCAGGCC ACTGTTCTATG C[G/A]CACTGGC TTTGAGGCATT CACATC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75181 KIAA0699 PROTEIN - HOMO SAPIENS (HUMAN), 847 aa (fragment).	0	9

3553	cg43947535	1017	GGCAGCACCCC TCCAGAGGCA GCC[A/G]GGGAG GCCTCTCCACCA GGCCTCTGC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21399 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRON REGULATORY PROTEIN 1) (IRP1) (FERRITIN REPRESSOR PROTEIN) (ACONITATE HYDRATASE) (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONITASE) - Homo sapiens (Human), 889 aa.	0	9
3554	cg43958488	241	GTTGAGCACTGG ATTCAGGCTAGAG G[A/gap]GGGCTC CCAGGTCAGTCT GAGAGTT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
3555	cg43958488	79	ATTTTCAAAGTC ATTGACCTCTTG T[A/G]TCAGATT AAGGCAAAGAAG AAGAT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
3556	cg43970044	357	GGTCTCCACCTG AAACTTCTGCC T[C/T]GGGATTGA CAGCCATCCATA AGAAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75129 KIAA0634 PROTEIN - HOMO SAPIENS (HUMAN), 1321 aa (fragment).	0	9
3557	cg43976962	836	GAGGGTGCTGT GGTCACAGCTCG CG[G/gap]CCCCG GCCACCGAGGC CCAGTTCCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92854 SEMAPHORIN - HOMO SAPIENS (HUMAN), 862 aa.	0	9
3558	cg43976962	842	GCTGTGGTCACA GCTCGCGGCCCC CG[G/gap]CCACC GAGGCCAGTTC CCTTCCAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92854 SEMAPHORIN - HOMO SAPIENS (HUMAN), 862 aa.	0	9

3559	cg43251586	1145	TTGATCAACAGT TGACAGTTAGTT G[C/T]GAGGAAA GGGTCCAAAAG GCATGGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76041 NEBULETTE - HOMO SAPIENS (HUMAN), 1014 aa.	0	10
3560	cg43923753	466	GTCACCTCCTGC AGCCATACCGTC A[G/gap]GCCAGC TTGGCCTAAAAG CTGTTAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
3561	cg43923753	467	TCACCTCCTGCA GCCATACCGTCA G[G/gap]CCAGCT TGGCCTAAAAGC TGTTATC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
3562	cg43925660	124	ATGCCTTGTTTT TTTTTTTTTTT[A /T]TGGCTGTTAT GCTTTTAATGGA AGC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13772 ARA70 - HOMO SAPIENS (HUMAN), 614 aa.	0	10
3563	cg43950416	42	CAGCAGCAGAG GGAGAGCTCGG GGC[G/T]TGAAG GGGAAACAGCG GAAGACCTA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10
3564	cg43950416	4189	AGGTAGGGTTCA GGGACTGATTGG T[C/gap]CCCCATT GCCCTCAGGTCA GTIGTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10
3565	cg43950416	4192	TAGGGTTCAGGG ACTGATTGGTCC C[C/gap]ATTTGC CCTCAGGTCAGT TGTTTAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10

3566	cg43917151	113	TGCCAACTCCTG AGCTAGGACCTG G[G/T]AACACAAA GTAAATAGGAC ACGAT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC98480 LYOSOMAL PEPSTATIN INSENSITIVE PROTEASE - HOMO SAPIENS (HUMAN), 563 aa.	0	11
3567	cg43983056	1243	CCACACACGTT AGACAAATTTTT [C/T]TTTTTTTC CAAGATTTTAGT AGTA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3568	cg43983056	1313	TACTTTCACTCC TTCAGTGTTAA A[T/C]AGAAACCC AAACAGTGCCAA CAGTA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3569	cg43983056	2744	CTCTAAGGTACC TCCCATCCCCC C[C/gap]ACCCCC AAAATCCCGCTG ATTTCCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3570	cg44015570	435	TAAAAAGTAA GCCACATCTGCA A[C/gap]TTACAC AATCCAAATGG CTAGAGC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13136 LAR-INTERACTING PROTEIN 1B - HOMO SAPIENS (HUMAN), 1202 aa.	0	11
3571	cg43329920	303	GCAGGGATGCTT AAGGAAGGCC CG[C/gap]CCAGT ATGAAAGCTGAG GATIGCCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12
3572	cg43329920	305	AGGGATGCTTAA GGAAGGCCCG CC[C/gap]AGTAT GAAAGCTGAGGA TTGCCTCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12

3573	cg43918566	2146	CCAGACTCTTCC TGGA CTGGCTTG C[C/gap]TCCTCC CCACCTCCCCAC CCTGGAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3574	cg43918566	2534	AGTCGTTTACC CTCTTCTATTGA A[T/A]TGCCCTTG GATTTCCCTCTC CCTTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3575	cg43918566	2581	CTTCCCTGCC ACCCTGTCCCT A[C/A]AATTGTG CTTCTGAGTTGA GGAGC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3576	cg43918566	2668	CCTATCACCTCC AGCACAATCCCA G[C/T]GAAAAAG GTGTGAAGCACC CACCAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3577	cg43924515	390	ACATGCTTGGTC TTTCTGGCTTGG C[C/gap]AACTCC TTCTTGAAACT AAGGGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29728 (2'-5')OLIGOADENYLATE SYNTHETASE 2 (EC 2.7.7.-) ((2'-5')OLIGO(A) SYNTHETASE 2) (2-5A SYNTHETASE 2) (P69/P71) - Homo sapiens (Human), 726 aa.	0	12
3578	cg43932638	175	AGCTGCCGCTG CCACCAGAGCC GGC[G/gap]GGG CATCGCGCTGCT CATTATCCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43892 BICAUDAL-D - HOMO SAPIENS (HUMAN), 975 aa.	0	12
3579	cg43950437	295	GAGTAGCTGGG ATTACAGGCGCA CG[gap/C]CAATA CGCCCGGCTAAT TTTTATT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0	12

3580	cg44918447	227	AATCCAGCACT TTGGAAGGCTGA G[A/G]CAGGAGG ATCAGTTGAGGC CAGGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3581	cg44918447	239	TTGGAAGGCTGA GACAGGAGGAT CA[G/C]TTGAGG CCAGGAGTTCAA GACCAGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3582	cg44918447	276	AGTTCAAGACCA GCCTGGGCAAC AT[A/G]GTGAGA GCCTGTCTCTAC AAAAAAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3583	cg44918447	475	TGAGACCTTGTC TCAAAAAA A[A/gap]AAACGC CTCCCCCTACC CCAGACA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3584	cg43961443	242	AATTATTTCTTC GAGCCCGCTCT G[C/gap]GCTGCG CCGGCCTCCCC GCGCCCGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14393 GROWTH-ARREST-SPECIFIC PROTEIN - HOMO SAPIENS (HUMAN), 678 aa.	0	13
3585	cg43966200	530	CTCAATTGTTTAT ATATATTTTTTTT /gap]ACAAGTTTT AACCTTTTGAA AAAC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13
3586	cg43966200	733	ATTTTATTCATT TTAAATCAAAGA G/A]ACCATTCCA TTTCCTAACAAA CAGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13

3587	cg43966200	817	CAGTCTTCCCT GTTTGAACAAG TT/CJT TTTTGAG AATTCTTAGTTT AGTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13
3588	cg43975253	415	AACAGTAGATT GTGCAATATGGA TIG/AJT TCTTAC TACAAGAAAAA ATTAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3589	cg43975253	52	TTGGGTGATGCA GAAAGCCACAAA TT/GJT TAAAGG ACACTAAGGTTT TAATA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3590	cg43975253	54	GGGTGATGCAG AAAGCCACAAAT TT/GJAAAGGA CACTAAGGTTT AATAAG	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3591	cg43929104	2930	ACAAGAGGAAGT GCCTGCGGGT CC/T/CJT TTTTAG AAGCTTTGTGGG TTGATT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3592	cg43929104	3069	GTCAGTATTCA GGGTTCTACATT TT/gapJATCTGTA AAATGTGACTTT TTTTTT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3593	cg43929104	3086	CTACATTTTATCT GTAAATGTGACI T/gapJTTTTTTTT TTTTATCACAACA GAA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14

3594	cg43929104	3098	TGTAATAATGTGA CTTTTTTTTTTTT T/gap]TATCACAA CAGAAAGTAAAT GTTGC	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3595	cg43929104	3099	GTAAATGTGAC TTTTTTTTTTTTT T/gap]ATCACAA AGAAAGTAAATG TTGCT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3596	cg43929104	3099	TAAATGTGACT TTTTTTTTTTTTT gap/]TATCACAA AGAAAGTAAATG TTGCT	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3597	cg43929104	387	AGCGGAGCCGA GTTGAGGCAGC GC[C/gap]TAGCG GTGAATCGGG CCCTCACCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3598	cg43929104	3568	CATTTTGATTCT GAAAGAAAGCT G[G/gap]CTTTGC CCATTCTTATTA AAAAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3599	cg43933104	1960	GCATACCTCTGGC AATGTTGTTCTTT [gap/A]AAAAAAG CATGGATTGCAT TTATAT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31641 KIAA0668 PROTEIN - HOMO SAPIENS (HUMAN), 1085 aa (fragment).	0	14

3600	cg43933104	1966	TCTGGCAATGTT GTTCTTTAAAAAA [gap/A]GCATGGA TTGCATTTATATA GTGTT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31641 KIAA0666 PROTEIN - HOMO SAPIENS (HUMAN), 1085 aa (fragment).	0	14
3601	cg43948117	2921	ACCTGTCAAGTG TCAACCCATACC CTT[C]GCAGAAG GCATGGGCTGC CACICGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15040 KIAA0329 - HOMO SAPIENS (HUMAN), 1411 aa.	0	14
3602	cg43949523	136	AGCGTGGTGTT C AAAGGCTTTTAG C[C/gap]TCATCT CATATCAGTCTA GTCAGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15035 KIAA0321 - HOMO SAPIENS (HUMAN), 1542 aa (fragment).	0	14
3603	cg43968223	164	GGCATCTCTTAG C GCGGGCAGGAC GG[C/gap]CCCCC CAGGCTCAACTC AGGACAAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3604	cg43968223	218	AACGGGACTGA C GCGGCCCCCATG GCC[C/gap]TCGG CCTGTGGCCACT GAGCTCCGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3605	cg43968223	388	TCCATGGCTCAG G CATCGTCCTTCT G[G/gap]CTTCCC AGCCCCGGGCC GAACGTTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3606	cg43991855	247	GCCTCTAAGTT A AGCCCTGCAACC A[A/gap]AGAGTT CCTCCAGGGAA GGAACGCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15037 KIAA0323 - HOMO SAPIENS (HUMAN), 724 aa (fragment).	0	14

3607	cg44018598	473	GGCAGTTCTAAA TAGCAAGTGCTT C[C/gap]ACAAAA ATAAAAAAACG ATAATGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
3608	cg44018598	592	CTATTCAGCTGG GTAATATTTTGAT [gap/]GTTTATCA TGTGCACTTGCT TGCTCT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
3609	cg44022133	4398	TATTATTAAATGA TGTGGTCTATGG [A/gap]AAAAAAA TAAAAATCTGAC TTAGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0	14
3610	cg43298473	3230	CAGCAGTTTGCA GTGGGTAAGG AG[G/gap]CCAAG CCCATTTGTGTA ATCACCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD32135 CYTOSOLIC PHOSPHOLIPASE A2 BETA - HOMO SAPIENS (HUMAN), 1012 aa.	0	15
3611	cg43936094	85	CAACATTTATTT ATCATAAAAGTTI C/AJAGCAAATAA AACTATATACAA GATC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC62018 P53 TUMOR SUPPRESSOR-BINDING PROTEIN 1 - HOMO SAPIENS (HUMAN), 1972 aa.	0	15
3612	cg43149413	3078	TTTGCCACGTA CCACGGTCTGG CT[G/gap]GGGCC CAGGCCCGGAT GCAGAGGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3613	cg43149413	3101	CTGGGGCCCG GCCCGGATGCA GAG[G/gap]CCTG CAGGGCCTCTGT CAATTGTAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16

3614	cg43149413	3135	GCCTCTGTCAAT TGACGCGCCAC CIG/AJAGTGCCTT CAACACAGCTTG TCTCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3615	cg43149413	3148	GTACGCGCCAC CGAGTGCCCTTCA AC/A/CJAGCTTG TCTCTTGCCTGC CACTGT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3616	cg43149413	3277	GTAATATGTAC ATTTCTCAGGCT A[G/gap]GGCCAG CAGGGCTGCC CGAGTCTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3617	cg43928515	1062	GTGAAGTAGCTG AACAAAAAAGCTT A[A/gap]AGAGAT TGCAATGTCAATT TTTAAGC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3618	cg43928515	16	TTTTTTTTTTTT TT[T/C]TTAATTTA GGAAGATTTTAT TTTTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3619	cg43928515	214	CACCGGTGTTC TCCCTCCACCT G[C/T]GTATGGG GTTTACTGTTATA GAATT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3620	cg43928515	2886	AACATACAAAC TTTGTTTTTTTT T/gapJAATATATA TACACAGTACAA GGCTG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16

3621	cg43928515	3260	TGGGGAGGAAT GAGACTGGCCC CAT[C/T]GCTGCG GCAAAAGCAAAC TGGGCTT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3622	cg43928515	3265	AGGAATGAGACT GGCCCCATCGCT G[C/T]GGCAAAA GCAAACTGGGCT TGAGGC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3623	cg43934724	428	AGAGGAATCTAG CGCGTCTGGCA GG[G/gap]CTGCG CTTCTTCACCTG CCCCTTAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15058 KIAA0350 - HOMO SAPIENS (HUMAN), 917 aa (fragment).	0	16
3624	cg43945577	2338	CAAGAAACAGA AGACAAAGCGG AC[G/T]TGAGGA GGAAGGGGACA GTGGCAGT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3625	cg43945577	2581	CACTCTGCTGAA CAGAAATTTATTT [C/T]TGAGTCAAA TATAATTTATTAT TAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3626	cg43945577	2696	CGTTTGCAAGAA GAGTTCCAGTTG A[C/T]GTGTGTT TGGTTCCATGGC GGGGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3627	cg43945577	2744	GGTACCCTAGG GATTCATCTGTT TT[C/T]TTCACCT CCCTTTGCATCT GAGATC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16

3628	cg43945577	2784	CATCTGAGATCC TGCTGGAAACCA C[G/A]GCAACCT GTATCCACTATT AGGAGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3629	cg43955093	1087	TCTCCTTTGTCA GGAATGCAAAA A[A/gap]TCACAC ACTCCTACCAGG IGTTTTA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3630	cg43955093	1257	GCTCACGTTTGG GTACACATCATT T[T/gap]CTTGCA GTATTTCTAAAA GCTTTGC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3631	cg43955093	1277	CATTTTCTTGCA GTATTTCTAAAA G[C/gap]TTTGCC AGAGTCAAAAAT CCAAGTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3632	cg43955093	1288	AGTATTTCTAAAA GCTTTGCCAGAG [T/C]CAAAAATCC AAGTTTGATTCT TAAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3633	cg43955093	1295	CTAAAAGCTTTG CCAGAGTCAAAA A[T/C]CCAAGTTT GGATTCTAAGCA GCCTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3634	cg43955093	1450	CTCATGTTACTA ACAGGCTGTAAC T[G/C]ATCAGCTG GATTAAGGAAAA AAGCT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16

3635	cg44014894	631	TTTCTACATCTG CAAGACAAGTTT G[G/gap]CTTCAG CCATTATGTATA GATAGAT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC51331 CREB-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 2442 aa.	0	16
3636	cg43055918	353	ACATTCTCCCTT GAGGGAATAAAA A[A/gap]GTGATT ATTAAATAATGA GTAAAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
3637	cg43936393	383	AAACAAGTTTCA GTAAAAATAAAA A[gap/A]CTAAAA CAACACTGAAG TAGAGTT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3638	cg43936393	398	AAAAATAAAAC TAAACAACAC T[G/T]AAGTAGAG TTTTGTAAATACA ACTG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3639	cg43936393	719	CTTAGGGAGGT GAGAACCTCCTT G[G/gap]CATATG CCCTACCTTAAT CTGAGCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3640	cg43947963	156	AGCACAGAGACT GGGAGGGGTT GA[gap/C]CCCCA CTCCAGAACACC AATACCTC	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14667 KIAA0100 (HUMAN COUNTERPART OF MOUSE E1 GENE) - HOMO SAPIENS (HUMAN), 2092 aa.	0	17
3641	cg43947963	86	ATATCCTACGGG GAAGGGTAGGG GA[C/gap]CCATG GCCAGCCCTGG CTCCTACTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14667 KIAA0100 (HUMAN COUNTERPART OF MOUSE E1 GENE) - HOMO SAPIENS (HUMAN), 2092 aa.	0	17

3642	cg43949150	166	CTGTCTGGAGG GGCTGAGGCTTC GG[C/gap]CTCGG GAGGCTGAAGC AGGAGGCAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
3643	cg43949150	167	TGTCTGGAGG GCTGAGGCTTCG GC[C/gap]TCGGG AGGCTGAAGCA GGAGGCAGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
3644	cg43964911	1457	TAGCTCACAGGT GAGGGGGTTTA GG[C/G]CCCTC TAGGGAGCGCC TGAGGCCA	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa.	0	17
3645	cg43980727	406	CCTCACTCCAGC ACACTCAGCCAG G[T/G]GCCCTGGC AAGATGACACAT TTCCCTG	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa.	0	17
3646	cg44023800	167	CCAGACAGACGA GGCCCCGGGAAG GG[gap/C]AGCCC AGGGGACTGGG GTCTCTCCT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14521 GIANT LARVAE HOMOLOGUE - HOMO SAPIENS (HUMAN), 1015 aa.	0	17
3647	cg43957585	101	CCACAGACAGG CCTAGTATGGCT AC[G/A]GTACCGT ATATAAAGACA ATTGCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13433 ESTROGEN REGULATED LIV-1 PROTEIN - HOMO SAPIENS (HUMAN), 752 aa.	0	18
3648	cg43979984	189	TAACTTTGGAC AACTTAAACCTTA TTCCTAGTGACAT TGCTGTCTAATA ATCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92539 HYPOTHETICAL PROTEIN KIAA0249 - Homo sapiens (Human), 896 aa.	0	18

3649	cg44001797	1080	GCGCCTGCAGC ACGTTGCCTCCA GG[G/gap]CCCAG CCTCCAGAGAGC CTCAGAGC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3650	cg44001797	185	TGCTGTCAATT GCAATGCCTGG GG[C/gap]CAAGC CAGGCCAGTGG ACTTGTTG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3651	cg44001797	324	ATGGGCTTGTGG AAGGGAGGCAT GC[C/gap]GCCGC CAGCATGCATGC CAGGGGTC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3652	cg44001797	719	AAAGTGAACGTA CTGAGACCGACA G[G/gap]ACAGCA AGAAGGCATTG CACATT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3653	cg42555863	2867	GGAGAGGAGCC CCATGCCCAGCC TG[G/gap]CTGAG CCCGAGATTCCG TCCTCCCC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14526 KIAA0290 - HOMO SAPIENS (HUMAN), 906 aa (fragment).	0	19
3654	cg42716880	95	GCAGTTTGGG GTGGGGGACAA AGA[C/gap]CCCC CTCCAGCTCCTA AACTGGGTC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43360 F21856_2 - HOMO SAPIENS (HUMAN), 679 aa.	0	19
3655	cg43917942	2499	AGATAGCGAGAT CTAAATCTCTGC C[gap/A]AAAAAA AAAAAAACTT AAAAAT	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19

3656	cg43917942	2500	AGATAGCGAGAT CTAATCTCTGCG C[A/gap]AAAAAA AAAAAAACTTA AAATTA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3657	cg43917942	2514	AAATCTCTGCCA AAAAAA A[A/gap]CTTAA ATTAAAAACACA AAGAGC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3658	cg43917942	2831	CTCCCGCCCTG GCTCAGCTCCCG CG[G/gap]CCCCG CCCGTCCCCCT CCCAGGAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3659	cg43927434	97	TCTTTTAAGGC AAAGCACCCGCA G[G/gap]TCAAGC CCCGCCCCGTC CCCCAGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0	19
3660	cg43975166	3601	CCGCTGCTGCTG GGAAAGACAGCA G[C/T]CTTGCG CGTCCCACAATC CTGCGC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00267 SUPT5H PROTEIN - HOMO SAPIENS (HUMAN), 1087 aa.	0	19
3661	cg43982840	541	ATTACTGAAGGA AATAGAAACTA T[C/A]TTACAAGT AGAACAGCCATA GACAA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15063 HYPOTHETICAL PROTEIN KIAA0355 - Homo sapiens (Human), 1070 aa.	0	19
3662	cg44022290	177	AGAGGGGGCCT CCCCCTGAGGC CCC[gap/C]ATTG GCCCCCTCCCA GGTATCCAAG	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14145 KIAA0132 PROTEIN - HOMO SAPIENS (HUMAN), 624 aa.	0	19

3663	cg43918691	157	AACGTCTAGGGG TGAGGGGCTGT GG[C/gap]CTCCA GTCGGCCCCAC AGCCTTTGA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3664	cg43918691	158	ACGTCTAGGGG GAGGGGCTGTG GC[C/gap]TCCAG TCGGCCCCACA GCCTTTGAG	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3665	cg43918691	349	ACTCGGCGGTG GCCCCGGGCTG CGC[C/gap]CAGG ATAGTGTTTATC AAATGTGAC	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3666	cg43918691	350	CTCGGCGGTG CCCCGGGCTGC GCC[C/gap]AGGA TAGTGTTTATCA AATGTGACA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3667	cg43918691	456	TTGTCTCTCATG GCTTCTCTCGGA G[gap/C]TACCGG AAGTTGGGCCTG GATAACG	gap	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3668	cg43918691	66	TTTTTTTTTTTT TTTTTTTTTTTTA TCCGGGCACCA ACGTTGGTTTTA ATG	A	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3669	cg43921004	591	AGATGTCACAAA TTATAGCGGCAC C[C/T]GTTACAGAT TTAGGGTGAGTT TCTGA	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60506 GRY-RBP - HOMO SAPIENS (HUMAN), 623 aa.	0	20

3670	cg43921598	2636	AAAGCACCCGTA GTAGCAAAACA T[A/gap]AAACAAA TAAAACTTCCCC CACATC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43439 MTG8-LIKE PROTEIN (MTG8 RELATED PROTEIN) (EHT) - HOMO SAPIENS (HUMAN), 604 aa.	0	20
3671	cg43958732	4278	TCTAAATAAATTG CTGTATTGTGCTT T/AJAATGTAAAA AAAAA AAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3672	cg43958732	4281	AAATAAATTGCT GTATTGTGCTTA A[T/A]GTAAAA AAAAA AAAAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3673	cg43958732	4283	ATAAATTGCTGT ATTGTGCTTAAT G[T/A]AAAAA AAAAA AAAAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3674	cg43317567	2185	TTCATCTCACTT CCAAATTTGGTT C[G/C]AAAGCAC AGTACCTAAAA AGTTCA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60318 MCM3 IMPORT FACTOR (KIAA0572 PROTEIN) - HOMO SAPIENS (HUMAN), 1872 aa (fragment).	0	21
3675	cg44019279	4170	ATGCTTAATACG TGTCGGTCATAT A[C/T]AGTATTGA ATTTTACTGTAT AGTA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14149 HYPOTHETICAL PROTEIN KIAA0136 - Homo sapiens (Human), 950 aa (fragment).	0	21
3676	cg43936123	163	ACGCTAGCACAG GGCCTGCCGCA GG[G/gap]CCTGG ATGCGGGCAAC GCAGGCGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60289 KIAA0542 PROTEIN - HOMO SAPIENS (HUMAN), 968 aa.	0	22

3677	cg43936220	185	AGTCTCACTCAG AATATTTAATTGG [C/T]TTAAATGA GAAATGAATCT TTTT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75132 KIAA0637 PROTEIN - HOMO SAPIENS (HUMAN), 1171 aa.	0	22
3678	cg43959772	3077	AGGGGTGCGTA GGTAATGGCGTC GG[G/T]ACCGCT CGGTCGCTGTG GAGGGTA	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3679	cg43959772	561	AATATTTACTAGA ACAACATTTAAA C/AJGTATCGTCG GTCCGCAGAAG CCTGG	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3680	cg43959772	882	AGGCAAGCCTCT AGATAGGCGGG GC[C/gap]AAGCC CTCCCGTGCCC ACCCTCTT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3681	cg43959772	886	AAGCCTCTAGAT AGGCGGGGCCA AG[C/gap]CCTCC CCGTGCCACCC CTCTTTCCC	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3682	cg43955358	2322	AAACAACCTGA GCCTGTGCATAT A[A/gap]GGCATT TACATATGATGA CCTTGCA	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)

3683	cg43955358	2360	TGATGACCTTGC ATCCTATAATAC A[A/gap]GTAATT GCATACTTAATA TCTGTAA	A	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
3684	cg43955358	77	CACAGAGGTAAC AATGACATTGTC C[CT]ACTAGACA CAGTAGTTCAAG ACATA	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
3685	cg43925474	1066	CACAGATCAATA CCACCTTGACTT G[T/G]TGACCCA GAGAATTCTAAT TAGATT	T	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3686	cg43925474	1303	TCTCTCCCAATT AAAAAACAAGA G[T/gap]TTTTTTG CTAGCTTGACAA TTTTAT	T	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)

3687	cg43925474	2277	CGGCTTTTATAA GAAAAA A[A/gap]GACGAA TCTGTAATGAAG AAAAAA	A	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3688	cg43925474	489	CATACTTTAATAT TATGTTGGTCCA C/T]GGGGTATAC ACATTTTAACAAA AGA	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3689	cg43925474	971	ATGGAAGAAAA CAAAACAAGCAT C/T]A]TTTCAAGA AGAAATGAATTG GATAT	T	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3690	cg43973809	2511	CCCCACCCCA GCCTGGGGGTC TGG[T/G]CTGGG GCAGGGATTGCT CAGTGGAA	T	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p36.1)
3691	cg43973809	2559	GAAGCAGGACT GGGGTCTGGC GTG[T/C]CCCCCTC CCTGGGCTCCA TCACCCC	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p36.1)
3692	cg43973809	3160	CCGAGAGTCCA GGCCTTGCCCTCC CC[C/gap]GACCG CCATGGAGGGG GCAGCCCGG	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p36.1)

3693	cg41573476	3166	AGAAATAACTA TTATAAGTTAGG T[<u>gap</u>]/T[GACAAAT GATGTTGATTAT GTAAGG	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3694	cg41573476	610	CCCTCCTACTCA GGATAAGACTTT C[G]/TAAATCTCC GGAGCTGAAAAA GGATC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3695	cg41573476	611	CCTCCTACTCAG GATAAGACTTTC G[A/C]/ATTCTCCG GAGCTGAAAAAG GATCC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3696	cg41573476	612	CTCCTACTCAGG ATAAGACTTTTCG A[A/T]/TTCTCCGG AGCTGAAAAAGG ATCCT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)

3697	cg41573476	613	TCCTACTCAGGA TAAGACTTTCGA A/T/ATCTCCGGA GCTGAAAAAGGA TCCTG	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3698	cg43117949	37	TCTGTCCACCAG CTGAGAAGGACA A[gap/A]GGGCGG AAGGCAGCTGCA CAGAGCA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10745 INTERPHOTORECEPTOR RETINOID- BINDING PROTEIN PRECURSOR (IRBP) (INTERSTITIAL RETINOL- BINDING PROTEIN) - Homo sapiens (Human), 1247 aa.	0	10 (10q11.2)
3699	cg43117949	4091	TATATATGTATAT ATATATGGCTTTI C/T/CAATAACCA CCTAAATTTTAAC AAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10745 INTERPHOTORECEPTOR RETINOID- BINDING PROTEIN PRECURSOR (IRBP) (INTERSTITIAL RETINOL- BINDING PROTEIN) - Homo sapiens (Human), 1247 aa.	0	10 (10q11.2)
3700	cg43920702	134	GGCTCTTGTCAC CCACTCCTAACC C[gap/C]TCTGCA GATTCCTCCTCGG GATGCTC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3701	cg43920702	338	GAACTAGGATT TCCAAATTCTGG A[gap/A]GCAGGA CTGAAGTTATTT GGGGCAG	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3702	cg43920702	36	TTTTTTTTTTTT TTTTTTTTTTTTTA TTTTTTTTTTAAC AAAATGTATTCAT C	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)

3703	cg43920702	439	AGGGGCTGAGT GGTCCTAGGCTC CC[ap/C]GGGCT GGAGGTGGGAC CTGTGCTCC	gap	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3704	cg43920702	464	GGGCTGGAGGT GGGACCTGTGCT CC[ap/C]TTGGG TTAAGGGTGAAA CCTCAGCT	gap	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3705	cg43920702	812	TGGGCTCAGAGT TGGGGGACTAA GG[G/gap]CGGAG CCTGGGTCCCA CAAGCGGT	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3706	cg43269831	365	AAGAACTGTGGC CCCAGGATAAAA A[A/G]AATACAGT GAGAACAAGAC CTCAG	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15586 N-ACETYLGLUCOSAMINE-6- SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6- SULFATASE) - Homo sapiens (Human), 552 aa.	0	12 (12q14)
3707	cg43950650	382	AGTAAAGGGCG TTCCAAGTCTTG A[ap/T]TTTTTTT TTTTTTTTTTTT AGCAG	gap	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99700 ATAXIN-2 - HOMO SAPIENS (HUMAN), 1312 aa.	0	12 (12q24)
3708	cg43950650	402	CTTGATTTTTTT TTTTTTTTTTTTTg ap/T]AGCAGTAAT AGCAGCAAGAAT CACT	gap	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99700 ATAXIN-2 - HOMO SAPIENS (HUMAN), 1312 aa.	0	12 (12q24)

3709	cg43979900	1019	TCCTTCTTCCAG CCACCTGGAAAA A[C/T]GTTACAG AGAGTTATAGTG GTTAC	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3710	cg43979900	1116	AATTAATCTGCT AATATCTATTACC [G/A]CAGAAATAG TGTTAGAGGTAG TTTA	G	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3711	cg43979900	1147	ATAGTGTTAGAG GTAGTTTATTAA [G/C]AGGCGTTTT TAAATCATCCC ACTC	G	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)

3712	cg43979900	1152	GTTAGAGG TAGT TTATTAAAGAGG C[G/A]TTTTTAA ATCATCCCACTC ATCAT	G	A				SILENT- NONCODING	UNCLAS UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3713	cg43979900	157	AACCACTGAATC ACACAACATGGA C[C/A]AATCTCAA ATCATTATGCTG ATGGA	C	A				SILENT- NONCODING	UNCLAS UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3714	cg43979900	292	ATTCCTATCAAT GGCTGCCCAACAA TTT[C]GGGAGTG AAAGGAACTGAC TGAGCA	T	C				SILENT- NONCODING	UNCLAS UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)

3715	cg43978900	470	AAATAAATTACA CCTCTATAATGT TTTCGTTTTAAA AAATATTAGATA CATCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3716	cg43978900	616	TAGCTAAGCCTA TGTTAGACTCTT A/C/TAAATTCCT AAATAGTAGAAT TAGTT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3717	cg43973740	669	AGGTCCTGAAGG TGAGTGTCCGGA G[G/gap]TGCTGG GTAAACACATC ACAGGTA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa.	0	16 (12q12)
3718	cg44928323	10345	TAAAATTGGTTT GATACTCAGAAA ATTAAACAAGAATT TAATTTTTTAAAT TT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
3719	cg44928323	11285	GACTTGTTAAAG AGGAAACCAGGA A/C/TTCAGTCAT GTTTTGTCCTG GATAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)

3720	cg44928323	11963	ATGATAAATTAC TGTCCTTTCCAT C[C/T]GGGCCTA AACTTTGGCAGT TCCITT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
3721	cg44026807	2058	GGAGGAAGAAG CCCCGTTTCCAG GG[C/gap]ATCCG CAGCCAGGGT AGGGAGAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14397 GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR) - Homo sapiens (Human), 625 aa.	0	2 (2p23.3)
3722	cg43960198	2178	CGGCCGGGCC GGGGCTGAGGT CAG[C/gap]CTCA CTGCCTGCTTAT TGCCTCTTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3723	cg43960198	2474	TGCAAGGCTGG CAGCCCCCACC CCC[gap/C]ACCC CCCAGGCCGCC TTGAGAAGCA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3724	cg43960198	2491	CCCACCCCCACC CCCAGGCCGC CTT[gap]GAGAA GCACAGTTTAAC TCACTGCG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3725	cg43960198	2505	CCAGGCCGCCCT GAGAAGCACAGT TTT[gap]AACTCAC TGCGGGCTCCT GAGCCTG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)

3726	cg43960198	2700	GGCCCCATGCCT CTCCTCCCTCTC T[gap/C]GGCAGG GCCCATCCTGG GCAGAGG	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3727	cg43960198	2708	TGCCTCTCCTCC CTCTCTGGCAGG G[C/gap]CCCATC CTGGGCAGAGG GGCCTGGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3728	cg43960198	2711	CTCTCCTCCCTC TCTGGCAGGGC CC[C/gap]ATCCT GGCAGAGGGG CCTGGGGCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3729	cg43960198	2734	CCCATCCTGGGC AGAGGGGCTG GG[G/gap]CTGGG CCAGAGTCCAG CCGTCCAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3730	cg43956384	2427	GTACCTACTGGA GCCGCAGAAAG GA[A/gap]GTCCA CTCAGTCACATC CAGAAAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13866 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 664 aa.	0	22 (22q13.1)
3731	cg44025634	3380	TTTGTGGGGAA AACTATTAATTT T[T/G]TGCAATGG AAAGATCAACAG ACTA	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)

3732	cg44025634	3873	TGGCAGATGTCA CATGAGTAGAAT TTC/TCTGCCCAG CCTTAACATGCAT TCAGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
3733	cg44025634	3985	GACACATGGTTG TGAATACAATGA TIG/AJTATTTCTT TATTTTCACATAC ACTC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
3734	cg44025634	4039	TAAAGAGCAAG AGTACACATCAA C[gap/A]AAAAAT GGAACAAGGCT TTGGCTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
3735	cg43955813	3033	TATATGTATGTAT ATATGTATATGT G[gap]AAAAACAG TTTGATAGTTG GAATA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0	4 (4q12)
3736	cg43993542	322	CGGTTTCTGGG CTGGGCTTTCTG C[C/gap]TTACTC ACTCCTTCTCCC TCCTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16471 PROLACTIN RECEPTOR PRECURSOR (PRL-R) - Homo sapiens (Human), 622 aa.	0	5 (5p13)
3737	cg43993542	449	CTGATGTGGCAG ACTTTGCTCCCT G[G/A]CAAAACTA AAGAACTCTCCT ATTCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16471 PROLACTIN RECEPTOR PRECURSOR (PRL-R) - Homo sapiens (Human), 622 aa.	0	5 (5p13)
3738	cg43952287	161	TGTAAAAAAGCA AACAGTGCCAAT G[G/gap]CCACTT TGGTAAAAACAC ACAGTGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0	5 (5pter)

3739	cg43952287	92	TTTTTTTTTTTT TTTTTTTTTTTT[C /T]CTGGTTGACA AATTTTCTTTACT TA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE-TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0	5 (5pter)
3740	cg43952287	93	TTTTTTTTTTTT TTTTTTTTTTTT[C /T]TGGTTGACAA ATTTTCTTTACTT AT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE-TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0	5 (5pter)
3741	cg43955232	7346	GAGAGAAATTACA CTTTTTTTTTTTT gap/T]AAGTGGC GTGAGAGGCCTTT GCTTCC	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54253 ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN) - Homo sapiens (Human), 816 aa.	0	6 (6p23)
3742	cg42907760	2137	CTGCCCTGCTCT GTGACAGAGCCT G]gap/G]AGACTT GGAGGTCCAGA GGCCCCCCC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3743	cg42907760	2149	GTGACAGAGCCT GAGACTTGGAG GT]gap/G]CCAGA GGCCCCCACC AACCAGCCC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3744	cg42907760	2174	CCAGAGGCCCC CCACCAACCAGC CC]gap/C]AGCCA CTGTTGCTGGCT GTGTCGTT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3745	cg42907760	2174	CCAGAGGCCCC CCACCAACCAGC CC]gap/C]AGCCA CTGTTGCTGGCT GTGTCGTT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)

3746	cg42907760	2272	CTGTTGCCACTT ACGGGGGCTGG AG[A/gap]AGGCC TGGATAAAGACA GAAGGGCG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3747	cg42907760	2273	TGTTGCCACTTA CGGGGGCTGGA GA[A/gap]GGCCT GGATAAAGACAG AAGGGCGG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3748	cg43958842	632	CCATTGGAATTT CAATCCAAGCAG C[A/G]TATTTTAC ACACACCTGAAG GAAAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P41252 ISOLEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (LERS) (IRS) - Homo sapiens (Human), 1266 aa.	0	9 (9q21)
3749	cg42373006	59	TACACAAATGAA GTCTTTGGTGA TIG[A]AATTCAAG TCAAAACAAATA ATAGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60267 KIAA0512 PROTEIN - HOMO SAPIENS (HUMAN), 632 aa.	0	X
3750	cg43921793	1986	GGATCTGCAGCA GCTGGGCTGCC TC[C/gap]GATGG TGGAGAGCTGG ATGAAGGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X
3751	cg43921793	42	CGACTTTTTTTTT TTTTTTTTTTTTTT GJCAGACTTTTCA GCTTTTATTACAA A	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X

3752	cg43921948	3315	AACAATGTGATT GGATTCCTTTAT G[G/C]CAAAATC GAGAGAAAGCTG CCATCCA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3753	cg43921948	3494	GAATGTTAGCCA TGACTTGGGCTT T[C/G]TGAAAGTT GGCTATAATTTC TCTAT	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3754	cg43921948	3989	TTGATGATGTGG AAATGCTGCAGG A[T/C]TAAATAAC TTGAAGAGCCCTT TATAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3755	cg43921948	4592	TATGGTACTAAG GAAGTCCTGTTT T[T/gap]CAAAAAT GGAAGCCCACTT CTCAGA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3756	cg43921948	4665	AAAAGTGAAGGGA GAAACACACACA C[A/G]CAAAAAA CAAGTATTGGC TTGTC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X

3757	cg43921948	4673	GGGGAACACA CACACACAAAA AA[gap/A]CAAGT ATTGGCTTGTC ACAGGAAT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3758	cg43921948	4717	CAGGAATCTGAT TGCATTAAGTGA A[A/gap]GGATTA TTTAGAATATGTT AATGCA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3759	cg43921948	5894	CAGGTGATGTCT GGTCAACTGGCC TT[A/G]CCTTCAGC TAGAATCCTGTT AGGTC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3760	cg43921948	5975	CTTGGTAATCTT CCATCCACTGCC C[C/A]TGACCCCTG TTCCCTGTCTAT AAATC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3761	cg43921948	6017	CTATAAATCCCC AGTTTTCATGG T[G/A]TATTCAGA GCTGAGTCCAGT CTCTC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X

3762	cg42866508	1928	TTCTCCAGTCAG AGTAGATGATGA G[G/gap]CCCATG CCCCTCACCCCC ACGCCCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76007 TRIPLE LIM DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 615 aa.	0	X (Xp11.2 3)
3783	cg43927750	276	ACTGTATTGAG ATGTCTTACTTG GTT/GJAGACCAAT TAAACTATGACA TAAAA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
3784	cg43927750	631	ATTGAAATGCAT AAACACAATACT TTT/gap]CAAGAAT ACGCTCAACACA TGTACA	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
3785	cg43277466	593	TCGCCAAGCAGA CACAGAAATCCC C[A/G]TGTGGG GAATGCAGCAGC TCTGCC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	XY
3766	cg43061097	4045	TGATGCATGTTG GCTGAGATGATC ATT/GJGGAGATG AGTGACACCCAGA GCTCAC	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39482 OLIGOPHRENIN-1 LIKE PROTEIN - HOMO SAPIENS (HUMAN), 814 aa.	0	
3767	cg43061097	4046	GATGCATGTTGG CTGAGATGATCA TTG/TJGAGATGAG TGACACCAGAGC TCACA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39482 OLIGOPHRENIN-1 LIKE PROTEIN - HOMO SAPIENS (HUMAN), 814 aa.	0	
3768	cg43273039	4922	ATAAATTAAATTT TATTGTGTAAAA ATTJAAATTATTAC ATAAATGTGTTT TT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75763 SYNAPTONEMAL COMPLEX LATERAL ELEMENT PROTEIN - HOMO SAPIENS (HUMAN), 1530 aa.	0	

3769	cg43273039	4924	AAATTAAATTTTA TTGTGTAATAAA ATJATTATTACAT AAAATGTGTTTT GA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75763 SYNAPTONEMAL COMPLEX LATERAL ELEMENT PROTEIN - HOMO SAPIENS (HUMAN), 1530 aa.	0	
3770	cg43277456	2654	GACCGACAGTC GTGAGGATGGC AGA[G/gap]CTGC TGCAATCCCCCA CATGGGGAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	
3771	cg43277456	2673	GGCAGAGCTGC TGCAATCCCCCA CA[T/C]GGGGATT TCTGTGCTCTGCT TGCGCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	
3772	cg43291710	555	GACAGTCTGAAG CATTAAAAAATTC [G/A]TAAAAAACA GTAACACTGACA AAAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA34522 KIAA0802 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	0	
3773	cg43916588	1102	GGTCCATGTTGT TCCAGAGTCCCC T[G/A]AGTTTCAG GTTCAGCTGATG TAGAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75150 KIAA0661 PROTEIN - HOMO SAPIENS (HUMAN), 1001 aa.	0	
3774	cg43916588	352	GCCACCAGGAT GAAAGCAGGGTT AG[G/gap]TCCAG GGACCCAGTAGA GCCTTGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75150 KIAA0661 PROTEIN - HOMO SAPIENS (HUMAN), 1001 aa.	0	
3775	cg43918446	1527	CTAAAAACTGAT TTGCAAACTTGA A[C/A]GTCTAGAT GTGTGTAGGAAG ATTTT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	

3776	cg43918446	1559	ATGTGTGTAGGA AGATTTTAAAT TTCJAGGCAAAT GGTCTCTAAAGA GACC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3777	cg43918446	1570	AAGATTTTAAAT TTAGGCAAATG G/gapJTCTCTAAA GAGACCAATTTT GCTTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3778	cg43918446	1926	TGTTTTCCCA GGAACATTGAT G[A/C]CTGAGGA GACTTGAAAAGA GACCTA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3779	cg43918446	1930	TTTCCCAGGA CTATTGATGACT G[A/G]GGAGACT TGAAAAGAGAGACC TAAAGT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3780	cg43918446	2125	TCTCCATGTGA GTAGGTCAAAGT CTT/CJCCGTCCTC CCTGGCCAGGT GGAAGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3781	cg43918446	444	CAAAAATAACA ATCCAACAAGAG TTC/AJATGTTACC CATTCTTAGCCA TTAAC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3782	cg43918446	529	TGTACCCCACTG GGACCAAATACA A[A/gap]CATGAG ACACTAGGGTGG CTTGTC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	

3783	cg43918446	601	AAGGAACCTTAT CATGGGCTGAGA GTTA]TAGATAGA TAGCTTAGAACA ACATT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3784	cg43918446	655	AAAGTGGGTGCT TCTACATGAGGA CTT/gap]TTTTTTC CCCCCAAGTAGA AAAATA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3785	cg43918446	661	GGTGCTTCTACA TGAGGACTTTTT TTT/gap]CCCCC AAGTAGAAAAAT AATTAAA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3786	cg43920875	2433	GTTCTGACTCCC AGTACGGTGTG TIGT]GCGCCGC TAGGATATCCTT GTCAAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF- 2, MITOCHONDRIAL PRECURSOR (IF- 2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0	
3787	cg43920875	2434	TTCTGACTCCCA GTACGGTGTGT G[G/]CGCCGCT AGGATATCCTTG TCAAGG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF- 2, MITOCHONDRIAL PRECURSOR (IF- 2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0	
3788	cg43923595	310	CCGGCAGTCCCT GCCCAGTCCCTC C[G/]CTCTGCTTC CTCCCACTCTTC CACAT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99467 LYMPHOCYTE ANTIGEN 64 PRECURSOR (RP105) - HOMO SAPIENS (HUMAN), 661 aa.	0	
3789	cg43932090	19	TTTTTTTTTTTT TTTTT]G]AAGG TTCTCAAGAATTT TATTATAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	

3790	cg43934688	2862	GTCCTTCATATGT CAACTACAGAAA A[A/G]AAAAAAA ATAGAAATTGAA GGATT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3791	cg43934688	2863	TCCTTCATATGTC AACTACAGAAA A[A/G]AAAAAAA TAGAAATTGAAG GATT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3792	cg43934688	4242	ACTTTTATGTCA TCGTAAAGCTG A[gap]AAAAAATC CCTTTGTTTCTAT TTAT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3793	cg43934688	4248	TATGTCATCGTA AAAGCTGAAAAA A[A/gap]TCCCCTT GTTCTATTATA AAAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3794	cg43935504	70	ATTTAGCACAG TTAAATTTTTTTT T/GJTGTAAACAC AAACAAGATAAA TTTA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15044 KIAA0335 - HOMO SAPIENS (HUMAN), 1263 aa.	0	
3795	cg43936083	239	AAGTCAACAGGG AAAGAAGTGGGT A[C/gap]CCCCCTT TGCCAGAAGCTA ATTGTT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3796	cg43936083	323	AAGATGTAGGCA GTGGCGGCAGG CC[C/gap]TGCGC CCACAGCTCCTC GCCTGTCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	

3797	cg43936083	335	GTGGCGGCAGG CCCTGCGCCCA CAG[C/gap]TCCT CGCCTGTCCTT GACCACAGA	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3798	cg43936083	432	ATGATAGGGAA CAATAGAGGGA A[C/gap]CCAGCC TCAACCCAAGTC AGAAGGT	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3799	cg43940146	185	AAACTCATTACT ATAAATTATTCTT I[A/C]CAGTACTTT GCAAATTCAGAA TTTC	A	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15910 ENHANCER OF ZESTE HOMOLOG 2 (ENX-1) - Homo sapiens (Human), 746 aa.	0	
3800	cg43940465	662	CCTTGGGTCAG TGTGTTAATTAG G[G/gap]CTGAGA GCCTGGGTGAAA GGCAAGA	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment).	0	
3801	cg43951590	167	CTGATAAACAC ATACAAAAGTTA A[A/G]AGACAGCT CGATTTTCATCTT CCTCC	A	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14684 HYPOTHETICAL PROTEIN KIAA0179 - Homo sapiens (Human), 740 aa.	0	
3802	cg43951590	2663	TACAAAATCATA AAAAAGGCCCA TTT/AJTTCTTAA GGTATAATTTATA GCGC	T	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14684 HYPOTHETICAL PROTEIN KIAA0179 - Homo sapiens (Human), 740 aa.	0	
3803	cg43960583	6448	CTGCTGTTTGCT TAAAAAATAAA A[A/gap]CACCCCT TGTCATGTATTT CTGTAT	A	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93073 HYPOTHETICAL PROTEIN KIAA0256 - Homo sapiens (Human), 635 aa.	0	

3804	cg43971555	235	TGAGCTTCAGGC GGTTGTCCCGAA G[G/gap]GTCAAG TGGCCAGCAGG GTCTGGTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0	
3805	cg43971555	236	GAGCTTCAGGC GGTTGTCCCGAA GG[G/gap]TCAAG TGGCCAGCAGG GTCTGGTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0	
3806	cg43975476	95	TATTATTTCCTT TGGAAGAAGAAA [C/A]CAGAAAAA AACTTCCTGATT GTAA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75141 KIAA0650 PROTEIN - HOMO SAPIENS (HUMAN), 848 aa (fragment).	0	
3807	cg43979857	123	ACGCAAGACAGA TGATGCAGGG AA[C/T]GGGTGTC CACTCTTTCTTG TTCTCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60327 KIAA0584 PROTEIN - HOMO SAPIENS (HUMAN), 738 aa (fragment).	0	
3808	cg43981392	25	TTTTTTTTTTTT TTTTTCTGCAAT/ C]TGAGGAACA GTTCACTGATT ATT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15297 WIP1 - HOMO SAPIENS (HUMAN), 605 aa.	0	
3809	cg43985672	614	AGTGGCTGGGA CAAGCTGGCGG GG[C/gap]CAAG CACTGTTGAAGC AATAGGGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15017 ORF - HOMO SAPIENS (HUMAN), 692 aa (fragment).	0	
3810	cg44001705	274	TGTTTTCCATAC AAGACTGTCACG C[A/G]AAGGATCA ATTTGTGCATGT GCCAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00539 NUCLEAR PROTEIN SA-1 - HOMO SAPIENS (HUMAN), 1258 aa.	0	

3811	cg44003843	6105	CAGAAATGTAAG TCAACTTAAGAA C[A/G]GTGAATGA ATGTAAAAACAT TCAGT	A	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0	
3812	cg44003843	6131	GTGAATGAATGT AAAAACATTTCAG T[C/T]GAGACCAT ATGCATTTTCTG TGCTG	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0	
3813	cg44009187	1459	ATGTCGTCACG CGGCTAACTTGA C[C/gap]TGCGGG GTCTAAGGAAAG TCAACTT	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0	
3814	cg44009187	18	TTTTTTTTTTT TTTT[G/T]ATGGT TTCCATTTTTC CTTTAAT	G	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0	
3815	cg44022781	275	ATCTCTTGAGCT CTTCCCACTGA C[T/G]TGTCATTC ACAGGCATTCAA ACTGT	T	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14692 KIAA0187 PROTEIN - HOMO SAPIENS (HUMAN), 1282 aa.	0	
3816	cg44036048	65	TTTATTTTCAGTTT TGGCTCTTAAGC[C/gap]ACTTCCAT TGGAAGAAGAA ACTCC	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:CAB45768 HYPOTHETICAL 94.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 851 aa (fragment).	0	
3817	cg44130923	5459	ATGTCCATAAAG TGGCGTGAAGTG A[A/G]ACGTTCTC TTTGGTGGTCAA CCCCG	A	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) - MUS MUSCULUS (MOUSE), 1726 aa.	0	

3818	cg44921672	1595	GCAAAAAATTAG CCAGGCATGGT GG[C/T]ATGCAC CTGTAGACCCAG CTACTTG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O60879 DIAPHANOUS PROTEIN HOMOLOG 2 - Homo sapiens (Human), 1101 aa.	0	
3819	cg44921672	1648	AGGCTGATGCAG GAGGATCGCTTG A[A/G]CCTGGGA GTTTGAGGTTGC AGTGAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O60879 DIAPHANOUS PROTEIN HOMOLOG 2 - Homo sapiens (Human), 1101 aa.	0	
3820	cg44932392	194	AATTTTATGTCCT TTAAGATACATT A[gap]AAAAAAA AAAAAAGACACA TCAAC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
3821	cg44932392	208	TAAGATACATT AAAAAAA A[A/gap]GACACA TCAACTGCAAAC GTGAAGG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
3822	cg43942696	1416	TTCTGGGCCCTG TCTGCGGTTCCA C[A/G]TGATGATAC TGTGGGTGAGAC GGCAT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROXYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3823	cg43942696	1438	CACATGTGATAC TGTGGGTGAGAC G[G/C]CATGGCC CATTCTGCACT TGCCCA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROXYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8

3824	cg43942696	172	TCAAGACAGTGG TTACAAAAAAA A[A/gap]GTACTC TTCTGGCTACAC ACTTTAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3825	cg43942696	260	CAATCACAATT CCAGGATTAAAA A[C/T]CATCTATT CTTAAATCCTAC ACTGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3826	cg43942696	274	AGGATTAAAAAC CATCTATTCTTAA [A/G]TCCTACACT GTTTtagagCAT CAAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3827	cg43942696	480	CAAAACAACCAA AAATTACCATGA C[C/T]CGGTACA GGAAAAACAGGA AGACTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3828	cg43942696	69	AACAACACATT TTGCTTTATTAG G[C/T]GTTCCATG GTAATATAACAC AGAGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8

3829	cg43957189	387	CAGATGGGTGG GGCAGGGTGGG GTT[C/gap]CCCC CATCTGACCCCTC TAGGGCTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
3830	cg43957199	392	GGGTGGGGCAG GGTGGGGTTCC CCC[C/gap]ATCT GACCCCTCTAGGG CTCTGGGGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
3831	cg44002959	3908	CCTTGTGGGG GACCAGGGCAG GGC[C/gap]TGGG ACAGGGAAGGG GGTGAGTTAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92513 MYELOBLAST KIAA0239 - HOMO SAPIENS (HUMAN), 571 aa (fragment).	1.4e-316	5
3832	cg43958391	253	CCCCCGGAAC AGAAAGGCAGTGA TG[C/gap]CAAAT GCCAAGGAAGC AGCTTAAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14545 FLN29 - HOMO SAPIENS (HUMAN), 582 aa.	2.4e-316	12
3833	cg43958391	254	CCCCCGGAACA GAAGGCAGTGAT GC[C/gap]AAATG CCAAGGAAGCA GCTTAAAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14545 FLN29 - HOMO SAPIENS (HUMAN), 582 aa.	2.4e-316	12
3834	cg43937128	170	CACAACTTGATG GTTTTTTTCTTT C/TTTTTGCAAAA GGACAATCTATA TGCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X

3835	cg43937128	299	GGCTGGAGGAG GTATACAGGATA AC[A/gap]AAAAA AAAAAATAGAA AAAAATAA	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3836	cg43937128	311	TATACAGGATAA CAAAAAA A[A/gap]TAGAAA AAATAAGAAAG TGGTTCC	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3837	cg43937128	311	ATACAGGATAAC AAAAA A[gap/A]TAGAAA AAATAAGAAAG TGGTTCC	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3838	cg43979183	1210	CCATGCCCTGACA AGTTCTGAAGAG G[A/gap]AAAAA AAATTGTTTAA TCCAGT	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3839	cg43979183	1219	ACAAGTTCTGAA GAGGAAAAA A[A/gap]ATTGTTT TAATCCAGTTTC TGCTCG	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3840	cg43979183	1220	CAAGTTCTGAAG AGGAAAAA A[A/gap]TTGTTT AATCCAGTTTCT GTCTGC	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3841	cg43979183	1300	CCCTTTATGAAA AGATAAAGCAGA A[C/G]AAAAAGTGA AATATATCTTCA GATTA	C	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	

3842	cg43979183	754	TCTCAATATACA CACAGATTAAAGA GTT/gapTTTTTGC CTTGGCAAAAAT AAACT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3843	cg43979183	759	TATACACACAGA TTAAGAGTTTTTT [gapTT]GCCCTTGG CAAAAATAAAAC TGAAGT	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3844	cg43979183	872	AAAGATTACAAT ACATTATTAACTT [A/C]CTTTTAA CACAGAGTAAAG TTAC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3845	cg43979183	873	AAGATTACAATA CATTATTAACTTA [C/A]TTTTTAAAC ACAGAGTAAAGT TACT	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3846	cg44002835	22	GTCGACTTTTTTA TTTTTTTTT[AT]TA TAAAAGGTCAC TTTTATTTTGCC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13585 MELATONIN-RELATED RECEPTOR (H9) - Homo sapiens (Human), 613 aa.	5.0e-312	12
3847	cg44002835	406	GAGTCTGACAGT GTTCCGGGCTGCT G[C/gap]CTTTATA GTCTGTGTTCTC AAAGTT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13585 MELATONIN-RELATED RECEPTOR (H9) - Homo sapiens (Human), 613 aa.	5.0e-312	12
3848	cg43948793	394	GCCACACAAATC TGTTGTGGGCTA A[G/C]GATGAGG ATACAGAGAAAA GAAAAA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15051 HYPOTHETICAL PROTEIN KIAA0036 - Homo sapiens (Human), 598 aa.	5.5e-315	6

3849	cg42710561	1866	TGAGGAAATGTA TAAATACACACA T[A/G]GTATAAAA TTACATGTTAATA CAAT	A	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92521 PIG-B - HOMO SAPIENS (HUMAN), 554 aa.	6.1e-311	15
3850	cg43938133	1324	CACCTTCGGAAGT CCCAAGGGCAG TG[C/gap]GGATG ACCGATTGGCC ATGGAAGA	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14195 DIHYDROXYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (UNC-33-LIKE PHOSPHOPROTEIN) (ULIP PROTEIN) - Homo sapiens (Human), 570 aa.	6.6e-310	5
3851	cg43938133	1846	ACTTATTCAAAC CTGCAGTCAGAG A[C/T]AATGGTTT CTCCTAAGCAAT TAAAA	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14195 DIHYDROXYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (UNC-33-LIKE PHOSPHOPROTEIN) (ULIP PROTEIN) - Homo sapiens (Human), 570 aa.	6.6e-310	5
3852	cg43277973	62	TTTTCTTTTCAC AGTCCGCCTCTT gap[C/T]AATCTTG GACTGGAGGATA TACAG	gap	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P36269 GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA- GLUTAMYLTRANSFERASE 5) (GGT- REL) - Homo sapiens (Human), 586 aa.	8.0e-314	22
3853	cg44015618	348	GGCAGGTTGATC TGGAACGGGC TG[G/A]CATGCTA GGGATGGTGGA GAAGTAG	G	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75148 KIA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	8.7e-312	11
3854	cg44928804	2623	AATGAGAAAGGC CAGAGGCTGCAA A[A/gap]GACAGT CAAAGGACACGA GAGAAAG	A	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)

3855	cg44928804	3388	CCTCGGTTCTAT GCATATATGGAT T[A/gap]GCTATAA AAATGTCAATA AGATTG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3856	cg44928804	3435	ATTGTACAAGGA AAATTAGAGAAA G[G/T]CACATTTA GGTTTATTTTTT ACAC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3857	cg44928804	3493	TAAATAGGGTA AATCCTATTAGA A[gap/A]TTTTTTA AAGAACTTTTTT AAGTT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3858	cg43956210	1844	ATCATGTAAAT AAGATATTAGAC T[G/gap]TTTTTTG AATAAAATATTTT TATTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
3859	cg43982721	1884	CTCTCCTAGACG CCCAGGACCGG CC[G/gap]CCCTG TGAGCCGTGCTG GCCCCACC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	
3860	cg43982721	1937	AGGCCGCGGG CCCCAGGGCAC TCG[C/gap]CCCC CTCCTTAGCAAT TTCTTTTGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	

3861	cg43955051	136	AATTTATGGTAA CAATCATTTCTTT [T/C]AAATGTCTA ACTTATTTAACC CCTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD10823 SQUALENE EPOXIDASE (EC 1.14.99.7) - HOMO SAPIENS (HUMAN), 574 aa.	1.9E-305	8
3862	cg43264444	216	GGAAGAGGGAA AAAGGTTGCTTC TG[T/C]TTTATTTT CACATCTGTAAT TTTAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene REMTREMBL- ACC:G513351 PROTEIN 1 - ARTIFICIAL SEQUENCE, 530 aa.	2.4E-305	11 (11q21)
3863	cg43991434	194	CATCTGCCCAGT CCAGACCCCTACC G[C/T]TCCCCCTGC CCCAGGAGGTC CTTTAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3864	cg43991434	427	ACAATCTGGTGT CTGCCCTGTCCAC A[C/T]GGTGTGG GGCCCAGGGTT GCCCTCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3865	cg43991434	59	TTTTTTTTTTTT TTTTTTTTTTTTTG TTAAGCTGCCAC ACGACTTTATTT GTG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3866	cg43991434	828	TCCCCACAACAG AGCAGGGCTGG GC[C/gap]AGCAG AAGACGTTAAAA CCCCAAATC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3867	cg43962078	2297	TCCTTCTGTCCTT TTAAGTGTAACCTT GTTGAATTCCTT GATTTATTTTATT GCA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43776 ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.22) (ASPARAGINE-- TRNA LIGASE) (ASNRS) - Homo sapiens (Human), 548 aa.	2.2E-304	18

3868	cg43982078	2507	ATAATCCTGAGG CATAGAAATTGA A[A/G]AATTGTGTA AAAATAGAAATTG CCTTA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43776 ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.22) (ASPARAGINE-- TRNA LIGASE) (ASNRS) - Homo sapiens (Human), 548 aa.	2.2E-304	18
3869	cg43985349	3532	TGCCATGGTGCG GGCCGGGGCGG AC[G/A]CGTTCCC ACCTTTGGGACC GGACGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC69991 GLYPICAN-4 - HOMO SAPIENS (HUMAN), 556 aa.	2.7E-304	X
3870	cg43951838	334	CTTCTGAGTGT GAACCTGGCTCG G[C/gap]CTGAAG CCTAGAGCTGGC TTGAAGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3871	cg43951838	82	TTTTTTTTTTT TTTTTTTTTTT TTTGGGCAGTTC ATTTCTTTATTT TT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3872	cg43951838	84	TTTTTTTTTTT TTTTTTTTTTT GTTGGCAGTTCA TTTTCTTTATTT TTC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3873	cg43142595	591	CCTGGTGCTGCT GAGATGGGCGC TG[C/gap]CTCCT CCCACCCACAGC GCGTCATC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	

3874	cg43142595	592	CTGGTGCTGCTG AGATGGGCGCT GC[C/gap]TCCTC CCACCCACAGC GCGTCATCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3875	cg43142595	703	CCCGCACCCAG ACCGTGCCGTCT GG[C/gap]AGGCA CTTTCGGCCTCA GTGCCACG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3876	cg43142595	745	AGTGCCACGGC CCCCTCCCCAG GCC[A/G]CTCAC ACTCCTGGGGG GCCACAGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3877	cg43142595	753	GGCCCCCTCCC CAGGCCACTCAC AC[T/C]CCTGGG GGCCACACAGAG GTGTCTGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3878	cg43142595	910	GGCGGGGCCCT TGACACTGAGGC TG[ap/C]TCCCG CCCCACACAGCA GCCTGGCGA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3879	cg43317253	3037	GGTCCTGTTTTT TAAAAA A[A/gap]CTGTTG TAGAAATTCCTTA TTTGA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P42568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2E-301	9

3880	cg43317253	3219	ATTAAATCTTTC TTTGGGGAATAA ATTCTTGGTTAT TCTGCCATAACA GAT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P42568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2E-301	9
3881	cg43917155	2849	CATACTGTGTCT GTGAGTTTCTTC A[A/G]TTACAAAT GGGCATTTAGTA TAGTT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
3882	cg43917155	3090	GATCTCTTTGCT GAATTAATGAGT T[C/A]TTAACATG TGGACCCCAACTG CCTGT	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
3883	cg43988371	4038	TTCTGTGACTAA TCACTGAACCTAG A[C/T]GAATGTTA AATTTTATGTC TGAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA34487 KIAA0767 PROTEIN - HOMO SAPIENS (HUMAN), 573 aa (fragment).	4.1E-301	22
3884	cg44916847	322	ATGTCAACCTGC CCGACCCTCTGG G[G/gap]TGAAC GGATGTGGACAC TGGAGGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
3885	cg44916847	496	TGTACATGTAAC ATGTGGCCATGC C[C/gap]AGGCAT CCCAGCATCTAT CCAGAAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
3886	cg44916847	507	CATGTGGCCATG CCCAGGCATCCC A[G/A]CATCTATC CTGAAGTCAGTG TAAAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SP TREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1

3887	cg43296397	575	GACACTGAGAG GTTTCCATCTGC AGTTCGCGCCAAG GGCTGCAGGTTG TGCCATG	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14134 ATAXIA-TELANGIECTASIA GROUP D- ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 588 aa.	7E-299	11
3888	cg43923376	1791	TGAGCAGGAGTT TGAACAGACCTG A[G/gap]CCCCAG GCACCGAGGAG GGTGCTGG	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P06865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N- ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
3889	cg43923376	1867	GGCTTCCACTGC ATCCTGGCCAGG G[G/gap]ACGGAG CCCCTTGCCTTC GTGCCCC	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P06865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N- ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
3890	cg43280144	514	TCAGAAATTTAA GCCTCCCCACCT G[A/C]AAGATTAC ATATATAAAACTC CCAC	A	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15320 MEA6 - HOMO SAPIENS (HUMAN), 804 aa.	7.4E-295	
3891	cg43255486	1897	CTCCACCCATCC AGTGGAATCTGG G[G/gap]CGCGGC CACAGGGGACG GGATGAGG	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.7E-294	17
3892	cg43998124	189	CCAACTCTGTGA ATTAGTATTAAG C[A/G]TAACATC ACATATGTAAAC GCGAG	A	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75174 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment).	4.7E-293	

3893	cg4398124	343	CTTGCAACAA GAATTACTAATT [A/C]AAGTGTA AATTTTGCAAAG GGAA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75174 KIA0689 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment).	4.7E-293	
3894	cg43981656	1171	TGAATATTGTAA ATATTACAATTG G[gap/G]TATTAG AAAGCCATGATG AATCCAG	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3895	cg43981656	1269	ACCAGGCTTACC ATGTTCTAAATA [C/T]TCAAGAAA TATCTTTAAAAA AAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3896	cg43981656	1294	TCAAGAAAATAT CTTTAAAAAAA [gap/A]GGACTGC AATTTAACAGTA ATCTGT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3897	cg43981656	1345	ATATCTTTAGCT GCCATTAAAAA A[G/A]AAAAAGA ACAACCAAAAC AATGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3898	cg43981656	809	TCAGGAAGAAA ATACTTTAAGA C[A/G]TGCCAATT TGAAAAGGCATC AAAGT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3899	cg43981656	820	AATACTTTAAAG ACATGCCAATTT G[A/T]AAAGGCAT CAAAGTAAAAA ATAAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10

3900	cg43981656	821	ATACTTTAAAGA CATGCCAATTTG A[A/T]AAGGCATC AAAGTAAAAAAA TAAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3901	cg43981656	833	CATGCCAATTTG AAAGGCATCAA A[G/A]TAAAAAA TAAAGCAAATG CTAAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3902	cg43981656	841	TTGAAAAGGCAT CAAAGTAAAAAA A[gap/A]TAAAG CAAATGCTAAAA ACTACTT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3903	cg43935280	272	AAAAATTTTTTT TTTTTTTTTTTTTC TTTCTGAGGAAG CCGAGAAACTTT AAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3904	cg43935280	444	ACCCAAGAGAG GCTGTGCGGCA GAG[C/gap]CCTG CACCCACAGGC CTTTGACAGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3905	cg43935280	446	CCAAGAGAGGCT GTGCGGCAGAG CC[C/gap]TGCAC CCACAGGCCTTT GACAGCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3906	cg43935280	530	TCACTCGACGCA CACCCGGTGCAT C[A/G]CACTGGC ACCTAAAGACAG GCCGTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5

3907	cg44003023	7608	AAGCAAAGAGGA AAACTTTGGAC A[G]TCGTAAAGA CTAGAAATAGTCT TTTAA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40200 T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN) - Homo sapiens (Human), 569 aa.	9.9E-291	3
3908	cg44128920	1686	CGAGTCACGCTC AATTGAACCCCTG C[C]TAGAGACG GGAAGAGGGGG GC[GTGCG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3909	cg44128920	1735	CGGCTGCTGCTT CTGGGCCACGG GG[A/G]GCCCCA GGACCTATGCAC TTTAATT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3910	cg44128920	1749	GGGCCACGGGG AGCCCCAGGAC CTA[T/G]GCACTT TATTTCTGACCC CGTGGCT	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3911	cg44128920	1914	CATGTTTACAT CTTTTCTTTCTGC [C/gap]GCTCGGC TCCGGCCATTT GTTTAA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3912	cg40886359	150	TCCCTCTCTGCA GAACCTCTCCTT T[A/gap]CCCCCC ACCCCCACCAC TGCCCCC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18627 LYMPHOCYTE ACTIVATION GENE-3 PROTEIN PRECURSOR (LAG-3) (FDC PROTEIN) - Homo sapiens (Human), 525 aa.	1.6E-290 (12p13.3 2)	12
3913	cg42742569	3325	AAAAATGGATAC CAAAAGCACTAT T[A/T]GTCACCCA AGCTAAGTGGAA TAGCT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15091 HYPOTHETICAL PROTEIN KIAA0391 - Homo sapiens (Human), 567 aa.	2.5E-290	

3914	cg43949262	81	GTAGAGGCACAC ATTGGACTCTGA C[G/A]ATTCCCCT TGCAGCAGACAT TTGTG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
3915	cg43995003	1944	TTGCCATCAGTG ATCTCACTAAAA A[gap/A]TATACA GCTACTTCCAG CTAATCT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
3916	cg43926814	360	AATAATTCAAAG TAGAATTTTCTAT [C/gap]CCCCCCC ATTCTCCAGTA ATAAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
3917	cg43926814	367	CAAAGTAGAATT TTCTATCCCCC C[C/gap]ATTCTC CAGTAAATAAAA GTAGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
3918	cg43931799	255	CCTATGTCGGC CGGGCCCTCCG GA[G/gap]GCTGA GGGGGGAACAG CGCGGCCAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83001 KIAA1049 PROTEIN - HOMO SAPIENS (HUMAN), 550 aa (fragment).	7.6E-289	22
3919	cg43055270	2134	AAATATCAGAGT AAACCTTTCTAG A[A/gap]CAGTAC AAGGTTAAAGAG GTGAGGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13884 BETA1-SYNTROPHIN - HOMO SAPIENS (HUMAN), 538 aa.	2.2E-288	8
3920	cg43055270	2305	GCCGAATAGTTG AGAAATGGACAT T[C/T]TTACCTAC TCCTCCTAGCCC CCTAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13884 BETA1-SYNTROPHIN - HOMO SAPIENS (HUMAN), 538 aa.	2.2E-288	8

3921	cg43969619	2350	TCACACACATGT CATCAGGGCCCT C[<i>gap</i> /C]TGCACT CCACATGATGAG GTCAGAC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00973 BETA-1,4 N- ACETYL GALACTOSAMINYLTRANSFER ASE (EC 2.4.1.92) (N- ACETYLNEURAMINYL)- GALACTOSYLGLUCOSYL CERAMIDE) (GM2/GD2 SYNTHASE) (GALNAC-T) - Homo sapiens (Human), 533 aa.	2.5E-287	12
3922	cg43249686	1818	CCTCGCCCCCG CCCCCACC GGG TGA[A/G]AGTGTC GTCTCCGCTTCT CTCGGTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q01101 ZINC FINGER PROTEIN IA-1 (INSULINOMA-ASSOCIATED PROTEIN 1) - Homo sapiens (Human), 510 aa.	1.4E-286	20
3923	cg43128343	1678	CACCTCTCTCCT CCACTCTGAGCC C[C/ <i>gap</i>]CTGACC TTCCAAACCTCA ATAAACT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3924	cg43128343	1679	ACTTCTCTCCTC CACTCTGAGCCC C[C/ <i>gap</i>]TGACCT TCCAAACCTCAA TAAACTA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3925	cg43128343	1921	CCTCTCCCGCC GCTGCCATAACC C[C/ <i>gap</i>]AATGTC TGGGCCCTGCG CAGCCCCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3926	cg43968641	993	GTAATATAGGTG TGCACAAAAGG G[A/ <i>gap</i>]AAACAC CCTATTTTCATTT TCAATT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (K1AA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3927	cg43968641	265	AAAGTTAATTTCTT TTTCTAATTTCTT T/G]CTCATACAC CTGAGTTATTTA AAAA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (K1AA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8

3928	cg43968641	508	AGGACCAGTGAA GAATAGCTCCAA T[G/T]TGACACTA GACACAAAATAC CTTTG	G	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3929	cg43968641	555	TTTGGGGGCAAA GACAGGGGCAAA GC[T/C]GTGTGC CGGTGGTGAAGT GAGAAAG	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3930	cg43968641	825	TTTTGACTCATG AGGCAAAGCTGT T[G/gap]CCACAA TCAGTGGCGACT CAAGTCA	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3931	cg43061073	119	AGCTATTTTAA CTAATGTAACCA gap/TTTTTTTTAA AAAAAGAAACTA TTTA	gap	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14117 DIHYDROXYRIMIDINASE (EC 3.5.2.2) (DHPASE) (HYDANTOINASE) (DHP) - Homo sapiens (Human), 519 aa.	8.6E-285	8
3932	cg43969352	296	GTTACAAATTTAA AAAAAGAATACA A/TJCAGAAATAAT TAATAACTTTAAGT GA	A	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60317 KIAA0571 PROTEIN - HOMO SAPIENS (HUMAN), 638 aa.	1.7E-284	11
3933	cg42709686	2604	GACAGTGATTAA TGGTTCTGTTGG C[C/gap]AAGGCT TCTCCCTGTCGG TGAAGGA	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYL GALACTOSAMINE-4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa.	4.3E-283	
3934	cg43943490	2217	TGCCCTGGGGTCA TGAAAGGCAGAG C[C/gap]TGCAGC ATGCAGTATGGC AGCCGGG	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:CAA10276 ARIADNE-2 PROTEIN (ARI2) - HOMO SAPIENS (HUMAN), 493 aa.	1.3E-281	3

3935	cg43948325	272	GATCCTAGCCTT GGGCCAGGGA TG[G/gap]CACAG GCTGAATGGAAG GGCTGGGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3936	cg43946325	65	GCTCTTTTTTTT TTTTTTTTTTT[A /TJAGGCTTCTGG TAGGGACATTTT ATT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3937	cg43946325	66	CTCTTTTTTTTT TTTTTTTTTTT[A /TJGGCTTCTGGT AGGGACATTTTA TTT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3938	cg44010409	223	CTCCAAATCCCA CCCAGTGCAAG TTC/TJGGGAA GGTAGGGTGTG AGCIGCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
3939	cg44010409	239	AGTGCAAGTCTG GGGAAGGTAGG GT[G/TJGAGCTG CTGCTGAAGGCT GTCCCC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
3940	cg43931431	1146	CTTCTTGTGAAC CAGGGATACACA C/A/TJTCAGACAT TGGCAAACAGTA GTACA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14154 HYPOTHETICAL PROTEIN KIA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5
3941	cg43931431	320	ACATAAAATTGC AGTATGAACTGA T[G/TJGACAAGAA CTCTGGGCCAG GAGTCA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14154 HYPOTHETICAL PROTEIN KIA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5

3942	cg43930921	329	CCGGAGCTCGC CTTGGTGCTGGG CA[C/gap]CAGTG GGCCCTGCCA GGCCTGTCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3943	cg43930921	330	CGGAGCTCGCC TTGGTGCTGGG AC[C/gap]AGTGG GCCCTGCCAG GCCTGTCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3944	cg43930921	340	CTTGGTGCTGGC CACCAGTGGC CC[C/gap]TGCCA GGCCTGTCCTCT CCTTTTG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3945	cg43930921	344	GTGCTGGGCAC CAGTGGGCCCC TGC[C/gap]AGGC CTGTCCTCTCCT TTTTGAGCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3946	cg44931278	33	TTTTTTTTTTT TTTTTTTTTTTAA TTACTACAAAAT AAGCACTTTACT AA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
3947	cg44931278	34	TTTTTTTTTTT TTTTTTTTTTTAA TTCTACAAAATA AGCACTTTACTA AC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
3948	cg43998884	2376	GGCAATGCCCGT CCTCTGGCTTGG GTTCTAATTCTT CGGTGACACTG GCGTTG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51688 N-SULPHOGLUCOSAMINE SULPHOHYDROLASE PRECURSOR (EC 3.10.1.1) (SULFOGLUCOSAMINE SULFAMIDASE) (SULPHAMIDASE) - Homo sapiens (Human), 502 aa.	1.1E-279	17

3949	cg43998884	2629	CCATACTGGGGT GGGCTGGAGGA GG[ap/C]CACAG GCCAGCTATTGT AAAAGCTT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51688 N-SULPHOGLUCOSAMINE SULPHOHYDROLASE PRECURSOR (EC 3.10.1.1) (SULFOGLUCOSAMINE SULFAMIDASE) (SULPHAMIDASE) - Homo sapiens (Human), 502 aa.	1.1E-279	17
3950	cg43958498	2184	GTCTGGCAATTT TGATTTCTGAAC TTC/TTGTGCTAC CTCAGAGGCCA GCTTCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75688 2'-5' OLIGOADENYLATE SYNTHETASE (P59OAS) - HOMO SAPIENS (HUMAN), 514 aa.	2.2E-279	12
3951	cg44001088	178	TCCACCACAGTA AACATACAAAGT TTT/AJTGTGCAAG AGAAAAGGTCAT ATGGA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
3952	cg44001088	179	CCACCACAGTAA AACATACAAAGT TTT/AJTGTGCAAG GAAAAGGTCATA TGGAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
3953	cg44031765	1170	ATTCACCTCAAG TCAGGTGAGACC C[A/G]TACATCAT GGTCCCCCACTC ACAAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.6E-279	22
3954	cg44022026	1864	TCCTTCTGGGGA AATAAATGAGTG T[C/gap]TGTTCAT GCAGCTAAAAA AAAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43292 HGAA1 - HOMO SAPIENS (HUMAN), 621 aa.	1.2E-278	8

3955	cg44002920	142	AGCACAGTTCAA AGTCATTAAATC CIG/AJGTACAAA GAAATGGCTCTC ACTTC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3956	cg44002920	171	AAAGAAATGGC TCTCACTTCCTG G[gap/G]ATTGGC ACCAGACATCCT ACCAGCT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3957	cg44002920	176	AAATGGCTCTCA CTTCCTGGATTG G[gap/G]CACCAG ACATCCTACCAG CTGCAAT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3958	cg43987191	1808	ACTCAAGACTTA TGGAACAGGGAT G[gap]CGAGGC CTCTCTCAGGAG CAGGGGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P19235 ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R) - Homo sapiens (Human), 508 aa.	8.5E-278	19 (19p13.3)

3958	cg43984386	281	ACGAGCTCTCGC CCACTCGCCGG AG[G/gap]AGACG GCCCTGGACTCC CAACCCCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00401 N-WASP - HOMO SAPIENS (HUMAN), 505 aa.	5.9E-277	
3960	cg439863979	502	GATAGAAGGGA GCAGCATCAGAC AC[A/T]TTTTTC AGGCCCTGGTTT CATGTG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3961	cg439863979	503	ATAGAAGGAGC AGCATCAGACAC A[T/A]TTTTTCAG GCCCTGGTTTCA TGTGC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3962	cg439863979	504	TAGAAGGAGCA GCATCAGACACA T[T/A]TTTTTCAGG CCCTGGTTTCAT GTGCC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3963	cg439863979	505	AGAAGGAGGCA GCATCAGACACA T[T/A]TTTTTCAGG CCCTGGTTTCAT GTGCC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3964	cg439863979	582	TATTCACCTAAC AATTTTTTTTTT T/gap]GTAAGGC TACTTTTGTAGC TTTT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3965	cg439863979	583	ATTCACCTAAC AATTTTTTTTTT T/gap]GTAAGGCT ACTTTGTAGCT TTTTG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14

3966	cg43963979	702	CAATTCAATTCG TTGCCCTTTTGAG G[C/gap]CACTGT GGCCATGAACAG CCCTGCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3967	cg43963979	712	CGTTGCCCTTTTG AGGCCACTGTG GC[C/gap]ATGAA CAGCCCTGCTAC TATCTGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3968	cg43988211	104	CAATTCCAGAGG GGCCTGGCTGT GG[C/gap]CAAAG CTGTGCCAAACG GTGGGAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3969	cg43988211	105	AATTCCAGAGG GCCTGGCTGTG GC[C/gap]AAAGC TGTGCCAAACG TTGGGATC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3970	cg43988211	182	TGAGACCATGGG CGAGGCTCCCC AC[G/A]CTATCTC CACCAACACAGT CATGAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3971	cg43988211	302	CTCATCCTGAGA GGCATTGGGTG CC[C/gap]ACTCA CTGGCTGGATGC TGGGCTGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3972	cg42935995	134	TGACCTTGCACC ATAATTATGGT A[G/A]TTTCTAGG TTAGAAGATACC TTAGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1E-274	

3973	cg42935995	484	ACTGGGTTAGCT GGATTTTGTCTT T[G/gap]AGCTTT GAGAAGGCCTA GTTCTCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1E-274	
3974	cg43929467	1829	AAAGACAAGGA CTGCTCTAGTGT T[G/C]AGGGATG TAGCTCAGCTTT TGGGCT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPLICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3975	cg43929467	2628	CATCTCAAAAA AAAAAAAAGCGG G[T/gap]GGGGGG GAGTTGGGCTGT GTTGGAA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPLICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3976	cg43929467	2733	TTGCTAGGTCAG AATGAGAGACTG G[T/A]GGGTCTGT CTACCTGTTTCT TCTAC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPLICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3977	cg43947753	3093	TCAATGGTGTAG CAACGTGGGTTT A[C/gap]CCAAAA CACCTTTTATAC AAAAGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.1E-274	12
3978	cg43947753	3095	ATTGGTGTAGCA ACGTGGGTTTAC C[C/gap]AAAAACA CCTTTTATACAA AAGACA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.1E-274	12

3979	cg43994885	55	TTTTTTTTTT TTTTTTTTTTT CJTTTGTTGACA AATGTTGTTATT G	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43147 KIAA0397 - HOMO SAPIENS (HUMAN), 488 aa.	1.2E-272	17
3980	cg43333012	406	TCAGCTCCCTCT TCTTGGTATTAC A[A/G]AATTTCAT ACTTATCCACTA GAAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.5E-272	11 (11q23.3)
3981	cg43328330	1629	CTCTCGCCTTCC AGCAATTCCCG C[A/gap]GTGCTA CAAATGGGAAGT CAGAGAC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16222 UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) (ANTIGEN X) (AGX) (AGX-1) (SPERM- ASSOCIATED ANTIGEN 2) - Homo sapiens (Human), 505 aa.	5.5E-271	1
3982	cg43970492	169	TCTATAAGATGT ATCTCCCCAAAG A[T/G]CACAATTAA CTCCTCAAGTCA ACATC	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3983	cg43970492	201	AACTCCTCAAGT CAACATCTGCCT A[T/C]CCCCAACT TCCCCTTTTTTC CTCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3984	cg43970492	391	AGCATTTGATAT GTGCACCCAGCT A[G/A]TTAGGCAT GAAACAGGGGC ACAGGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3985	cg43958878	1627	GAACGCCGAACGTG TGCCATGGGAG CG[C/gap]CCGCA GGGGAGGAGT CCTTGCAGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9

3986	cg43958878	1641	CCATGGGAGCG CCCGCAGGGG AGG[A/G]GTCCTT GCAGTTGGTGCC TACGGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
3987	cg43958878	1659	GGGAGGAGTC CTTGCAGTTGGT GC[C/gap]TACGG AGCCCGTGCCCT CCGGAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-268	9
3988	cg43926574	2586	AAATTAAATTGG ATATTAAATTGTA [A/T]AGACATCAT TTATTAAATTTAA ACT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.1E-268	7
3989	cg43926574	3018	TATTAACCTGCC CTTTACACAAA T[C/T]ACACAAA AGTTTCCTGATC TC[GT]	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.1E-268	7
3990	cg43927211	29	TTTTTTTTTTTT TTTTTTTTTTTAA TTGCCAGAGGTG AGATCTTTATTG ACT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15057 HYPOTHETICAL PROTEIN KIAA0041 - Homo sapiens (Human), 632 aa (fragment).	1.3E-268	3
3991	cg43951018	86	TTTTTTTTTTTT TTTTTTTTTTTTT[ATTGCTTCACTG CTTTATTTTGAA A	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16851 UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE 2 (EC 2.7.7.9) (UDP- GLUCOSE PYROPHOSPHORYLASE 2) (UDPGP 2) (UGPASE 2) - Homo sapiens (Human), 507 aa.	1.8E-268	2

3992	cg43326821	251	GGCTAACCTTGC CGCGGGCCGAG CC[C/gap]TGCCT CGCCATGGACCA GGACTATG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75869 R33374_1 - HOMO SAPIENS (HUMAN), 493 aa.	6.1E-268	
3993	cg43949042	268	GGAGAGGTGGG CTCTGGCAGCG GGT[G/]TGAGG TGGCAGTGAGAA GCCAGGCC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa.	6.1E-268	
3994	cg44022853	30	TTTTTTTTTTTT TTTTTTTTTTTTT/ AJAGCAATTGTT TATGTTTAATTTA C	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12891 LYSOSOMAL HYALURONIDASE (PH-20 HOMOLOG) (LUCA-2) (LUCA2) - HOMO SAPIENS (HUMAN), 473 aa.	2.1E-267	3
3995	cg43031103	742	CTTCAAAGTAGC CTGCTGGGAGC CTT[A/]GATCATC AGAGGATGTTCA TCAGAG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.3E-266	
3996	cg42919561	363	GGTGACTCTGGA GTTCTTGAGGGG C[G/]CCGTGCC CTGACTGTGGAT GTGAGC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00515 LADININ - HOMO SAPIENS (HUMAN), 517 aa.	7.2E-265	
3997	cg43313186	2105	GTTTGTTTTTCC CCTCAGCCCTGC C[A/C]CCGTGGG GAGTCTGGTTTT TCTCTT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265 (20q11.2)	20
3998	cg43313186	2196	GCCTGTGAGCAC ACAGGCAGCCC GG[C/A]CCAAAAA AAAAA AAAAA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265 (20q11.2)	20

3999	cg43313186	2197	CCTGTGAGCAC CAGGCAGCCCG GC[C/A]CAAAAA AAAAA AAAAA	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)
4000	cg43942622	1782	GGGAGCGGCAA GGCAGGGCAGG CGG[C/gap]CCCA GGAACCTGCCCA GTGCACAGG	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4001	cg43942622	297	CATAAAATATC ACCTCAACTCAT C[C/G]CTGACAC ACGCATGTCCTC CCAAGG	C	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4002	cg43942622	41	TTTTTTTTTTT TTTTTTTTTTT[C TTTGTCACAAA AATGATACATTTA TT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4003	cg43942622	582	GAAAGCCACCCA TAAGCCCCAGCT A[gap/G]TCTCCA GGAGAAAGCCC AGAAAGGT	gap	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4004	cg43934408	326	CACACCAGGCC CTGCTCTGCCGC AG[G/gap]AAAAT GGATTCCAGGC CACAGAGC	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4005	cg43934408	369	CACAGAGCTGTC AGGCCTTTGACT TTT[C]GCAGAGAC CAAGCACCCAG AGGCT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22

4006	cg43934408	715	ACCCCTTCTCCTA TGCCTCCAGG GT[<i>gap</i>]/TACTGT GTCTCAAAGAAC CTCTTCCC	<i>gap</i>	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4007	cg43934408	729	GCCTCCAGGG TACTGTGTCTCA AA[G/ <i>gap</i>]AACCT CTTCCCTCCTGG GAACCAT	G <i>gap</i>	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4008	cg43934408	729	CCTCCCAGGTA CTGTGTCTCAAA G[<i>gap</i> /G]AACCTC TTCCCTCCTGG AACCATT	<i>gap</i>	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4009	cg43934408	745	TGTCTCAAAGAA CCTCTTCCCTCC T[G/ <i>gap</i>]GGAACC ATTTCCACTCC TCTTTCT	G <i>gap</i>	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4010	cg43934408	747	TCTCAAAGAAC TCTTCCCTCCTG G[G/ <i>gap</i>]AACCAT TTCCACTCCTC TTTCTTT	G <i>gap</i>	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4011	cg43980328	183	AAGACTCATGAA GTATAATCTCTC ATT/CJCTTCTTTC TCTTCCCTCCTGC CCAAG	T <i>gap</i>	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4012	cg43980328	207	ATCTTCTTCTCT TTCCCTTGCCCA [A/G]GCCCTAAGT TAGGGTTCCCAT CCAT	A <i>gap</i>	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10

4013	cg43980328	273	GGTCAGGTGGC ATTGCTATCTCT G[A/G]GATTCCCT GCCCATGAAAGC CACAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4014	cg43980328	385	AAACTGTGTTT AAAACAAACA A[A/C]CCCAACCAC TGTGAAATATTTA TTTT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4015	cg43980328	455	TGATTAAACCAG TGCAGAAAAATA C[C/T]AAGTACAT TGGGTGAACGAT GAGCT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4016	cg43980328	469	CAGAAAAATACC AAGTACATTGGG T[G/A]AACGATGA GCTAGCTGTTCT AGTAT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4017	cg43980328	523	CTTTTGTATCC AGTTAAGACCAT C[G]AGCATATAC AACATCATCACT AACT	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4018	cg43980328	535	CAGTTAAGACCA TCAGCATATACA A[C/T]ATCATCAC TAACTCAACAAT GTAGC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4019	cg43980328	572	CTCAACAATGTA GCTGCAGGGTAA C[A/C]TGTGGATA CCCTGTGTGCTC TACTG	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10

4020	cg43056973	129	GAGTGCCTCAGC AGCTTCTCCACA T[G/C]CTCTTCAG TCCCCAAAGTTG GAGAA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20711 AROMATIC-L-AMINO-ACID DECARBOXYLASE (EC 4.1.1.28) (DOPA DECARBOXYLASE) (DDC) - Homo sapiens (Human), 480 aa.	5.2E-262	7 (7p11)
4021	cg43922182	2206	CCTCCTTTTTCG GTTTCCTCTTGT C[gap/T]TTTTTTT TTTATTTTATTATA CGAAG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
4022	cg43922182	2216	CGGTTTCCTCTT GTCTTTTTTTTTTT gap/T]ATTTTATT ACGAAGTTTCAT TCTT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
4023	cg44013054	271	TACACACACACA CACACACACACA C[Agap]CTTACA CACATGCACACA TCCTAAG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15391 B-LYMPHOCYTE ANTIGEN CD19 PRECURSOR (B-LYMPHOCYTE SURFACE ANTIGEN B4) (LEU-12) (DIFFERENTIATION ANTIGEN CD19) - Homo sapiens (Human), 556 aa.	3.3E-261 (16p11.2)	16
4024	cg40296063	103	AGCCCTATGGT GGGATGGCAC CG[Cgap]CCTAC CGCCGAGAGAG TTGAAGCTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O94810 REGULATOR OF G-PROTEIN SIGNALING 11 (RGS11) - Homo sapiens (Human), 467 aa.	3.3E-261	
4025	cg43971058	1035	CATTAGTAACAT AACTCAACATCC TT[C]AATTGGT ATAGATGTGACA CATT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60455 POLYADENYLATE BINDING PROTEIN- INTERACTING PROTEIN-1 - HOMO SAPIENS (HUMAN), 480 aa.	3.7E-261	
4026	cg27359628	100	TTCCCATGCCCC TCCCACGGTCAG C[A/T]CCCCGATG GCCTGGGTGAG GGCTGA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	

4027	cg27359828	123	GCACCCCGATG GCCTGGGTGAG GGC(T/A)GATAG GCTGCTCTGACA CCATGGGG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	
4028	cg27359828	125	ACCCCGATGGC CTGGGTGAGGG CTG(A/G)TAGGCT GCTCTGACACCA TGGGGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	
4029	cg27359828	76	ACAAGGGGAATA AAGTGGGACCCT TT(C)CCCATGCC CCTCCACACGGTC AGCAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	
4030	cg43916582	242	AACAGTTATCTC AGAGGGTCAACC A(C/T)ACAATGTC ATACAGAGACGC TGGTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75475 LENS EPITHELIUM-DERIVED GROWTH FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	2.3E-259	
4031	cg43980777	364	TCTTTTGAGGCT TTACAATTACAAA T(C)GACAATGAT GTCAACCCATT ATCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
4032	cg43075307	103	GTATAGACCAAC ACTGTCCAACCA A(T/C)AGAACTTT CTGCCATGATGG CATAT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60623 DIPHTHAMIDE BIOSYNTHESIS PROTEIN-2 - HOMO SAPIENS (HUMAN), 489 aa.	1.3E-258	
4033	cg43075307	90	GAAATAAGAGTC AGTATAGACCAA C(A/G)CTGTCCAA CCAATAGAACTT TCTGC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60623 DIPHTHAMIDE BIOSYNTHESIS PROTEIN-2 - HOMO SAPIENS (HUMAN), 489 aa.	1.3E-258	

4034	cg43258841	140	GAAATACATTCT TTTCACATGATA A[T/C]GTTTTCGC CCTTATTTATGG TCITT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q14449 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.7E-258	
4035	cg43999171	48	TTTTTTTTTTTT TTTTTTTTTTTT[A /T]TTACCAAAACC CAACATTTATTG AGA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	3.8E-257	6
4036	cg43255855	1805	TAAGCTAAAAAA CAGGCTGAAAAA G[G/A]AATTCCCA AAGAGAGTTAAC AAAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43148 KIAA0398 - HOMO SAPIENS (HUMAN), 476 aa.	1E-256	18
4037	cg43918866	1419	CCTCAGCCTCCC AAGTAACTGGGA A[T/C]ACAGGTAC CCACACCCACAC CCAGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15519 CASPER - HOMO SAPIENS (HUMAN), 480 aa.	3.5E-256	2
4038	cg43963125	1099	TAGAGGAAACT GTAATATAAATG C[gap/A]TTTTTTT TTTTTGCITTTA AAGGA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20
4039	cg43963125	403	GGGTCTAGTACA GAATAGACAGTA A[A/T]TCTTTGTT GAAAGAACTCTT TTATT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20
4040	cg43963125	563	TCAAGACTTTGC TCACTAGTCAGA C[C/T]GTAATTTT TAGAAGGAATAG GAGCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20

4041	cg43949732	1699	TGAAGAACTGAA GGAGTCCTGCAT C[T/gap]TTTTTTT TTTATCTGCTTCT GTTTA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4042	cg43949732	1709	AAGAGTCCTGC ATCTTTTTTTTTT T/gap]ATCTGCTT CTGTTTAAAG CCAAC	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4043	cg43949732	1709	AGGAGTCCTGCA TCTTTTTTTTTTT gap/T]ATCTGCTT CTGTTTAAAG CCAAC	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4044	cg43949732	1828	GTTTGTAGTTCCTT ACAAACAGGGT [G/gap]GGGGG GGAAGGCGTG CAAAACT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)

4045	cg43949732	1836	TCCTTACAAACA GGGTTGGGGG GG[G/gap]AAGGG CGTGCAAAACT AACATTGA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4046	cg43274303	746	ATTGGGACCACC GGCTGGTGGTG CA[G/T]GTCCAGA ACATTCTGGGGG CTGCAG	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15175 PARANEOPLASTIC ANTIGEN - HOMO SAPIENS (HUMAN), 535 aa (fragment).	7.6E-254	17
4047	cg43943285	1459	ATTGACCCACAA AGTTTCAGAAAT TT[C/T]CTGAAAG TTTCCTCCTTTT TCTC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04469 FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA) - Homo sapiens (Human), 453 aa.	4.2E-253	4
4048	cg43971614	736	CCTTTATCAAAA AAAAATTCTATTC [C/T]TTTATTCA GTTTTTAAACATA CCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.3E-253	5
4049	cg43040311	560	ATGGAATAGATT TTGCCAAACCTC A[C/T]TGCATATT TACAGTATTTTAA GCAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q00425 PUTATIVE RAS INHIBITOR - HOMO SAPIENS (HUMAN), 471 aa (fragment).	5.3E-253	20
4050	cg43040311	84	TTATGTGCAAAA TTCCATTAAAAA [A/gap]TCATTTAC AAAAGTACAACA CAGTA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q00425 PUTATIVE RAS INHIBITOR - HOMO SAPIENS (HUMAN), 471 aa (fragment).	5.3E-253	20
4051	cg44034555	386	GAAGTGAGGGC CCAAAATAGGGA GT[G/T]TGGGTG ATGAGGGTGGA GTTCAAAT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.8E-252	1

4052	cg43962954	103	CTGAGTGTACG GGCCAGGGA AG[G/gap]CTGGA GCCAAACCAAG TCTCTGG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4053	cg43962954	110	TCACGGGGCCA GGGAAGGCTG GAG[C/gap]CAAA ACCAAGTCTCTG GGGGCGGGG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4054	cg43962954	111	CACGGGGCCAG GGGAAGGCTGG AGC[C/gap]AAAA CCAAGTCTCTGG GGGGCGGGG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4055	cg43962954	211	TAGAGACGGA GAAGTCCAGTGT GC[T/C]GTTCCAC CTCCCTCCAAGT CCCAAG	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4056	cg43962954	328	AGGCCGGCGTG GTCAGGTCGGG GGC[G/A]GGAGG GCCGGGCCTGG CTCTGTCTC	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4057	cg43962064	213	CTGTCAACCTTT TATTGGAGTGG A[A/gap]CACATG AGGTTCAAGCTCG TGCCGGG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20

4058	cg43962064	305	ACACTGACGCCA CACTGAGCAGGA T[G/gap]CACGGC CCGGGGCTCAC ACTGTCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4059	cg43962064	420	GGGACTGTGGC TCAGCTGACCCG TG[G/gap]CACAG CTGCACCTAAGA CATGGCCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4060	cg43962064	461	GACATGGCCCTGA GCTAGCGGGA AC[A/G]GCTCACA GTAGCGATACAT TCACAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4061	cg43962064	487	GCTCACAGTAGC GATACATTACA G[G/gap]ACACAG TTGGTGTCAGAG AAAGGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4062	cg43962064	620	CAGCAGCTCATG CCCGGCATCCG CC[C/gap]ATGCT GGGAGACTCCCT GAAAGGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4063	cg43962064	647	TGCTGGGAGACT CCCTGAAAGGTG G[G/gap]CACCTG CCGTCATGAGG AGGTGTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4064	cg43924291	1180	ATATGCTTTAAG ACGCTTTCGTCC A[T/gap]TTCATAC CGCTCATTCTCA AGCGCC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	

4065	cg43924291	1182	ATGCTTTAAGAC GCTTTCGTCCAT TT[<i>gap</i>]CATACC GCTCAATCTCAA GCGCCAC	T	<i>gap</i>				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	
4066	cg43924291	1182	TGCTTTAAGACG CTTTCGTCCATT T[<i>gap</i>]TCATACC GCTCAATCTCAA GCGCCAC	<i>gap</i>	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	
4067	cg42300443	318	TGGTGGAGCTTT GGAGCTGAGGC GG[G/ <i>gap</i>]CAAGG CCTCTCAGATGG TCACGCTG	G	<i>gap</i>				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55249 ARACHIDONATE 12-LIPOXYGENASE, EPIDERMAL-TYPE (EC 1.13.11.31) (12- LOX) - Mus musculus (Mouse), 662 aa.	6.5E-249	
4068	cg44027341	2085	ATTGTACCTAAG TAAATTTCTTTA [A/G]GTCAGAAG CCCATTAAATA GTTAC	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00439 PHENYLALANINE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4- MONOOXYGENASE) - Homo sapiens (Human), 452 aa.	1.6E-246	12
4069	cg43996564	127	CAAACTCAGTAG GAGTGCAAGGG CT[G/A]TACCCCC GGAGCTAGACA GCCCTGGG	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
4070	cg43996564	402	ACCTTGCCAAGT AGATGCATATGG A[<i>gap</i> /G]CATGGA ATGAATGGTGTC TGCTGTG	<i>gap</i>	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
4071	cg43996564	405	CTTGCCAAGTAG ATGCATATGGAC A[T/ <i>gap</i>]GGAATG AATGGTGTCTGC TGTGGT	T	<i>gap</i>				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3

4072	cg43980318	1501	TGAGAGGGAGG GGAAAAGACITTT CTT[<i>gap</i>]AAATAT TTCATTTATGAC CTGCAAA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4073	cg43980318	1529	ATATTTCAATTTAT GACCTGCAAAATTI T/CJAAGAATAAA GACACTGAAGTA AGTT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4074	cg43980318	1561	AAGACACTGAAG TAAGTTTGAAGC C[<i>gap</i>]/TCTACAG TTGTTTCCAGTC TTTTCAG	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4075	cg43980318	1700	CTCTCATGGTGC CACGTTTTTTTTT [<i>gap</i>]/TCAATGTTT AGTAATAGTATA ATCCA	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4076	cg43980318	1700	CTCTCATGGTGC CACGTTTTTTTTT [<i>gap</i>]/TCAATGTTT AGTAATAGTATA ATCCA	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4077	cg43965612	131	CAGTAGCTGAAG GGCCCTGAGCA GA[G/ <i>gap</i>]CTGGT GCTGGGAGGGG CCGGCATGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O43236 BRAIN PROTEIN H5 (PEANUT-LIKE PROTEIN 2) - Homo sapiens (Human), 478 aa.	6.9E-244	17
4078	cg43920589	1996	TTTATATCACTGT TTTTCACTGTTT T/CJTGTGGACAA ATAATGGTTGCT TTGC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18

4079	cg43920589	2080	ACCTACCCAAA GCTGTAGTCACA C[G/A]TCCTAAAG GCCAAGCAAACC CACCG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18
4080	cg43920589	2104	CGTCCTAAAGGC CAAGCAAACCCA C[C/T]GGGATGG TGGGGGGTCTT GGAGCCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18
4081	cg43985156	167	GGTGACGGGCT CCGGGCTCCCG AGG[T/gap]GAAG AGCATCGGGG CTGAGGGGATG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.8E-243	17
4082	cg43985156	1811	CTTCTCTCTCTG AAAAAACTAATT [T/A]AAATTTGCT TTTCTTTTITTTA ACT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.8E-243	17
4083	cg43315249	146	CATTAACTCCC CAGGTTAAACAC C[T/C]TGTAATT ACCTTGAAGCTC TTTAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45712 HYPOTHETICAL 63.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 564 aa (fragment).	2.7E-242	17
4084	cg43315249	303	ACTTCAGAGAAA AATCCCAGATGA C[G/A]GCACTGG ACAGGTTATAAA GAGTTG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45712 HYPOTHETICAL 63.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 564 aa (fragment).	2.7E-242	17
4085	cg43292372	786	AGCCCTTGGGAA GCCCATCTCAGG G[G/A]GATCCAG GAGCAGATGGC CAAAAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14740 SMAD7 PROTEIN - HOMO SAPIENS (HUMAN), 426 aa.	1.5E-241	

4086	cg44021361	109	TTATTTGGAAGG GCAGAGTCCAAC C[C/A]ACCCAG GTCCTGAGGGTA GACTCA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa.	6.3E-241	3
4087	cg43917689	1962	CAGGGCCAAGA GCGCCTCACAAA GG[G/gap]CTGCT GCCTTGAACCTG GCCTGGGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa.	3.5E-240	3
4088	cg43976131	1814	GCGGAATGGA AGCAGTTTATGG AGT[C]TAAGTGG GGCTCTGCTATT TCCCC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4089	cg43976131	1888	TTCCAGGGCAGA GTGAGGGGCAG AC[G/A]GGATGA GGCTCTTCTGTA AAGTCCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4090	cg43976131	199	CGAGGCAGGGT CCCCAAGTGA GGC[G/A]GGGCG GGACGTGAGAG GATGGGGC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4091	cg43928134	204	ATTCAAATGGAA ACAGACAATTTA A[C/A]AAAGAGAA GTAAAAAAATTTA TTGC	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4092	cg43928134	208	AAATGGAAACAG ACAATTTAACAA A[G/A]AGAAGTAA AAAAATTTATTGC AGTA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8

4093	cg43928134	210	ATGGAACAGAC AATTTAACAAG A[G/A]AAGTAAA AAATTTATTGCA GTATT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4094	cg43928134	213	GAAACAGACAAT TTAACAAAAGAGA A[G/A]TAAAAAA TTTATTGCAGTAT TCGC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4095	cg43981846	1430	AATATGTGTTGT ATGCTCTTTTTCG [T/gap]TTTTTTTT TAAAAAAAAGAA TAACT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD33924 LOMP PROTEIN - HOMO SAPIENS (HUMAN), 797 aa.	1.2E-239	13
4096	cg43981846	1439	TGTATGCTTTTT TGCTTTTTTTTTT /gap]AAAAAAAAG AATAACTTTTTT GCC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD33924 LOMP PROTEIN - HOMO SAPIENS (HUMAN), 797 aa.	1.2E-239	13
4097	cg43950854	1462	ACTGAAGAACCA TAAAGAAAAGAT G[A/gap]AAAAAA AAACTATCAAAG AAAGATG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
4098	cg43950854	1471	CCATAAGAAAA GATGAAAAAAA A[A/gap]CTATCAA AGAAAGATGAAA TAATAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
4099	cg42750818	85	GCCAGGTTATAC CCTAGGACGGT GT[C/gap]CTTCC CTCCCTCCTAGG GTGGGAGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	2.9E-238	1

4100	cg43922856	1099	AGTTGAACGTGC CAAAGAGATACC ATTCTCAGTTGG ATTTCTAGGGT CAACA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2E-237	12 (12q22)
4101	cg43923262	1651	GCTAATGCCGAT CATCTTTGCCAC C[A/G]CCTGGGG AGAGCCTGCTTG GGAATG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15527 8-OXOGUANINE DNA GLYCOSYLASE 1 (EC 3.2.2.-) - HOMO SAPIENS (HUMAN), 424 aa.	4.8E-236	3
4102	cg41637661	54	TGGGCCGCCAG ACTCGGGAGAG GCT[C/G]CGTCTT GTGCAAGGGTC CTGTGGGC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O43913 ORIGIN RECOGNITION COMPLEX SUBUNIT 5 - Homo sapiens (Human), 435 aa.	6.1E-236	
4103	cg43932322	52	TCTTTTTTTTTT TTTTTTTTTTTTTG TTATTTTTTTTTG TTTTTCCAATTT A	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88941 GLYCOPROTEIN PROCESSING GLUCOSIDASE I - RATTUS NORVEGICUS (RAT), 834 aa.	6.5E-236	2
4104	cg43933215	299	GTCCTCCCCAGC CAAGTCAGGTGC C[C/T]AGCCCAG ACCCCTGCCCTGG CAAGGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	1.6E-235	5
4105	cg43330158	1507	ACCTGAGCCACC CTCAGCAGGAG CT[G/gap]GGTG GCCCTGAGCTC CAACGGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	
4106	cg43957219	3538	GAGAGGAACATT CCATTATTGTGA [G/T]TGGATTTC TCTGGAGGGCAT GTAC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00345 HSP1-A - HOMO SAPIENS (HUMAN), 452 aa.	4.3E-235	X

4107	cg43955823	317	CTTATCTGTTCA AATATACCTGGA A[G/A]GGAATAC ACAGAGGGTTCA GCAGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05048 CLEAVAGE STIMULATION FACTOR, 50 KD SUBUNIT (CSTF 50 KD SUBUNIT) (CF-1 50 KD SUBUNIT) - Homo sapiens (Human), 431 aa.	5.5E-235	20
4108	cg43930174	1732	GTGGCAGGACT CGTGGGCCCTCT CC[G/A]GCCTGTT TCCCCTGCCACT CCAGCC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
4109	cg43930174	275	CCTGTGGACC GTTCTCCTAGC CC[G/T]GTGGTTT GGAACCAAGTGG CTTTGGG	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
4110	cg43948360	432	GCAAGGCAGCG GAGGGCAGTG GGG[C/gap]CCCA GCATCCCCTGAA GCCTCACCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
4111	cg43948360	435	AGGCAGCGGAG GGGCAGTGGGG CCC[C/gap]AGCA TCCCCTGAAGCC TCACCTGCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
4112	cg43962127	205	TCAGATCAGCAG ACCGAGTCGAA T[G/C]TGATTCTT CAAAGCAAGTAT TGCCT	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4113	cg43962127	253	CTTTACCCCTTGT CCTGAATGCAGT C[C/T]GTCATATG ACCACTAACTTG CATGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7

4114	cg43962127	270	ATGCAGTCCGTC ATATGACCACTA A[C/T]TTGCATGT GACCAAAATGTTT GCAGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4115	cg43962127	317	CAGAGTGTTTT TAGATATGCTCT C[G/A]GTGAGCC GTCATCCGTCAA TCCAAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4116	cg43962127	97	GTCTTATTTCCA GTAAATATTCA[C/A]ATAATGTCA AAAGAATGAAAT GATA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4117	cg43952917	525	TCTTACTTTGGC AAGAGAAACAG A[G/A]GTATTTT GCTCCTCTTCTA CCCAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q99611 SELENIDE; WATER KINASE 2 (EC 2.7.9.3) (SELENIUM DONOR PROTEIN 2) - Homo sapiens (Human), 448 aa.	1.5E-232	
4118	cg43940463	220	AAGAACCACTCC TAGCCTCCGCAG G[G/gap]CTCTTT TGGGAACCCCTC CCTGCTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.1E-232	
4119	cg43966506	2018	TCACCATGTTGG CCAGGCTGGTCT C[G/A]AACTCCTA ACCTCAGGCGAT CCACC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92966 SNRNA ACTIVATING PROTEIN COMPLEX 50KD SUBUNIT - HOMO SAPIENS (HUMAN), 411 aa.	8.3E-232	9
4120	cg43966506	2914	AGGTCTAGACCA TCAGATAGATTT A[C/T]TCAAATAT TTTCTGGGAACC TTTAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92966 SNRNA ACTIVATING PROTEIN COMPLEX 50KD SUBUNIT - HOMO SAPIENS (HUMAN), 411 aa.	8.3E-232	9

4121	cg43983092	127	TAGCTAATTATTT ACAAACTCATTTT T/gap]AAAGACTA GAATTTTAAATC GAAGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29607 HYPOTHETICAL 53.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 448 aa.	1.7E-231	1
4122	cg43983092	922	TCCTGGTTTCCT TTTTGGCCCCG C[C/gap]ACAGAA AAGATGGATGTA GTAAGAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29607 HYPOTHETICAL 53.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 448 aa.	1.7E-231	1
4123	cg43947107	420	GACCAAGCAGA GACTAGGCCTCA GG[C/gap]TAGCC CAGCAGGGCTTC CTGTGTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75528 ADA3-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 432 aa.	2.8E-231	3
4124	cg43948144	1510	TAATATGTTTATT AGTTCTCTTTGG[A/gap]AAAAAACT ACCACTGTGGTC TTAAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
4125	cg43948144	1541	ACTACCACTGTG GTCCTTAAAGGG A[G/A]CAAAATAT ACCATAGGCTAA AACTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
4126	cg42676981	426	CCGAGACAGGT GTGCATGGTGG GTG[C/gap]CCCC TGCTGATGGTGT GAGGTCAGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15
4127	cg42676981	544	CTGCTGGAGCGT GCCAGAGTCCG GA[G/gap]GCCTC ACTCCAGGTCGG CCTCCACC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15

4128	cg42676981	545	TGCTGGAGCGT GCCAGAGTCCG GAG[G/gap]CCTC ACTCCAGGTCGG CCTCCACCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15
4129	cg43968343	1175	TACATTGAGGAA AGTGAGATTCAC A[gap/G]CACAAA TACCAAGATGAC CAATGAA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4130	cg43968343	1420	CAGAGGGGACT CTCCGTACCCCT TC[A/G]GGAGGG TTTTGGGCAATA AAGCCAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4131	cg43968343	1453	TTTGGGCAATA AGCCAAAATCTG T[A/G]CTTAAATA GGTGTGTCTCAT AAGAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4132	cg43968343	1488	GTGTGTCTCATA AGACAAATTTTAA [A/G]CTCATTAT TAAAGGTCCTGA TGGA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4133	cg43968343	1508	TTTAACTCATT ATTAAAGGTCCT[G/A]ATGGACATT CCAAACTAGTAA CTTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)

4134	cg43968343	1750	TGCCTAACGCCA CGGGTCCACC GGTTCJGGGGT CACAGCTGCTGG CTGGTGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4135	cg43968343	546	GGAGGAAAGAG AAAGTGATCTTT ACTTAAJTTTTTTC ATGGAACCCACCG GGGAT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4136	cg43968343	547	GAGGAAAGAGAA AGTGATCTTTAC TTTAAJTTTTTTCAT GGAACCCACCGG GGATC	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4137	cg43968343	548	AGGAAAGAGAAA GTGATCTTTACT TTTAAJTTTTTTCAT GGAACCCACCGG GGATCT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4138	cg43968343	551	AAAGAGAAAGTG ATCTTTACTTTTT TTTCTTCATGGAA CCACCGGGGAT CTTTT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4139	cg43968343	705	AAATGGCATTAA AAATATCTACAG GTAACJAGGACTA CCACGAAATACA ATATT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)

4140	cg43968343	801	CACATGTCCCAT TGTATCACTATA C[A/T]TTTTTATAA TAAAAAATCGTA AATT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4141	cg43987280	142	CTTGACATGCAC ACATATATGGAT C[A/C]AAAAAGTAT GTACAACTAGAA AAACG	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4142	cg43987280	144	TGACATGCACAC ATATATGGATCA A[A/C]AAGTATGT ACAACTAGAAAA ACGGA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4143	cg43987280	176	GTACAACTAGAA AAACGGACTCCA A[G/C]CAAAAATG GAAAACATGTTT CCAATG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4144	cg43274910	1083	GAGGTCACATGT AGCTGAGTGTGA A[A/gap]CCAAGA AAAATACGAAGC TTCAAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4145	cg43274910	1125	GCTTCAAAAAGTA CTGTGCGTTGTA T[T/C]TCTTCATT CTCTGGCAGGCT GGGAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4146	cg43274910	393	CACCTAGAAGAA TGCCTGGAACAC A[T/C]TAACCTTC ATTACTAATGTTT TTGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	

4147	cg43274910	581	TCCATACACTCC CTCCACTGAGAA A[G/A]AGACAAAT GGCTTAGGCTAC AAGGT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4148	cg43918854	1838	CTGGCCAAGTCT GGCCAGCCTGG CC[C/gap]TGCAG GTCTCCCATGAA GGCCACCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22
4149	cg43918854	1990	GCAAGAAAGCCT CCTCAGCCCGG GG[G/gap]CTATG GCCCTGACCCCA GCTCTCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22
4150	cg43918854	2000	TCCTCAGCCCGG GGGCTATGGCC CT[gap/T]GACCC CAGCTCTCCACT CTGCTGTT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22
4151	cg43918854	2039	CACCTCTGCTGT AGAGTGGCAGCT C[C/T]GAGCTGG TTGTGGCACAGT AGCTGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22
4152	cg43918854	2062	CCGAGCTGGTGT TGGCACAGTAGC T[gap/T]GGGGAG ACCTCAGCAGG GCTGCTCA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22
4153	cg43918854	2067	CTGGTGTGGCA CAGTAGCTGGG GA[gap/T]GACCT CAGCAGGGCTG CTCAGTGCC	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22

4154	cg43969669	1576	GCTGTTGCTGTT GCTGTTGCTGTT G[G/gap]GCATCT TGCTGCTAATCC TGAGGCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4155	cg43969669	1577	CTGTTGCTGTTG CTGTTGCTGTTG G[G/gap]CATCTT GCTGCTAATCCT GAGGCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4156	cg43969669	1614	TAATCCTGAGGC TGGTAGCAGAT G[C/gap]ACATTG GAAGCTCCCACC CCATATT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4157	cg42896238	1684	TGCTTCAGCAA CCGGACCAGGA GG[G/gap]CCAGG GCCGGATGTGG GGACCCCTCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75800 BLU PROTEIN - HOMO SAPIENS (HUMAN), 440 aa.	1.4E-227	3
4158	cg43978295	248	TATCTTACCGCA ACAGCAAAGAGG A[G/gap]GCTCAG CCTTCCCCAGTT CCCTGAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4159	cg43978295	255	CCGCAACACCAA AGAGGAGGCTC AG[C/gap]CTTCC CCAGTTCCCTGA GTTACACAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4160	cg43978295	256	CGCAACACCAA GAGGAGGCTCA GC[C/gap]JTCCC CAGTTCCCTGAG TTCACATT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6

4161	cg43978295	342	CAGGACCAATCA ATGTCCCGGA GG[G/gap]CAGAG AGGGTGGTGGG GCCACACTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4162	cg43978295	395	CCATATGGAAAG ACAGTATTCTCA G[A/T]TGAGGGC AGGACTTTTTTG TGGGAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4163	cg43978295	87	CCTTTTTTTTT TTTTTTTTTTTTT AJTAAATATTCAT TATCCTTCATTAA A	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4164	cg43978295	89	TTTTTTTTTTTTT TTTTTTTTTTTTT TTAATATTCATTA TCCTTCATTAAAA A	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4165	cg42913861	1886	ACCGTGACCCC GTTCCCGCGGG GG[G/gap]CTGGA AGAAGCCACCCC GGGACTGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4166	cg42913861	448	TGCTGCTATAAA AATAACTTTTTT [gap/T]CAAAATGG CAGTTTCTGACT AATCAT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4167	cg42913861	680	GCGCTCGGCCA AGGGCAACTTCT GG[A/G]CACACG CAGATCGGCAAG TGCTATG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)

4168	cg42913861	778	GGCGGGCAGGT GAGTGGGCAGG GGC[<i>gap</i> /C]ACGT CCACGGCCAGC CCTGATGGCT	<i>gap</i>	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4169	cg42913861	802	GCACGTCCACG GCCAGCCCTGAT GG[C/T]TGGCC CACATGGGCAAC TTCTGCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4170	cg42913861	933	CCATCCTCAGCA GTTCAAGAATGC C[T/A]CCTCCCG CCATTTCCTCCT GCGGT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4171	cg44932825	112	CATGCCTGGAG GTTAGTCTGGGG GGT[C]CGGCGG GATGGACACACA GACAGAC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43463 SU(VAR)3-9 HOMOLOG - HOMO SAPIENS (HUMAN), 412 aa.	9.8E-227	X
4172	cg43971224	248	ACCCCATAGACA CAGGCAGCATTA A[G/C]TCATAATT TTTAAATTAACTG TCAC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15907 CMP-N-ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,6- SIALYLTRANSFERASE (EC 2.4.99.1) (BETA-GALACTOSIDE ALPHA-2,6- SIALYLTRANSFERASE) (ALPHA 2,6- ST) (SIALYLTRANSFERASE 1) (B-CELL ANTIGEN CD75) (ST6GAL) - Homo sapiens (Human), 406 aa.	1.5E-225	3 (3q21)
4173	cg43918561	2555	CTAGACGCAGCC CGCAGGCAGCC CC[C/A]CACCCG CCGCCTCCTGCA CCGAGAG	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224	11 (11p15.5)

4174	cg43952397	2935	TGGTCITTCAGT CAACGTGCTAGA ATT/ACCGATGAC TTATTAATCTCTA ATT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4175	cg43952397	6176	CAAGAAGGCTG GGGCTGGCCCT GGG[G/gap]CTCA TCATGATGCTTT CCTGGATCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4176	cg43952397	7497	ATTCAAAGGGAC GCCAGCCATCCT T[G/A]GTGACAG GGGCCCAACTT AGCATC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4177	cg43986954	672	AATCATTTATTGT TCCTTACAGTGA T/C]GATGGAAGA ATGTACAGGTGT CCCC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC68871 METHYL-CPG BINDING PROTEIN MBD2 - HOMO SAPIENS (HUMAN), 411 aa.	9.4E-224	18
4178	cg43984330	86	AAAGAAACGGCC TTGTCCCCAAAG G[G/gap]TCTCCT CTTGAAGGAATG GGGGCAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P32121 BETA-ARRESTIN 2 - Homo sapiens (Human), 409 aa.	8.5E-223	17
4179	cg44916523	98	CCACCCTGCTTG GCCCAGGCTATG C[C/gap]TAGAAG CAAGTCAAAGGC AGGTAGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	
4180	cg44916523	12	TTTTTTTTTTT[A T]ATTTATTTTAC ATGAAAATCTTC C	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	
4181	cg44916523	13	TTTTTTTTTTT[A T]TTTTATTTTAC ATGAAAATCTTC CA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	

4182	cg44032871	202	CAGCTTCCTGAG GAGGGGCCGGC CC[T/gap]CTCCT CTTGCCCTGTT GAAGCTTG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4183	cg44032871	253	GCACAGGCTGG GGAGGCTGGCA CTG[C/gap]CAAC GCCATCCCTCCA TGTTGGGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4184	cg44032871	254	CACAGGCTGGG GAGGCTGGCAC TGC[C/gap]AACG CCATCCCTCCAT GTTGGGCAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4185	cg43960557	159	GCAACACTGCTT TATTAGGCCGGG C[C/gap]AGCCAG GAGCAGACACAC GGCTCCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
4186	cg43960557	174	TAGCCCGGCC AGCCAGGAGCA GAC[A/G]CACGG CTCCTCAGTACA CATTCCCC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
4187	cg43960557	2015	GTCGCGGATGG GCTGCAAGAGGT GG[G/gap]CGAAG CGCGCCTCCAC GTCCTCCAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22

4188	cg42500526	489	CGCTCTCTAGAG C CCAGGCACGAC CA[CA]TTGCTGA TTGGGGACAGG CTGTGCT	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99434 NEUROBLASTOMA - HOMO SAPIENS (HUMAN), 421 aa.	3E-220	1
4189	cg43313101	205	CTTTGCTTATTTT AAGTATTTTTTTTg ap/TJGCCTCCTGT ACAAAATACATA AAAG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62831 NEUROGLYCAN C PRECURSOR - RATTUS NORVEGICUS (RAT), 544 aa.	1.1E-219	3
4190	cg43994920	182	CAAGTGTCCAGG A CGACGTGGAAC CC[A/G]GGTGTC TTTTATGAATAAT CAAAAG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15394 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-219	3
4191	cg43041368	56	ATGAGAAAAGTA T CTTTATTCGTGC A[T/C]AATTTTTC AGTTCCATTCAA AATTA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15504 CG1 - HOMO SAPIENS (HUMAN), 423 aa.	1.6E-219	7
4192	cg43934903	181	TTGAGGAACCTA gap CGCCTGAACCT T[ap/A]AAAAAAA AATCTCTAAAGA CCTTAC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4193	cg43934903	190	CTACGGCCTGAA gap CCTTAAAAAAA A[ap/A]TCTCTAA AGACCTTACAGT CTGCTG	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4194	cg43934903	398	AAACTATTAGA A CCATATATTCTAT [A/G]TTTTTAAAG TGAATTATGCAT AAAA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1

4195	cg43934903	464	ACATGATTGCAG TAACATTCTCAA G[ap/A]AAAAAA AAACCCCTAGTAT ACTTTAG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4196	cg42891496	235	AAAGGCTGGCTC CCCTGGCCGAG GC[C/gap]TGGGA CTGATGCAAGAC AGCCAGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00224 HYPOTHETICAL 46.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 409 aa.	1.3E-217	8
4197	cg43994694	985	TACCTCAGGCCC TGCGGGTGCGT CT[G/A]GAGTTCC AAGGCATTTGGG GAACCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92554 MYELOBLAST KIAA0265 - HOMO SAPIENS (HUMAN), 401 aa (fragment).	2.1E-217	7
4198	cg43994694	1226	ACATCTGTAAGA CCACAAAAAAA A[A/gap]TGGGT TTACAGAAATACG AAGACCA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92554 MYELOBLAST KIAA0265 - HOMO SAPIENS (HUMAN), 401 aa (fragment).	2.1E-217	7
4199	cg43261326	495	ACAGAAAAATTT AAAGTGAATGTG ATT[C]GTTGGAGA GAGTGGGAAGG AAAAGT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99984 MRNA EXPRESSED IN OSTEOBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 413 aa.	3.3E-217	1
4200	cg43917040	240	CTCATTTATACAT TCCATGCCGTC [G/gap]GTTAAAA CTCTGCCTTTGAA TCGATG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16
4201	cg43917040	241	TCATTTATACATT CCATGCCGTCAG [G/gap]TTAAACT CTGCTTTGAATC GATGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16

4202	cg43917040	660	GCCTTCCAACCT GCCTCCCGGAG GG[G/gap]CTTTC AGCTGGAGACC CCATTGGAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16
4203	cg43959148	375	GACATCCTTCCA GATGGTTCCTG C[C/T]CCTAGGC CAACCTCCACAG TCATGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75955 FLOTILLIN-1 - HOMO SAPIENS (HUMAN), 427 aa.	1.4E-215	6
4204	cg43917498	199	GGCTCCAAGCAC GCCATATGAAGC A[C/T]GCCAATGT CACTTATGTGCC CTGAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4205	cg43917498	446	TCACTGTGAATA TCCTTTAGATTTC [G/A]TCTTGTTAA CTCAGTTTTTCAG TCAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4206	cg43917498	581	CAATGTAAAGAG AGCTCGAGTGTG G[gap/G]CCAAGG CATCGGACCTTA CACCTAA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4207	cg43917498	61	TATAATCTTTATT CTATAATTCTCC[A/G]CCAGTGCTA GAATTTTCTTCC CAAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4208	cg43917498	676	TTTCTTGTCTAAC AGTCTTTAAGGG[C/G]ACATAAGAA ACTCACGTTAA TTAT	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	

4209	cg43917498	703	CATAAGAACTC ACGTTAAATTATA TT/CjCCTGACATA TTATTATTCATG AAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4210	cg43941592	1434	CGCCCTCCTCAC CGCCCTTCCTCG G[G/C]AGTCACCT CCACTGGTGGAC CACGG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07988 PULMONARY SURFACTANT- ASSOCIATED PROTEIN B PRECURSOR (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(PHE)) (18 KD PULMONARY- SURFACTANT PROTEIN) - Homo sapiens (Human), 381 aa.	2.1E-215	2 (2p12)
4211	cg43941592	2088	CCTGTGTAATAC AATGTCTGCACC A[A/G]TGCTAATA AAGTCCTATTCT CTTTT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07988 PULMONARY SURFACTANT- ASSOCIATED PROTEIN B PRECURSOR (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(PHE)) (18 KD PULMONARY- SURFACTANT PROTEIN) - Homo sapiens (Human), 381 aa.	2.1E-215	2 (2p12)
4212	cg44006797	1111	CTGCTCTGCCCA TTTCCATTGGG G[gap/G]CCCCACA GGCAGGGTCT GTGCTATC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4213	cg44006797	227	CGGCTTCCTCAC AAAGGAGGCAG GG[C/gap]CCCAT CACAGGGTGTCC CACCCCTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	

4214	cg44006797	230	CTTCCTCACAAA GGAGGCAGGGC CC[C/gap]ATCAC AGGGTGTCACAC CCCTGAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4215	cg44006797	247	CAGGGCCCCAT CACAGGGGTGTC CA[C/gap]CCCTG AAAGGCTCTCCC AGCCTGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4216	cg44006797	253	CCCATCACAGGG TGTCACACCCCT G[A/G]AAGGCTC TCCAGCCTGGA AGAGCC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4217	cg44006797	296	GAAGAGCCAGAA CAAAGTGCAATTG G[A/G]CCCACTC CCACCCTCTCTG AGCTGC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4218	cg43955639	1535	TTAGGACCTGAA CAGGGGTCCTG CC[A/G]GGCTGG GGACCCTCTCTG GAAACCT CATTAGTGAAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.8E-215	
4219	cg43950766	390	CTGCATTTCATG G[G/gap]GGGG GGGGGTACAC AGTATTITA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.3E-214	22

4220	cg43950766	392	TTTAGTGAACCT GCATTTTCATGGG G[G/gap]GGGG GGGGTACACAGT ATTTTAAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD4491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.3E-214	22
4221	cg43947481	2202	ATCTTGCCATCC TCCCTTCTGGT T[C/G]TCTGCACC CACCTGTCCAC TGCAG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43978 CHROMATIN-SPECIFIC TRANSCRIPTION ELONGATION FACTOR FACT 140 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 1047 aa.	8.6E-214	14
4222	cg43935715	913	GAATGTTGCCCT CCATTCTAAGGA A[T/A]GCAAAACA AATCTAAATGAT CTTCT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION- RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8
4223	cg43935715	1088	TGCTGTAAAGC CAGGAGATTTTG T[T/C]GCCTGCTT TTGCTGCACATT AAGAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION- RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8
4224	cg43935715	823	CCTTACATCGAG TAACCCCAATTC C[G/A]CCCCCAC CCCAGTGCTCCT ACTCCG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION- RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8

4225	cg44914050	2439	GTCACACAGCTA ATGAGTTCTAAA C[G/A]GGGAAC GGACTCAGGCTT GTCTGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4226	cg44914050	55	TTTTTTTTTTTT TTTTTTTTTTTTTT CJTITTTTCCAGG CCACTTTTATTTA A	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4227	cg44914050	56	TTTTTTTTTTTT TTTTTTTTTTTTTT CJTITTTTCCAGG CACTTTTATTTA A	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4228	cg43948829	117	CTCTCAAGAGAA AGAAAGAGTTACT A[C/T]TGCAGGAA CAGACATTTTTT AAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4229	cg43948829	192	ACAGAAAACATT GTATTACACATA A[T/C]AATGTGGG GCTCTGTCTCTG CCGAC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4230	cg43948829	219	ATGTGGGCTCT GTCTCTGCCGAC A[G/gap]GGGCTG GGTTCGGGCATT AGCTGTG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4231	cg43948829	222	TGGGGCTCTGTC TCTGCCGACAGG G[G/gap]CTGGGT TCGGGCATTAGC TGTGCCG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2

4232	cg43948829	359	ACACGAGTCACC TCCAAAGAGCTG C[G/A]ACTGTTTG AGAATCTGCCAA GAGGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4233	cg43920203	55	TTATTGGCCAC AGAAGGATGA GG[A/G]CGCGTG AAGGGCTAGG GATAAGAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75065 KIAA0477 PROTEIN - HOMO SAPIENS (HUMAN), 1132 aa.	3.2E-213	1
4234	cg43920203	57	ATTGGCCACAG AAGGGATGAGG AC[G/A]CGTGAA GGGGCTAGGGA TAAGAATG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75065 KIAA0477 PROTEIN - HOMO SAPIENS (HUMAN), 1132 aa.	3.2E-213	1
4235	cg43062448	124	TTAACAGTGTA GAAGGAAAATCT C[A/C]GAAAAAGC AGATAGACAATG TAGAA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)
4236	cg43062448	239	ACATGTGGAAC TAAGTACACCAT TT[C]TAAGAAAG ACCAATTTCTAAT GCAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)
4237	cg43062448	261	ATTTAAGAAAG ACCAATTTCTAAT [G/C]CAAAATTTTC TGAGGTTTTCAG ATTT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)
4238	cg43062448	262	TTTTAAGAAAGA CCAATTTCTAAT G[C/G]AAATTTTC TGAGGTTTTCAG ATTT	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)

4239	cg43985159	1351	AAGGCATGATAG TGCAAGAGGTAA GTTCTTTTGATT TATAGAACATTTA TAGA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15018 ORF - HOMO SAPIENS (HUMAN), 419 aa (fragment).	1.3E-212	10
4240	cg43950854	424	ATAGGCAAAATTC AGAGGTGATTTTC A[CT]CATTTC AATTATCATCAA GAGTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O14524 HYPOTHETICAL PROTEIN KIAA0286 (HSA6800) - Homo sapiens (Human), 429 aa (fragment).	2.6E-212	
4241	cg43969195	1616	CAAGTTTGTGTA TCAGAGCGGGA GT[G/T]CGGGG AGGAAAGAAAA CAAAACAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HSA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
4242	cg43969195	289	CGGTGCGCCGG ACCCACGCCGG AGG[gap/C]CGAG CTACAGGCCCTG GCGCGGGAC	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HSA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
4243	cg43989944	1878	CCGCACTCACCT GGGGGTTGGG CA[G/A]TGCCGC GCTGTGCTGCCT GTCTTCG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4244	cg43999944	2096	GGTGGTGCAG CCAGCGTGGG GAA[A/C]GGGCA GGCAGCCTCCC GCTGCCAGT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4245	cg43989944	2849	TCTGGGTCTGTG TAGCTGGGGAG AG[A/G]ATGAGG CTGCAGAGATGG GGACCAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16

4246	cg43999944	3086	CTCCCACAAATTT ATCCCATGAGCA A[G/T]AACCACTT TATAGCTGGCAT ATATT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4247	cg43984681	1347	TGCGACACTCC CAAAGCCGTAAG G[G/gap]CCGACC CAGGCATCTTGG CCCCCAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.3E-210	19 (19q13)
4248	cg43049444	168	ATCACGTAGGCC AGGAGCCTCAG CG[G/C]TGCCCC TTCAGGCTCATC TGCCAAG	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4249	cg43049444	294	GCCCTTCCCACC TGTTGGTGACA A[A/gap]TCACAA GGTGGTAGAAGT TGCCAGG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4250	cg43049444	305	CTGGTTGGTGAC AAATCACAAAGGT G[G/gap]TAGAAG TTGCCAGGGACA GATAACA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4251	cg44013820	17	TTTTTTTTTTTT TTT[A/T]AAGAAG GTAGATAAAATTT ATTGCCA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4252	cg44013820	18	TTTTTTTTTTTT TTTA[A/T]AGAAG GTAGATAAAATTT ATTGCCAC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1

4253	cg44013820	19	TTTTTTTTTTTT TTTAA[AT]GAAG GTAGATAAATTT ATTGCCACT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4254	cg44013820	955	TTAAATATATCTA TTTAGTTTTTTTT /CJTTCCTTACC CTGAGATATTTA TTA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4255	cg43934675	455	CAGTCTCTGCAG GTACCAGATTCC C[C/T]GTTGTATC CAACTGCATACA TTTAC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75216 WUGSC:H_DJ1159O04.1 PROTEIN - HOMO SAPIENS (HUMAN), 379 aa.	1.1E-208	
4256	cg43932174	188	AAGCGCTGCAAA ATCCCTGGCGGT G[C/gap]CCGCAA TCTAACGCTCTAC AATAACC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4257	cg43932174	190	GCGCTGCAAAAT CCCTGGCGGTG CC[C/gap]GCAAT CTAACGCTCTACA ATAACCTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4258	cg43932174	288	AGACGGCAAGTC GCCGGGACGC CT[G/gap]GGGCT CTCAGCTGCTGA ACAATGAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4259	cg43932174	291	CGGCAAGTCGC CGCGGACGCCT GGG[G/gap]CTCT CAGCTGCTGAAC AATGACATC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20

4260	cg43932174	82	TTTTTTTTTTTT TTTTTTTTTTTT TTGCAATCTGCA AAAGACTTTATTA CA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4261	cg43995867	1354	TTGTTGTTTCTAA ATCTATATGAGA A/TTGGACAATAA GTATTTTATTAT AA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4262	cg43995867	1361	TTCTAAATCTATA TGAGAAATTGACA A/gap]TAAGTATT TTTATTATAACTC AGCC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4263	cg43995867	1364	TAAATCTATATGA GAATTGACAATA A/gap]GTATTTT ATTATAACTCAG CCCAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4264	cg43995867	1372	TATGAGAAATTGA CAATAAGTATTTT T/gap]ATTATAAC TCAGCCCCATACA TATAT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4265	cg43995867	1379	ATTGACAATAAG TATTTTATTATA A/gap]CTCAGCCC ATACATATATACT ATGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4266	cg43995867	1387	TAAGTATTTTAT TATAACTCAGCC C/gap]ATACATAT ATACTATGTATG CAGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)

4267	cg43995867	53	CTCGTGCCGTTA CGGCCATCAGG GC[G/C]GCCGCA GTGGCGTCCTG GAGCCCTC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4268	cg43293087	1916	GAATGGAGAAG GGTAATAGGTTG GT[gap/T]GCAGT GAATGGGCTGG GGGTGGGGT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21128 PLACENTAL PROTEIN 11 PRECURSOR (EC 3.4.21.-) (PP11) - Homo sapiens (Human), 369 aa.	2.3E-206	12
4269	cg43293087	2234	TAACCTCAATTAT GCATTTGTCCCC[C/gap]AACCCAC TGAGAACTAAAT GCTGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21128 PLACENTAL PROTEIN 11 PRECURSOR (EC 3.4.21.-) (PP11) - Homo sapiens (Human), 369 aa.	2.3E-206	12
4270	cg43916807	313	AGGCCAGGCTG CAGGGCGGGC AGA[C/gap]CCTG GGCCCCGGGTC TACGCTTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4271	cg43916807	315	GCCAGGCTGCA GGGGCGGCAG ACC[C/gap]TGGG CCCCGGGTCTAC GCTTTCTGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4272	cg43916807	551	AAGATCTCCACT TCGGTCTGCCAT T[gap/A]AAAAAAA AAAAAAATCTTTC TCTTC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4273	cg43916807	552	AAGATCTCCACT TCGGTCTGCCAT T[A/gap]AAAAAAA AAAAAATCTTCT CTTCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10

4274	cg43916807	565	CGGTCTGCCATT AAAAA A[<i>gap</i>]TCTTTCT CTTCTTTCTCTT TAAAG	A	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4275	cg43916807	565	GGTCTGCCATTA AAAAA A[<i>gap</i>]TCTTTCT CTTCTTTCTCTT TAAAG	<i>gap</i>	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4276	cg43916807	805	GGGTGCAGCA GGCATGACACCA AG[G/ <i>gap</i>]CAGAG CCCGCAGCAGG GGCCCCGGG	G	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4277	cg43948416	1041	ATTGTCCATCCC ATGAGGCAGGG CT[G/ <i>gap</i>]GGCCA TGCCAAGACAAT CTCAAGGA	G	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4278	cg43948416	454	CCTTCCTGCCCT TGGAATGGCGT G[C/ <i>gap</i>]CTGGGC AATAGGACAGG CCACAGT	C	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4279	cg43948416	455	CTTCCTGCCCT GGAAATGGCGT GC[C/ <i>gap</i>]TGGGC AATAGGACAGG CCACAGTG	C	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4280	cg43948416	758	CGCAGGAGGCC CCTGGAGCAGC CTG[G/ <i>gap</i>]CCTC AGCCAGGGCA GGTGCCCCAGA	G	<i>gap</i>				SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11

4281	cg43920385	1326	AATGGAGAAAGA AAGCCATTTTTC C/A/G]TAAAAAGG GATGGTTCATCA TTGTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4282	cg43920365	1468	ATCTAGACAGCC TAAATCTGATTT [A/G]GTCCTTATA AAAATAATATCTT GTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4283	cg43920365	2051	TCTTATGGAAT CTCTGTTATTAA G/A/C]TATTTCAA GATGAGACAACA CTGAA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4284	cg43920365	2188	AAGATGGGAACC TTATTTGAATGT G[T/gap]TTTTTTT TTTCCATGATGT CCAATT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4285	cg43920365	2198	CCTTATTTGAAT GTGTTTTTTTTT [T/gap]CCATGAT GTCCAATTTTGT TGTGGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3

4286	cg43920365	2198	CTTATTGGAATGT GTTTTTTTTTTT[g ap/TCCATGATGT CCAATTTTGTG TGGG	gap	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4287	cg43920365	2198	CTTATTGGAATGT GTTTTTTTTTTT[g ap/TCCATGATGT CCAATTTTGTG TGGG	gap	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4288	cg43958860	1311	CTAATGTGATCA TATGAGGACCTT T[gap/C]ATATCTG TCTTTTATTTAAC AAAA	gap	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P48745 NOV PROTEIN HOMOLOG PRECURSOR (NOVH) - Homo sapiens (Human), 357 aa.	6E-206	8 (8q24.1)
4289	cg44002669	333	GAGAGGCCAGG GAGGGCTGGC GGG[C/gap]CCCC CAGGCTGGGCC GAGCAGCGCA	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	
4290	cg44002669	338	GCCAGGGAGGG CTGGCGGGCC CCC[C/gap]AGGC TGGGCCGAGCA GCGCAAGTAG	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	
4291	cg44002669	348	GCTGGCGGGC CCCCCAGGCTG GGC[C/gap]GAGC AGCGCAAGTAGA GGAAGTCAG	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	

4292	cg43278557	1618	AGGCAGACCCCTC CCAGAGGCCCG CC[C/gap]AGGTG GGCATGGTCCC CCATTTTCT	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43581 SYNAPTOTAGMIN VII - HOMO SAPIENS (HUMAN), 418 aa (fragment).	1E-204	
4293	cg43948656	39	TTTTCTTTTTT TTTTTTTTTTTTT A]TTTGAAGAAT CAGAAATTTATTC A	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB41267 HYPOTHETICAL 66.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 609 aa.	1.1E-204	X
4294	cg43302693	106	ATTCCAGCCACA CCCAGGCCGTG GG[C/gap]AGCCA CCCTCCGAGACA CCTGGGCC	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4295	cg43302693	137	CCCTCCGAGACA CCTGGGCCGG GG[C/gap]AGGT CTCAGCAGAAGC GCCGTGGG	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4296	cg43302693	163	AGGGTCTCAGCA GAAGCGCCGTG GG[C/gap]AGCCA CCATCCGAGGCA CTTGGTGG	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4297	cg43302693	294	TCCTTTCTCAGA GAACTGGGCATA G[C/gap]CAGAGC TGGGGTGAGAA GCCCTTC	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16

4298	cg43302693	295	CCTTTCTCAGAG AACTGGGCATAG C[C/gap]AGAGCT GGGGTGAGAAA GCCCTTCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4299	cg43302693	344	CAGCCCTGCTGC ACCGAGGCTCTG C[C/gap]AGTTCT CATACCCCTCC CCATCCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4300	cg43302693	485	CTGCCCCACAGC AAGCTGCCCCATG G[G/gap]CCCGGG GTCAAGCCACCA CCCACAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4301	cg43302693	535	TGTCCAGGAGT CCGGCCAGCCC AC[C/T]ACATCCG CTCCCTAGCTCC GGCGAG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4302	cg44000884	706	TGGAAGCTGGGT TAGTTCATGCTA G[G/A]TGGCTGT AGCACTGACCTC ATGTAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43567 RING ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 381 aa.	4.8E-204	3
4303	cg44000884	939	TCAAAAGTCCTG TTTCAGTAATTG [A/C]TTAAACTGT AGAATACTAAAA AATA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43567 RING ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 381 aa.	4.8E-204	3

4304	cg43950996	1036	TGTAATTCCAAG AGGAGGGTGGG GA[G/gap]GCGAG GCCATAGTCTCC GAGTCCCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4305	cg43950996	1044	CAAGAGGAGGG TGGGAGGCGA GGC[C/gap]ATAG TCTCCGAGTCCC AGGACGATG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4306	cg43950996	1060	AGGCGAGGCCA TAGTCTCCGAGT CC[C/A]AGGACG ATGGCTGACAAT ACACCAA	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4307	cg43950996	819	AGGTGAACGCCA GTCCAGAAAGAA G[G/gap]TGCTGG AGCCCCCTGCTCT GTCCTCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4308	cg43950996	861	CTGTCCTCTCCA TCACGGTGCTCC C[C/gap]TAGGGC CTCCCAAGGCCT CCTTGGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4309	cg43950996	866	CTCTCCATCAGG GTGCTCCCCCTAG G[G/gap]CCTCCC CAGGCCTCCTTG GCTCAGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4310	cg43950996	873	TCACGGTGCTCC CCTAGGGCCTCC C[C/A]AGGCCTC CTTGGCTCAGTC CAGGTG	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1

4311	cg43950996	895	CCCCAGGCTC CTTGGCTCAGTC CA[G/A]GTGTCTG CAGGAGGAAGG TGTTGTC	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4312	cg44021565	115	GTTCAATTATTG CTTTAAGAGTTA C/TATACCATGA GACACACAGTTC TGTT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4313	cg44021565	191	CGCAGTGCTCAC GGGAGCAAGT GG[G/A]CAGGGG ACGGTCCAGATC GATGGCC	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4314	cg44021565	220	GGGACGGTCCA GATCGATGGCCA CC[C/A]ACTGAG CCGCTGCTACGT GGCCCCC	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4315	cg43942842	1577	TGCATCTTCAGT TAATGTAACAGG A/T/AJAAAAAGGC AATGGATTTTATT TTAT	T	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49903 SELENIDE, WATER KINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa.	1.9E-203	17
4316	cg43959472	122	TTTTTTTTTTT TTTTTTTTTTTTT GJGGCATCAGAA ATGCTGTTTATT CT	T	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
4317	cg43959472	123	TTTTTTTTTTT TTTTTTTTTTTTG /TJGCATCAGAA TGCTGTTTATTTC TC	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15